

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 19:58:51 : Search time 45.0389 Seconds  
(without alignments)  
15700.357 Million cell updates/sec

Title: US-09-750-240-1

Perfect score: 314

Sequence: 1 atgtcatgttagtgccct.....acacggcgaggacctgaa 314

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_101002.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	313	99.7	314	22	Human partial card
2	313	99.7	2127	19	Human adenylyl cycl
3	295.2	94.0	3549	22	Human cardiac aden
4	295.2	94.0	3552	22	Human cardiac aden
5	295.2	94.0	3582	22	Human modified car
6	295.2	94.0	4942	20	Human type VI aden
7	227.4	72.4	4046	14	Cardiac adenylyl c
8	199.2	63.4	5841	24	Mouse ischaemic co
9	198.2	63.1	4131	21	Type VI adenylyl c

C 10	39.8	12.7	236303	22	AAS11614	Human genomic DNA
C 11	38.2	12.2	3050	22	AS05036	Angiotensin conver
C 12	38.2	12.2	3174	21	AAQ77370	Human OREF ORF2925
C 13	38.2	12.2	3243	15	AAQ79401	Human NMDAR2 recep
C 14	38.2	12.2	3698	15	AAQ79400	Human NMDAR2 recep
C 15	38.2	12.2	4274	15	AAQ79407	Human NMDAR2 recep
C 16	38.2	12.2	4289	15	AAQ79405	Human NMDAR2 recep
C 17	38.2	12.2	4325	15	AAQ79404	Human NMDAR2 recep
C 18	38.2	12.2	4340	15	AAQ79372	Human N-methyl-D-a
C 19	38.2	12.2	4349	15	AAQ79406	Human NMDAR2 recep
C 20	38.2	12.2	4364	15	AAQ79403	Human NMDAR2 recep
C 21	38.2	12.2	160771	24	ABQ88179	Human osteoblast d
C 22	37.6	12.0	4046	14	AAQ42525	Cardiac adenylyl c
C 23	37.2	11.8	668	9	AA080926	Longisporus Typsi
C 24	37.2	11.8	1438	18	AA091179	Human apoptosis pr
C 25	37	11.8	1700	21	AA069681	Novel human protei
C 26	36.8	11.7	5317	23	ABL17087	Drosophila melanog
C 27	36.8	11.7	5538	23	ABL19835	Drosophila melanog
C 28	36.8	11.7	9579	23	ABL17086	Drosophila melanog
C 29	36.8	11.7	9579	23	ABL19834	Drosophila melanog
C 30	36.6	11.7	1734	22	AA010196	Pseudorabies virus
C 31	36.6	11.7	3243	20	AA082910	Human N-methyl-D-a
C 32	36.6	11.7	3243	21	AA095033	Human N-methyl-D-a
C 33	36.6	11.7	3243	21	AA087824	Human clone NMDA22
C 34	36.6	11.7	3243	24	AA047377	Human NMDAR2C codi
C 35	36.6	11.7	3243	24	ABA05910	Human NMDA recepto
C 36	36.6	11.7	3698	20	AA082909	Human N-methyl-D-a
C 37	36.6	11.7	3698	21	AA095032	Human N-methyl-D-a
C 38	36.6	11.7	3698	21	AA087823	Human clone NMDA22
C 39	36.6	11.7	3698	24	AA047376	Human NMDAR2C codi
C 40	36.6	11.7	3698	24	AB091819	Human NMDA recepto
C 41	36.6	11.7	4002	20	AA082915	Human N-methyl-D-a
C 42	36.6	11.7	4002	21	AA095038	Human N-methyl-D-a
C 43	36.6	11.7	4002	21	AA087829	Human NMDAR2 subun
C 44	36.6	11.7	4002	24	AA047382	Human NMDAR2C codi
C 45	36.6	11.7	4002	24	AB091914	Human NMDA2C enco

#### ALIGNMENTS

RESULT 1

AA08561

ID AAD08561 standard; CDNA; 314 BP.

XX AAD08561;

XX AAD08561;

DT 04-SEP-2001 (first entry)

XX Human partial cardiac adenylylase VI (ACVI) isoform #1 cDNA.

XX Human; cardiac; beta-adrenergic signalling protein; beta-ASP;

KW myocardiun; gene therapy; beta-adrenergic receptor; beta-AR;

KW adenylylase; adenylate cyclase; cAMP synthetase;

KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;

KW cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ss.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

Location/Qualifiers

1..312

/\*tag= a

/product= "Human partial cardiac ACVI isoform #1"

/transl\_except= (pos:229..231, aa:Xaa)

/note= "Xaa is an unknown amino acid; CDS does not

include stop codon"

/EC\_number= "4.6.1.1"

WO200148164-A2.

05-JUL-2001.

26-DEC-2000; 2000WO-US35411.

XX 27-DEC-1999; 99US-0472667.  
XX (REGC ) UNIV CALIFORNIA.  
XX Hammond HK, Gao M;  
XX WPI; 2001-418260/44.  
XX P-PSDB; AAE04308.  
XX Novel polynucleotide encoding a modified adenylyl cyclase polypeptide  
XX useful for enhancing cardiac function in mammalian hearts, and for  
XX treating heart disease, especially congestive heart failure -  
XX Example 5; Page 114; 153pp; English.  
XX The present invention relates to methods and compositions for enhancing  
XX cardiac function in mammalian hearts by inserting transgenes encoding  
XX beta-adrenergic signalling proteins (beta-ASP) which increase  
XX beta-adrenergic responsiveness within the myocardium using in vivo  
XX gene therapy. The beta-ASPs of the invention include beta-adrenergic  
XX receptors (beta-AR), adenylyl cyclases (also referred to as adenylyl cyclase,  
XX adenylyl cyclase and G-protein coupled receptor kinase  
XX (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
XX in mammalian hearts and for treating heart disease, especially  
XX congestive heart failure. The present cDNA sequence encodes human  
XX partial cardiac adenylyl cyclase VI (ACVI) isoform which is used for  
XX generating a third beta-ASP transgene, used in the exemplification  
XX of the invention.  
XX Sequence 314 BP; 60 A; 98 C; 108 G; 47 T; 1 other;  
Query Match 99.7%; Score 313; DB 22; Length 314;  
Best Local Similarity 100.0%; Pred. No. 1.7e-69;  
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGTCATGTTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAACACGCTGGGT 60  
Db 1 ATGTCATGTTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAACACGCTGGGT 60  
QY 61 GAACCAATGGCAGAGGTTGCGGGGCGCCGTGCGACTCGGGCAGGTGCTTCTGCAG 120  
Db 61 GAACCAATGGCAGAGGTTGCGGGGCGCCGTGCGACTCGGGCAGGTGCTTCTGCAG 120  
QY 121 CCCGCTATATGAGTGGCTCGGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 180  
Db 121 CCCGCTATATGAGTGGCTCGGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 180  
QY 181 CCTCGTCCCTCGGAGTGCAGCCCTTCAATCCGAGGGGGCGCCAGGAGGCAAG 240  
Db 181 CCTCGTCCCTCGGAGTGCAGCCCTTCAATCCGAGGGGGCGCCAGGAGGCAAG 240  
QY 241 GAACCTGGGCTCGGGAGTGGCCCTTGGCTTCGAGATACCGAAGTACACACACCG 300  
Db 241 GAACCTGGGCTCGGGAGTGGCCCTTGGCTTCGAGATACCGAAGTACACACACCG 300  
QY 301 GCGGGACCGCTGAA 314  
Db 301 GCGGGACCGCTGAA 314  
RESULT 2  
AAV23246  
ID AAV23246 standard; cDNA; 2127 BP.  
XX AAV23246;  
AC AAV23246;  
XX 17-JUL-1998 (first entry)  
XX Human adenylyl cyclase isoform VI encoding cDNA.  
XX Human; adenylyl cyclase VI; AC-VI; beta-adrenergic signalling protein;  
XX transgene; gene therapy; congestive heart failure; cardiac function;  
KW

KW adenovirus; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
XX CDS 1..2127  
XX /\*tag= a  
XX /product= "adenylyl cyclase isoform VI"  
XX /transl\_except= (pos:229..231,aa:Xaa)  
XX /transl\_except= (pos:315..317,aa:Xaa)  
XX /note= "no stop codon given; Xaa = unknown"  
XX misc\_difference 315  
XX /\*tag= b  
XX /note= "n indicates a gap of about 0.5 kb"  
XX WQ9810085-A2.  
XX 12-MAR-1998  
XX 05-SEP-1997; 97WO-US15610.  
XX 16-JUN-1997; 97US-0048933.  
XX 05-SEP-1996; 96US-0708661.  
XX (COLL-) COLLATERAL THERAPEUTICS.  
XX (REGC ) UNIV CALIFORNIA.  
XX Gao M, Hammond HK, Insel PA, Ping P, Post SR;  
XX WPI; 1998-193633/17.  
XX P-PSDB; AAW53345.  
XX Vectors containing transgene(s) encoding beta-adrenergic signalling  
XX proteins - useful for gene therapy of congestive heart failure  
XX Claim 60; Fig 12A; 114pp; English.  
XX The present sequence encodes human adenylyl cyclase isoform VI (AC-VI)  
XX from the present invention. The present invention describes a  
XX recombinant replication-defective viral particle (I) comprising a gene  
XX encoding a beta-adrenergic signalling protein (beta-ASP) operably  
XX linked to a promoter. Also described are: (1) a recombinant pro-viral  
XX plasmid (Ia) comprising a gene encoding a beta-ASP, as above, operably  
XX linked to a promoter and further comprising a replication-defective  
XX viral genome; (2) a (mammalian) cell transfected with (I) or (Ia); (3)  
XX an isolated polynucleotide comprising a sequence encoding a human  
XX adenylyl cyclase isoform VI (AC-VI), or a variant having AC activity;  
XX (4) a human AC-VI encoded by (3); (5) an isolated polynucleotide  
XX sequence which hybridises at high stringency to (3); and (6) a vector  
XX comprising the polynucleotide of (3). (I) can be used to form a  
XX filtered adenovirus particle preparation. (I) is used to enhance  
XX cardiac function in mammals.  
XX Sequence 2127 BP; 421 A; 637 C; 615 G; 452 T; 2 other;  
Query Match 99.7%; Score 313; DB 19; Length 2127;  
Best Local Similarity 100.0%; Pred. No. 2.2e-69;  
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGTCATGTTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAACACGCTGGGT 60  
Db 1 ATGTCATGTTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAACACGCTGGGT 60  
QY 61 GAACCAATGGCAGAGGTTGCGGGGCGCCGTGCGACTCGGGCAGGTGCTTCTGCAG 120  
Db 61 GAACCAATGGCAGAGGTTGCGGGGCGCCGTGCGACTCGGGCAGGTGCTTCTGCAG 120  
QY 121 CCCGCTATATGAGTGGCTCGGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 180  
Db 121 CCCGCTATATGAGTGGCTCGGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 180  
QY 181 CCTCGTCCCTCGGAGTGCAGCCCTTCAATCCGAGGGGGCGCCAGGAGGCAAG 240  
Db 181 CCTCGTCCCTCGGAGTGCAGCCCTTCAATCCGAGGGGGCGCCAGGAGGCAAG 240

Db 181 CCTCGTCCCTGGCAGGATGACGCTTCATCCGGAGGGCGGCCCAAGCAAG 240  
QY 241 GAACTGGGGCTGGCGCAGTGGCCCTGGGCTTCGAAGATACCAAGTGAACGACACCG 300  
Db 241 GAACTGGGGCTGGCGCAGTGGCCCTGGGCTTCGAAGATACCAAGTGAACGACACCG 300  
QY 301 GCGGGACCGCTGAA 314  
Db 301 GCGGGACCGCTGAA 314

RESULT 3  
AAD08563  
ID AAD08563 standard; DNA; 3549 BP.  
XX  
AC AAD08563;  
XX  
DT 04-SEP-2001 (first entry)  
XX  
DE Human cardiac adenylylase VI (ACVI) isoform #1 DNA.  
XX  
KW Human; cardiac; beta-adrenergic signalling protein; beta-ASP;  
KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
KW adenylylase; adenylylase; adenylylase; adenylylase;  
KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
KW cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
CDS 1..3504  
FT /\*tag= a  
FT /product= "Human cardiac adenylylase VI isoform #1"  
FT /EC\_number= "4.6.1.1"  
XX  
PN WO200148164-A2.  
XX  
PD 05-JUL-2001.  
XX  
PF 26-DEC-2000; 2000WO-US35411.  
XX  
PR 27-DEC-1999; 99US-0472667.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Hammond HK, Gao M;  
XX  
DR WPI; 2001-418260/44.  
DR P-PSDB; AAE04310.  
XX  
PT Novel polynucleotide encoding a modified adenylylase polypeptide  
PT useful for enhancing cardiac function in mammalian hearts, and for  
PT treating heart disease, especially congestive heart failure -  
XX  
XX Example 5; Page 122-129; 153pp; English.  
XX  
CC The present invention relates to methods and compositions for enhancing  
CC cardiac function in mammalian hearts by inserting transgenes encoding  
CC beta-adrenergic signalling proteins (beta-ASP) which increase  
CC beta-adrenergic responsiveness within the myocardium using in vivo  
CC gene therapy. The beta-ASPs of the invention include beta-adrenergic  
CC receptors (beta-AR), adenylylases (also referred as adenylylase,  
CC adenylylase and G-protein kinase) and G-protein receptor kinase  
CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
CC in mammalian hearts and for treating heart disease, especially  
CC congestive heart failure. The present DNA sequence encodes human  
CC cardiac adenylylase VI (ACVI) isoform which is used for generating  
CC a third beta-ASP transgene, used in the exemplification  
XX  
SQ Sequence 3549 BP; 699 A; 1025 C; 1061 G; 764 T; 0 other;  
Query Match 94.0%; Score 295.2; DB 22; Length 3549;

Best Local Similarity 97.1%; Pred. No. 7.1e-65;  
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGTTAGTGGCTCCCTGGTCCCTAAAGTGAACGAAACAGCTGGGGT 60  
Db 1 ATGTCATGTTAGTGGCTCCCTGGTCCCTAAAGTGAACGAAACAGCTGGGGT 60  
QY 61 GAACGAATGGCAGAGCGTTCGCGCGCCGCTGGCACTCGGAGGTGCTTCTGCACG 120  
Db 61 GAACGAATGGCAGAGCGTTCGCGCGCCGCTGGCACTCGGAGGTGCTTCTGCACG 120  
QY 121 CCCCGCTATATGAGCTCCCTCCGGGATGACAGCCACCCAGCCCTCGCGGGCCCC 180  
Db 121 CCCCGCTATATGAGCTCCCTCCGGGATGACAGCCACCCAGCCCTCGCGGGCCCC 180  
QY 181 CCTCGGTGCCCCGCGAGGATGACGCTTCATCCGGAGGGGGCGCCCAAGCAAG 240  
Db 181 CCTCGGTGCCCCGCGAGGATGACGCTTCATCCGGAGGGGGCGCCCAAGCAAG 240  
QY 241 GAACTGGGGCTGGCGCAGTGGCCCTGGGCTTCGAAGATACCAAGTGAACGACACCG 300  
Db 241 GAACTGGGGCTGGCGCAGTGGCCCTGGGCTTCGAAGATACCAAGTGAACGACACCG 300  
QY 301 GCGGGACCG 309  
Db 301 GCGGGACCG 309

RESULT 4  
AAD08567  
ID AAD08567 standard; DNA; 3552 BP.  
XX  
AC AAD08567;  
XX  
DT 04-SEP-2001 (first entry)  
XX  
DE Human cardiac adenylylase VI (ACVI) isoform #2 DNA.  
XX  
KW Human; cardiac; beta-adrenergic signalling protein; beta-ASP;  
KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
KW adenylylase; adenylylase; adenylylase; adenylylase;  
KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
KW cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
CDS 1..3507  
FT /\*tag= a  
FT /product= "Human cardiac adenylylase VI isoform #2"  
FT /EC\_number= "4.6.1.1"  
XX  
PN WO200148164-A2.  
XX  
PD 05-JUL-2001.  
XX  
PF 26-DEC-2000; 2000WO-US35411.  
XX  
PR 27-DEC-1999; 99US-0472667.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Hammond HK, Gao M;  
XX  
DR WPI; 2001-418260/44.  
DR P-PSDB; AAE04311.  
XX  
PT Novel polynucleotide encoding a modified adenylylase polypeptide  
PT useful for enhancing cardiac function in mammalian hearts, and for  
PT treating heart disease, especially congestive heart failure -  
XX  
XX Claim 6; Page 134-140; 153pp; English.  
XX

CC The present invention relates to methods and compositions for enhancing  
CC cardiac function in mammalian hearts by inserting transgenes encoding  
CC beta-adrenergic signalling proteins (beta-ASP) which increase  
CC beta-adrenergic responsiveness within the myocardium using in vivo  
CC gene therapy. The beta-ASPs of the invention include beta-adrenergic  
CC receptors (beta-AR), adenylyl cyclases (also referred as adenylylase,  
CC adenylyl cyclase and CAMP synthetase) and G-protein receptor kinase  
CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
CC in mammalian hearts and for treating heart disease, especially  
CC congestive heart failure. The present DNA sequence encodes human  
CC cardiac adenylylase VI (ACVI) isoform which is used for generating  
CC a fourth beta-ASP transgene, used in the exemplification  
CC of the invention.  
XX Sequence 3552 BP; 686 A; 1037 C; 1068 G; 761 T; 0 other;  
SQ

Query Match 94.0%; Score 295.2; DB 22; Length 3552;  
Best Local Similarity 97.1%; Pred. No. 7.1e-65;  
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGTTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAACACGCTGGGGT 60  
|||||  
DB 1 ATGTCATGTTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAACACGCTGGGGT 60  
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QY 61 GAACGCAATGGCGAGAGCGTTTCGGGGCCGCTGCGCACTCGGGCAGGTGCTTCGCACG 120  
|||||  
DB 61 GAACGCAATGGCGAGAGCGTTTCGGGGCCGCTGCGCACTCGGGCAGGTGCTTCGCACG 120  
|||||

QY 121 CCCCCTATATAGCTGCTCGGGATGCAGAGCCACCCAGCCCTCGGGCCCC 180  
|||||  
DB 121 CCCCCTATATAGCTGCTCGGGATGCAGAGCCACCCAGCCCTCGGGCCCC 180  
|||||

QY 181 CCTCGGTGCCCCGTCAGGATGACGCTTCATCCGGAGGGCGGCCAAGGGCAAG 240  
|||||  
DB 181 CCTCGGTGCCCCGTCAGGATGACGCTTCATCCGGAGGGCGGCCAAGGGCAAG 240  
|||||

QY 241 GAACGTCGGGCTCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACACACGCG 300  
|||||  
DB 241 GAGCTGGGGCTCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAAGTGACACACGCG 300  
|||||

QY 301 GCGGGACCG 309  
|||  
DB 301 GCGGGACCG 309  
|||

RESULT 5  
AAD08568  
ID AAD08568 standard; cDNA; 3582 BP.  
XX  
AC AAD08568;  
XX  
DT 04-SEP-2001 (first entry)  
XX  
DE Human modified cardiac adenylylase VI (ACVI) isoform cDNA.  
XX  
KW Human; cardiant; beta-adrenergic signalling protein; beta-ASP;  
KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
KW adenylylase; adenylylase; adenylylase; adenylylase;  
KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
KW cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT CDS 22..3525  
FT /\*tag= a  
FT /product= "Human modified cardiac ACVI isoform"  
XX  
PN WO200148164-A2.  
XX  
PD 05-JUL-2003

PF 26-DEC-2000; 2000WO-US35411.  
XX  
PR 27-DEC-1999; 99US-0472667.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Hammond HK, Gao M;  
XX  
DR WPI; 2001-418260/44.  
XX  
DR P-FSDB; AAE04312.  
XX  
PT Novel polynucleotide encoding a modified adenylylase polypeptide  
PT useful for enhancing cardiac function in mammalian hearts, and for  
PT treating heart disease, especially congestive heart failure -  
XX  
XX Claim 4; Page 143-150; 153pp; English.  
XX  
CC The present invention relates to methods and compositions for enhancing  
CC cardiac function in mammalian hearts by inserting transgenes encoding  
CC beta-adrenergic signalling proteins (beta-ASP) which increase  
CC beta-adrenergic responsiveness within the myocardium using in vivo  
CC gene therapy. The beta-ASPs of the invention include beta-adrenergic  
CC receptors (beta-AR), adenylyl cyclases (also referred as adenylylase,  
CC adenylyl cyclase and CAMP synthetase) and G-protein receptor kinase  
CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
CC in mammalian hearts and for treating heart disease, especially  
CC congestive heart failure. The present cDNA sequence encodes human  
CC modified cardiac adenylylase VI (ACVI) isoform which is used for  
CC generating a beta-ASP transgene, used in the exemplification of the  
CC invention.  
XX  
SQ Sequence 3582 BP; 703 A; 1036 C; 1067 G; 776 T; 0 other;  
XX

Query Match 94.0%; Score 295.2; DB 22; Length 3582;  
Best Local Similarity 97.1%; Pred. No. 7.1e-65;  
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGTTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAACACGCTGGGGT 60  
|||||  
DB 22 ATGTCATGTTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAACACGCTGGGGT 81  
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QY 61 GAACGCAATGGCGAGAGCGTTTCGGGGCCGCTGCGCACTCGGGCAGGTGCTTCGCACG 120  
|||||  
DB 82 GAACGCAATGGCGAGAGCGTTTCGGGGCCGCTGCGCACTCGGGCAGGTGCTTCGCACG 141  
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QY 121 CCCCCTATATAGCTGCTCGGGATGCAGAGCCACCCAGCCCTCGGGCCCC 180  
|||||  
DB 142 CCCCCTATATAGCTGCTCGGGATGCAGAGCCACCCAGCCCTCGGGCCCC 201  
|||||

QY 181 CCTCGGTGCCCCGTCAGGATGACGCTTCATCCGGAGGGCGGCCAAGGGCAAG 240  
|||||  
DB 202 CCTCGGTGCCCCGTCAGGATGACGCTTCATCCGGAGGGCGGCCAAGGGCAAG 261  
|||||

QY 241 GAACGTCGGGCTCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACACACGCG 300  
|||||  
DB 262 GAGCTGGGGCTCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAAGTGACACACGCG 321  
|||||

QY 301 GCGGGACCG 309  
|||  
DB 322 GCGGGACCG 330  
|||

RESULT 6  
AAX00461  
ID AAX00461 standard; cDNA; 4942 BP.  
XX  
AC AAX00461;  
XX  
DT 21-MAY-1999 (first entry)  
XX  
DE Human type VI adenylyl cyclase cDNA.  
XX  
KW Adenylyl cyclase type VI; human; hAC6; therapy; diagnosis; ds.



XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX FT CDS 145...3651  
XX FT /\*tag= a  
XX PN WO9901547-A1.  
XX PD 14-JAN-1999.  
XX PF 01-JUL-1998; 98WO-US13694.  
XX PR 01-JUL-1997; 97US-0886550.  
XX PR 01-JUL-1997; 97US-0070904.  
XX PA (CORT-) COR THERAPEUTICS INC.  
XX PI Tomlinson JA;  
XX DR WPI: 1999-106049/09.  
XX DR P-PSDB; AAW30599.  
XX PT Newly isolated and purified human type VI adenylyl cyclase (hac6)  
XX PT polypeptide - useful for identifying potential therapeutic agents  
XX PT that modulate hac6 activity, and for the diagnosis of  
XX PT hac6-associated diseases and disorders  
XX PS Claim 3; Fig 1A-I; 42pp; English.  
XX CC This DNA sequence encodes human type VI adenylyl cyclase (hac6, see  
XX CC AAW30599) that is expressed mainly in the heart and brain. hac6 has  
XX CC a similar putative structure to other adenylyl cyclase isoforms  
XX CC but, like type V, is distinguishable in that it has a larger  
XX CC N-terminus and a relatively shorter C-terminus as it lacks the C2b  
XX CC region. hac6 cDNA was initially isolated from a human heart cDNA  
XX CC library using an adenylyl cyclase PCR fragment as probe. It was  
XX CC used to design primers that were used in a PCR-based RACE to obtain  
XX CC the full-length cDNA sequence. The invention relates to the hac6  
XX CC gene, methods for the recombinant production of purified hac6 and  
XX CC the proteins made by these methods, antibodies against hac6,  
XX CC vectors, probes and host cells (especially HEK-293) transformed by  
XX CC genes encoding polypeptides having hac6 activity, along with  
XX CC diagnostic and therapeutic uses for these various reagents. hac6  
XX CC can be used as a tool to screen for agonists and antagonists that  
XX CC stimulate/inhibit hac6. Such compounds have therapeutic utility  
XX CC in treating diseases caused by aberrant activity of this enzyme,  
XX CC and diseases whose symptoms can be ameliorated by stimulating or  
XX CC inhibiting the activity of hac6.  
XX SQ Sequence 4942 BP; 953 A; 1404 C; 1512 G; 1073 T; 0 other;  
Query Match 94.0%; Score 295.2; DB 20; Length 4942;  
Best Local Similarity 97.1%; Pred. No. 7.5e-65;  
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 1 ATGTCTATGTTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAACACGCTGGGT 60  
DB 145 ATGTCTATGTTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAACACGCTGGGT 204  
QY 61 GAACGCAATGGGAGGAGGTTTCGGCGCCCTGGGACATCGGCGAGGTCTCTGCACG 120  
DB 205 GAACGCAATGGGAGGAGGTTTCGGCGCCCTGGGACATCGGCGAGGTCTCTGCACG 264  
QY 121 CCCCCTATATGATGCTGCTCGGGATGAGAGCCACCCAGCCCTCCCTGCGGCCCC 180  
DB 265 CCCCCTATATGATGCTGCTCGGGATGAGAGCCACCCAGCCCTCCCTGCGGCCCC 324  
QY 181 CCTCGGTGCTTGGCAGGATGACGCTTCATCCGGAGGGGGCCCAAGGAGGCAAG 240  
DB 325 CCTCGGTGCTTGGCAGGATGACGCTTCATCCGGAGGGGGGGCCCAAGGAGGCAAG 384  
QY 241 GAACTGGGCTGCGGGAGTGGCCCTGTTGGCTTCAAGATACCGAAGTGAACACGACCG 300

DB 385 GAGCTGGGCTGGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACGACGCG 444  
QY 301 GCGGGACCG 309  
DB 445 GCGGGACG 453  
RESULT 7  
AAQ42525  
ID AAQ42525 standard; DNA; 4046 BP.  
XX AC AAQ42525;  
XX DT 14-SEP-1993 (first entry)  
XX DE Cardiac adenylyl cyclase gene.  
XX KW Regulation; cardiac function; heart; heart failure; ss.  
XX OS Canis familiaris.  
XX FH Key Location/Qualifiers  
XX FT CDS 131...3627  
XX FT /\*tag= a  
XX PN EP543137-A  
XX PD 26-MAY-1993.  
XX PF 12-OCT-1992; 92EP-0117374.  
XX PR 18-NOV-1991; 91US-0793961.  
XX PA (AMCY ) AMERICAN CYANAMID CO.  
XX PI Ishikawa Y;  
XX DR WPI: 1993-168873/21.  
XX DR P-PSDB; AAR37309.  
XX PT Purified DNA encoding cardiac adenylyl cyclase - useful to screen  
XX PT for cpds. which stimulate activity of the cyclase  
XX PS Claim 1; Fig 2; 34pp; English.  
XX CC A canine heart cDNA library was constructed in lambda gt10 and was  
XX CC screened with a 970 bp AatI-HincII fragment from type I adenylyl  
XX CC cyclase cDNA probe (encodes the first cytoplasmic domain of adenylyl  
XX CC cyclase, which has significant homology to other previously known  
XX CC types of adenylyl cyclase). One positive clone, of 5.4 kb was obtd.  
XX CC Positive colonies were subcloned into pUC18 and further subcloned  
XX CC and sequenced bidirectionally. The 5.4 kb clone was used to  
XX CC rescreen the library and on overlapping clone contg. the 5' end of  
XX CC the gene was isolated. Together the two clones cover the complete  
XX CC canine cardiac adenylyl cyclase gene. The gene is suspected of  
XX CC being involved in the regulation of cardiac function and it is thought  
XX CC that decreased activity of adenylyl cyclase in the heart may be a  
XX CC major factor in the development of heart failure. Thus the adenylyl  
XX CC cyclase gene is useful to screen cpds. which stimulate the activity  
XX CC of the cyclase.  
XX SQ Sequence 4046 BP; 743 A; 1206 C; 1254 G; 843 T; 0 other;  
Query Match 72.4%; Score 227.4; DB 14; Length 4046;  
Best Local Similarity 89.5%; Pred. No. 7.7e-48;  
Matches 256; Conservative 0; Mismatches 27; Indels 3; Gaps 1;  
QY 1 ATGTCTATGTTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAACACGCTGGGT 60  
DB 131 ATGTCTATGTTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAACACGCTGGGT 190  
QY 61 GAACGCAATGGGAGGAGGTTTCGGCGCCCTGGGACATCGGCGAGGTCTCTGCACG 120

Db 191 GAACCAATGGGCAAGCGT---CCACGCGCGGAGCTGGACCAAGTGTCTTGTGCACG 247  
Qy 121 CCACGCTATATGAGTGTGCTTCGGGATGAGAGCCACCCACCCACCCCTGCGGGCCCC 180  
Db 248 CCCGCTATATGAGTGTGCTTCGGGATGAGAGCCACCCACCCACCCCTGCGGCTCCC 307  
Qy 181 COTCGTCCCTGCGGAGTATGAGCTTCATCCGAGGCGGCGGCCANGCAAGGCAAG 240  
Db 308 COTCGTCCCTGCGGAGTATGAGCTTCATCCGAGGCGGCGGCCANGCAAGGCAAG 367  
Qy 241 GAACCTGGGCTGCGGCGAGTGGCCCTGGGCTTCGAGATACGGAAG 286  
Db 368 GAGCTGGGCTGCGGCGAGTGGCCCTGGGCTTCGAGGAGCACTGAGG 413

## RESULT 8

AB199680  
ID AB199680 standard; cDNA; 5841 BP.  
XX  
AC AB199680;  
XX  
DT 07-MAR-2002 (first entry)  
XX  
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:716.  
XX  
KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;  
KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.  
XX  
OS Mus musculus.

XX WO200108188-A2;  
XX PD 22-NOV-2001.

XX PR 18-MAY-2001; 2001WO-JP04192.  
XX PR 18-MAY-2000; 2000JP-0145977.

XX PA (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
XX PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;  
XX WPI; 2002-034733/04.  
XX P-PSDB; ABB57257.

XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring  
XX expression levels of particular genes defined in the specification or  
XX by determining the expression profile of a gene group comprising these  
XX genes -  
XX  
XX Claim 2; Page 1771-1780; 2690pp; English.

XX The present invention describes a method for examining ischaemic  
XX conditions, comprising measuring the expression levels of particular  
XX genes (I) in a test sample or determining the expression profile of a  
XX gene group in the sample comprising genes selected from (I). The method  
XX is useful for examining the ischaemic condition (e.g. compressive  
XX ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring  
XX expression levels of particular genes (ABI99202 to ABI99912, encoding  
XX the protein sequences in ABB57020 to ABB57374) or by determining the  
XX expression profile of a gene group comprising these genes. The  
XX expression levels or expression profiles produced by these genes are  
XX used as an indicator when screening for ischaemic condition-improving  
XX drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914  
XX represent PCR primers for a mouse ischaemic condition related sequence,  
XX which are used in the exemplification of the present invention.

XX Sequence 5841 BP; 1214 A; 1558 C; 1673 G; 1396 T; 0 other;

XX Query Match 63.4%; Score 199.2; DB 24; Length 5841;  
XX Best Local Similarity 82.3%; Pred. No. 9.8e-41;  
XX Matches 241; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

Qy 1 ATGTCATGTTTAGTGGCTCTCTGTCTCTAAAGTGGATGAACGGAAACACGCTTGGGT 60  
Db 96 ATGTCATGTTTAGTGGCTCTCTGTCTCCCAAGTGGATGAACGGAAACACGCTTGGGG 155  
Qy 61 GAACGCAATGGGCAAGCGTTCGGGCGCGGTGGCACTCGGGAGGTGGCTTCTGCACG 120  
Db 156 GAACGCAATGGGCAAGCG---CCCACGCCACGCAATCGAGCAGTGGCTTCTGCACA 212  
Qy 121 CCCGCTATATGAGTGTGCTTCGGGATGAGAGCCACCCACCCACCCCTGCGGGCCCC 180  
Db 213 COTCGCTATATGAGTGTGCTTCGAGATCGGAGCCACCCACCCCTCTGCAGCTCAC 272  
Qy 181 COTCGTCCCTGCGGAGTATGAGCTTCATCCGAGGCGGCGGCCANGCAAGGCAAG 240  
Db 273 ACTCGTGGCTGCGGAGTATGAGCTTCATCAGGAGGCGGCGGCCANGGCTGTG 332  
Qy 241 GAACCTGGGCTGCGGCGAGTGGCCCTGGGCTTCGAGATACGGAAGTGAACAC 293  
Db 333 GAGCTGGGCTGCGGCTCAGTGGCTTGGGCTTTCGAGGAGCACTGAGGTGACCAC 385

## RESULT 9

AAA53923  
ID AAA53923 standard; cDNA; 4131 BP.

XX AAA53923;

XX DT 03-JAN-2001 (first entry)

XX Type VI adenyllyl cyclase coding sequence.

XX Adenyllyl cyclase; type I; type II; recombinant; enzyme; CAMP;  
XX cyclic AMP; adenosine monophosphate; screening; stimulation;  
XX inhibition; treatment; cholera; pituitary tumour; heart failure;  
XX ischaemia; endocrine disorder; cell necrosis;  
XX pseudohypoparathyroidism; endocrine deficiency; human; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
XX CDS 14..3556

XX /\*tag= a

XX /product= Type VI adenyllyl cyclase

XX US6107076-A.

XX PD 22-AUG-2000.

XX PF -04-OCT-1996; 96US-0726214.

XX PR 04-OCT-1995; 95US-0005498.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Gilman AG, Tang W;

XX WPI; 2000-578539/54.

XX P-PSDB; AAB02010.

XX Novel soluble mammalian polypeptide composition comprising adenyllyl  
XX cyclase activity for screening stimulators and inhibitors of adenyllyl  
XX cyclase, is activated by Galpha

XX Disclosure; Columns 75-78; 73pp; English.

XX A recombinant Adenyllyl cyclase is described which lacks membrane  
XX bound domains. Separation and purification of the recombinant  
XX enzyme is much easier compared with wild type enzymes and the  
XX recombinant enzyme is more stable than the wild type enzyme which  
XX allows easier screening of compounds that stimulate and inhibit  
XX Adenyllyl cyclase activity. The recombinant adenyllyl cyclase comprises  
XX a chimera of adenyllyl cyclase C\_1 and C\_2 domains linked covalently.

CC The domains may be linked by a linker peptide. The recombinant  
CC adenylyl cyclase is useful for screening inhibitors and stimulators  
CC of adenylyl cyclase activity. Inhibitors of the enzyme are useful for  
CC treating cholera, pituitary tumors, heart failure, ischaemia,  
CC endocrine disorders and cell necrosis. Stimulators of adenylyl  
CC cyclase are useful for treating pseudohypoparathyroidism and other  
CC endocrine deficiencies.  
XX  
SQ Sequence 4131 BP; 835 A; 1190 C; 1182 G; 924 T; 0 other;

Query Match 63.1%; Score 198.2; DB 21; Length 4131;  
Best Local Similarity 79.9%; Pred. No. 1.7e-40;  
Matches 246; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 1 ATGTCATGTTTGTAGTGGCTTCCTGGTCCCTAAAGTGGATGAACGGAACAGCCTGGGGT 60  
DB 56 ATGTCATGTTTGTAGTGGCTTCCTGGTCCCTAAAGTGGATGAACGGAACAGCCTGGGC 115  
QY 61 GAACGCAATGGGAGAGCGTTTCGCGGCGCTGGGACCTGGGACGAGTGGCTTCTGCACG 120  
DB 116 GAACGCAATGGGAGAGCG--CCACGCGCAGCGGACCGGCGCTGGCTTCTGCACG 172  
QY 121 CCGCGCTATATAGTGGCTTCCTGGGATGACAGCCAGCCGCCCTCGCGGGCCCC 180  
DB 173 CCGCGCTACATGAGTGGCTTCGAGTGGAGCCAGCCAGCCGCTCTGCAGCTCGC 232  
QY 181 CTTGCGTGGCCCTGGCAGGATGACGCTTCATCCGAGGGGGCGCCGACGAGGGCGA 240  
DB 233 ACTCGGTGGCCCTGGCAGGATGAGCTTCATCAGGAGGCTGGCGGAGGGGTGTG 292  
QY 241 GAACGCGGCTGGCGGAGTGGCCCTGGGCTTCGAGATACCGAAGTGACACGACACCG 300  
DB 293 GAGCTGGGCTGGGCTGAGTGGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 352  
QY 301 GCGGAGCC 308  
DB 353 GGGACAGC 360

RESULT 10  
AAS11614/C  
ID AAS11614 standard; DNA; 236303 BP.

XX AAS11614;

XX 24-OCT-2001 (first entry)

XX Human genomic DNA containing exons 2-17 of the CRIM1 gene.

XX CRIM-1; Human; human chromosome 2p21-16.3; ophthalmological;  
KW neuroprotective; renal; osteopathic; dental; vulnary; immunogen;  
KW antibody; gene therapy; neurodegenerative disease; eye disorder;  
KW cataract; bone morphogenic protein; BMG; renal disease; bone abnormality;  
KW tooth abnormality; wound; ds.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH exon 33104..33277  
FT /tag= a  
FT /number= 2  
FT 33278..77746  
FT /tag= b  
FT /number= 2  
FT 77747..77989  
FT /tag= c  
FT /number= 3  
FT 77990..79103  
FT /tag= d  
FT /number= 3  
FT 79104..79224  
FT /tag= e  
FT /number= 4

FT intron 79225..101022  
FT /tag= f  
FT /number= 4  
FT 101023..101144  
FT /tag= g  
FT /number= 5  
FT 101145..113377  
FT /tag= h  
FT /number= 5  
FT 113378..113560  
FT /tag= i  
FT /number= 6  
FT 113561..115985  
FT /tag= j  
FT /number= 6  
FT 115986..116183  
FT /tag= k  
FT /number= 7  
FT 116184..1135707  
FT /tag= l  
FT /number= 7  
FT 1135708..1135836  
FT /tag= m  
FT /number= 8  
FT 1135837..1146471  
FT /tag= n  
FT /number= 8  
FT 1146472..1146628  
FT /tag= o  
FT /number= 9  
FT 1146629..1148761  
FT /tag= p  
FT /number= 9  
FT 1148762..1148883  
FT /tag= q  
FT /number= 10  
FT 1148884..1150044  
FT /tag= r  
FT /number= 10  
FT 1150045..1150254  
FT /tag= s  
FT /number= 11  
FT 1150255..1153815  
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FT 1154032..1158580  
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FT 1158581..1158802  
FT /tag= w  
FT /number= 13  
FT 1158803..1173982  
FT /tag= x  
FT /number= 13  
FT 1173983..1174177  
FT /tag= y  
FT /number= 14  
FT 1174178..1181006  
FT /tag= z  
FT /number= 14  
FT 1181007..1181129  
FT /tag= aa  
FT /number= 15  
FT 1181130..1183612  
FT /tag= ab  
FT /number= 15  
FT 1183613..1183800  
FT /tag= ac  
FT /number= 16  
FT 1183801..1185152  
FT intron

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FT      /*tag= ad
FT      /number= 16
FT      exon      185153..187765
FT      /*tag= ae
FT      /number= 17
XX      WO200138519-A1.
XX      31-MAY-2001.7
XX      24-NOV-2000.--2000WO-AU01435.
XX      26-NOV-1999; 99AU-0004348.
XX      (UYQU ) UNIV QUEENSLAND.
XX      Little M, Yamada T, Holmes G, Georgas K, Kolle G, Wilkinson L;
XX      WPI; 2001-343951/36.
XX      Nucleic acids from human chromosome 2p21-16.3 and the encoded peptide,
XX      especially cataract formation -
XX      Claim 4; Fig 3; 16pp; English.
XX      The invention relates to nucleic acids from human chromosome 2p21-16.3
XX      and the encoded peptide (and mouse and chicken orthologues) that
XX      comprises a PEGECPLP group, an insulin-like growth factor binding protein
XX      (IGFBP)-like domain, cysteine-rich domains, an RGD (undefined) group
XX      and a transmembrane domain. The protein, e.g. CRIM1, interacts with
XX      peptides of the transforming growth factor superfamily. A composition
XX      comprising an expression construct comprising the nucleic acids of the
XX      invention or a mimetic which antagonises or mimics an activity of a CRIM1
XX      polypeptide may be used in a method for modulating the biological
XX      activity of a polypeptide of the bone morphogenic protein (BMP) family.
XX      In this way they may be used to prevent or treat an eye disease,
XX      especially cataract formation. They may also be used to treat
XX      neurodegenerative diseases, renal and kidney disease, bone and tooth
XX      abnormalities, wounds and skin damage, e.g. by use of the nucleic acid in
XX      gene therapy by using antibodies directed against CRIM1 polypeptides.
XX      The present sequence is a Human genomic DNA containing exons 2-17 of
XX      the CRIM1 gene.
XX      Sequence 236303 BP; 70199 A; 46544 C; 47996 G; 71563 T; 1 other;
XX      Query Match      12.7%; Score 39.8; DB 22; Length 236303;
XX      Best Local Similarity 55.4%; Pred. No. 1.8;
XX      Matches 77; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
QY      78 GCGTTCCGGCGCCGTCGACACGTCGGGAGTGGCGGAGTCCCTTCCCTCCGCGGAGTCCCGGCGGAG 137
DB      234505 GAGTGGGGGGCCCGGGGAGTGGCGGAGTGGCGGAGTCCCTTCCCTCCGCGGAGTCCCGGCGGAG 234446
QY      138 CCTCCGGGATGCAGAGCCACCCAGCCACCCCTCGGGGCCCTCCGTCGTCCTATATGAGCTG 197
DB      234445 CCTCAGGCGCGAGCTCCCTCCGCGCCCTCTCCGCGGAGTCCCGGCGGAGTCCCGGCGGAG 234386
QY      198 GGATGACGCTTCATCCCG 216
DB      234385 TCTCGGCTCTCTCTCCCG 234367
RESULT 11
AA050636/c
ID      AAS06036 standard; DNA; 3050 BP.
XX      AC      AAS06036;
XX      DT      12-SEP-2001 (first entry)
XX      DE      Angiotensin converting enzyme (ACEV) splice variant DNA #36.
XX
```

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KW      Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KW      granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW      platelet-derived endothelial cell growth factor; cardiovascular disease;
KW      cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; ds;
KW      vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW      myocardial infarction; coronary arterial thrombosis; renal disease;
KW      diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW      multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW      nonaroidotic pulmonary granulomatous disease; endothelial abnormality;
XX      vascular disorder; asbestosis.
XX      Homo sapiens.
OS      Homo sapiens.
XX      WO200136632-A2.
XX      25-MAY-2001.
XX      17-NOV-2000; 2000WO-IL00766.
XX      17-NOV-1999; 99IL-0132978.
XX      10-DEC-1999; 99IL-013455.
XX      (COMP-) COMPUGEN LTD.
XX      Levine Z, David A, Azar I, Khosravi R, Bernstein J;
XX      WPI; 2001-336004/35.
XX      P-PSDB; AAU02936.
XX      Novel alternative splicing variants e.g. variant of angiotensin
XX      converting enzyme (ACEV), useful in identifying candidate compounds
XX      capable of binding to the variant and to detect anti-variant antibodies
XX      -
XX      Claim 1; Page 335-336; 519pp; English.
XX      The sequence represents a DNA encoding an angiotensin converting enzyme
XX      splice variant (ACEV) polypeptide. The polypeptides of the invention
XX      include variants of granulocyte colony stimulating factor receptor,
XX      glucagon, interleukin 6, platelet-derived endothelial cell growth factor,
XX      cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and
XX      vasoactive intestinal polypeptide receptor 2. The polypeptides and their
XX      associated nucleic acids are useful for identification of binding
XX      molecules and detection of candidate compounds capable of binding the
XX      molecules. The sequences of the invention can be used in the treatment
XX      and diagnosis of various disorders including cardiovascular diseases such
XX      as arteriosclerosis, myocardial infarction and coronary arterial
XX      thrombosis, renal diseases such as diabetic nephropathy, muscular
XX      diseases such as hypertrophy, immune disorders such as immune complex
XX      nephritis, multiple sclerosis, cancer, sarcoidosis, nonaroidotic
XX      pulmonary granulomatous diseases such as asbestosis and vascular
XX      pathologies involving an endothelial abnormality such as deep vein
XX      thrombosis.
XX      Sequence 3050 BP; 520 A; 1032 C; 942 G; 555 T; 1 other;
XX      Query Match      12.2%; Score 38.2; DB 22; Length 3050;
XX      Best Local Similarity 46.0%; Pred. No. 2.4;
XX      Matches 127; Conservative 0; Mismatches 149; Indels 0; Gaps 0;
QY      13 AGTGGCCTCCTGTCCTCTAAAGTGGATGAACGGAACAGCCCTGGGGTGAACGCAATGGG 72
DB      2623 AGAGCCCCCAGGCCCGGAGAGCCAGGAGCCGTGGTGGACAGGTTGGAAGGTGAGGA 2564
QY      73 CAGAAGCGTTCCGGCGCGGTGGCACTCGGGCAGGTGGCTTCTGCACGCCCCCGCTATATG 132
DB      2563 CAGACAGCCCCCAGCAAAATGGCAGTGGCGGTGGCGGTGCAGGCAGACGTCGTCGTG 2504
QY      133 AGCTGCTCCGGGATGCAGAGCCACCCAGCCACCCCTCGCGGCGCCCTCGGTGCCCC 192
DB      2503 TGCTCCAGGGGGGGGGCCCTCGCTGCTGCGCCCTCTGTCAGAGCCCTCCCGGTAGATCGC 2444
QY      193 TGGCAGGATGACGCTTTCATCCGAGGGGGCGGCCCCAGCAGGCAAGGAAGTGGGGCTG 252
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DB 2443 AAGCATATCGACTGCGCTGGCCAGCGCTTCAGAGCCGAGTGGCGTGGCGGGCG 2384  
QY 253 CGGCGAGTGGCCCTGGCTTCAGAGATACCGAGTG 288  
DB 2383 CAGCGGGGCGGTGCACCGAGCGGCGAGCGTG 2348  
RESULT 12  
AAC77370  
ID AAC77370 standard; cDNA; 3174 BP.  
XX AC AAC77370;  
XX 08-FEB-2001 (first entry)  
DE Human ORFX ORF7925 polynucleotide sequence SEQ ID NO:5849.  
XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;  
KW vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;  
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
KW hypotensive; dermatological; immunosuppressive; antinflammatory;  
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;  
KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;  
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
KW cholesterol ester storage; systemic lupus erythematosus; infection;  
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
KW bone damage; cartilage damage; antinflammatory disease; coagulation;  
KW thrombosis; contraceptive; ss.  
XX Homo sapiens.  
XX OS  
XX PN WO200058473-A2.  
XX 05-OCT-2000.  
XX 31-MAR-2000; 2000WO-US08621.  
XX 31-MAR-1999; 99US-0127607.  
XX 02-APR-1999; 99US-0127636.  
XX 05-APR-1999; 99US-0127728.  
XX 30-MAR-2000; 2000US-0540763.  
XX (CURA-) CURAGEN CORP.  
XX PI Shinkets RA, Leach M;  
XX WPI; 2000-602362/57.  
XX P-PSDB; AAB43161.  
XX Novel nucleic acids and peptides derived from open reading frame X,  
XX useful for treating e.g. cancers, proliferative disorders,  
XX neurodegenerative disorders and cardiovascular disease -  
XX Claim 5; Page 5022-5024; 5507pp; English.  
XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
XX which represent the human ORFX open reading frames 1 to 3161. The ORFX  
XX sequences have activities such as: cytostatic; hepatotropic; vulnery;  
XX antipsoriatic; antiparkinsonian; nootropic; neuroprotective;  
XX osteopathic; anticonvulsant; antiarthritic; immunosuppressant;  
XX immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;  
XX antidiabetic; hypotensive; dermatological; antirheumatic; antithyroid;  
XX antinflammatory; antibacterial; antiviral; antifungal; antineumatic;  
XX antithyroid; and antianemic. The sequences can be used for determining  
XX the presence of or predisposition to, or preventing or treating  
XX pathological conditions associated with an ORFX-associated disorder. The  
XX nucleic acids can be used to express ORFX proteins in gene therapy  
XX vectors. The proteins and nucleic acids may be used to treat cancers,  
XX proliferative disorders, neurodegenerative disorders, osteoarthritis,

CC graft vs host disease, cardiovascular disease, diabetes mellitus,  
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
CC nocturnal haemoglobinuria, antinflammatory disease; to enhance  
CC coagulation; to inhibit thrombosis; and as a contraceptive.  
XX  
SQ Sequence 3174 BP; 737 A; 897 C; 904 G; 620 T; 16 other;  
Query Match 12.2%; Score 38.2; DB 21; Length 3174;  
Best Local Similarity 53.4%; Pred. No. 2.4;  
Matches 79; Conservative 0; Mismatches 69; Indels 0; Gaps 0;  
QY 137 GCCTCGGGATGAGAGCCAGCCACCCCTGGGGGGGGGGGGGGGGGGGGGGGGGGG 196  
DB 2049 GCGCCCTCCAGGCTGAGTTCCTCCAGCCAGCCAGCTCCGGGGGGGGGGGGGGG 2108  
QY 197 AGGATGACGCTTTCATCCGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 256  
DB 2109 AGGGCTTAGTCCAGTTCCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 2168  
QY 257 CAGTGGCCCTGGGCTTCGGAAGATACCGA 284  
DB 2169 CAGGCGCCCTGGCTAGCTGGACATCCA 2196  
RESULT 13  
AAQ79401/c  
ID AAQ79401 standard; cDNA; 3243 BP.  
XX AC AAQ79401;  
XX 06-JUL-1995 (first entry)  
XX Human NMDAR2 receptor subunit clone NMDA24 gene.  
XX N-methyl-D-aspartate; receptor; human; NMDA; cation-selective; channel;  
KW glutamate; hippocampus; rat; pcdnal; NMDA receptor; antagonist; ds.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FT CDS 1..822  
FT /tag= a  
FT /product= part of the NMDAR2C receptor subunit  
FT misc\_feature 540..551  
FT /tag= b  
FT /note= "11 bp insertion found in clone NMDA24"  
FT misc\_feature 1501..1525  
FT /tag= c  
FT /note= "24 bp insertion found in clone NMDA24"  
XX WO9424284-A.  
XX 27-OCT-1994.  
XX 20-APR-1994; 94WO-US04387.  
XX 20-APR-1993; 93US-0052449.  
XX (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.  
XX Daggett LP, Ellis SB, Liaw CW, Lu C;  
XX WPI; 1994-341863/42.  
XX P-PSDB; AAR66059.  
XX Isolated DNA encoding a human N-methyl-D-aspartate receptor  
XX subunit - used as probes in the identification and isolation of  
XX nucleic acids encoding related receptor subunits.  
XX Claim 11; Page 99-104; 156pp; English.



Db	3685	AGAGGCCCCAGGCCCCGGAGAGCACAGAGCCGTGGCTGGCAGAGGTCGAGAGGTGAGGA	3626
Qy	73	CAGAAAGCCTTCGCGCGCGCGTGGGACCTCGGGCAGGTGGCTTCTGCAGCGCCCCGCTATATG	132
Db	3625	CAGACAGCCCCCAGCAAAATGGCAGGTGGGCGTGGCAGCAGACGTGCTGCTCTG	3566
Qy	133	AGCTGCTTCGGGATGCAGAGCCACCCAGCCCCCCTGCGGGCCCCCTCGGTGCCCC	192
Db	3565	TGCTGCCAGGGGGGGCCCCCTGCTGTCGCCCTCTTGCAGCGCCTCCCGGTAGATCGGC	3506
Qy	193	TGGCAGGATGAGCCCTTCATCGGAGGGCGGCCCAAGCAAGGCAAGAACTGGGGCTG	252
Db	3505	AGCACATGACTGGCCCTGCGCCAAAGCGCTTCGAGGCCGAGTCTCCGTGCGGGCGGGCG	3446
Qy	253	CGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTG	288
Db	3445	CAGCGGGGCCGTGCACCCAGCGGGCAGCAGCTG	3410





GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model  
Run on: February 28, 2003, 21:13:01 ; Search time 539.139 Seconds  
(without alignments)  
16949.756 Million cell updates/sec

Title: US-09-750-240-1  
Perfect score: 314  
Sequence: 1 atgcatggttttagtgccct.....acaccggcggaacgcgtgaa 314

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : GenEmbl:\*
- 1: gb.ba.\*
  - 2: gb.htg.\*
  - 3: gb.in.\*
  - 4: gb.om.\*
  - 5: gb.ov.\*
  - 6: gb.pat.\*
  - 7: gb.ph.\*
  - 8: gb.pl.\*
  - 9: gb.pr.\*
  - 10: gb.ro.\*
  - 11: gb.sts.\*
  - 12: gb.sy.\*
  - 13: gb.un.\*
  - 14: gb.vi.\*
  - 15: em.ba.\*
  - 16: em.fun.\*
  - 17: em.hum.\*
  - 18: em.in.\*
  - 19: em.mu.\*
  - 20: em.om.\*
  - 21: em.or.\*
  - 22: em.ov.\*
  - 23: em.pat.\*
  - 24: em.ph.\*
  - 25: em.pl.\*
  - 26: em.ro.\*
  - 27: em.sts.\*
  - 28: em.un.\*
  - 29: em.vi.\*
  - 30: em.htg.hum.\*
  - 31: em.htg.inv.\*
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  - 33: em.htg.mus.\*
  - 34: em.htg.pin.\*
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  - 41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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2	313	99.7	314	6	AX189757	Sequence
3	295.2	94.0	3549	6	AX174473	Sequence
4	295.2	94.0	3549	6	AX189761	Sequence
5	295.2	94.0	3552	6	AX189766	Sequence
6	295.2	94.0	3582	6	AX189768	Sequence
7	295.2	94.0	5877	9	AB007882	Sequence
c 8	295.2	94.0	205248	2	AC117498	Homo sapi
c 9	293.6	93.5	193283	2	AC021647	Homo sapi
10	292	93.0	6463	9	AF250226	Homo sapi
c 11	283.2	90.2	171945	2	AC025557	Homo sapi
12	227.4	72.4	4046	4	DOGADENCYC	Canis famill
13	227.4	72.4	4046	6	I29958	Sequence 1
14	199.2	63.4	5841	6	AX305965	Sequence
15	199.2	63.4	5841	10	MUSADCYC	Mouse adeny
16	199.2	63.4	139619	2	AC074028	Mus muscu
17	198.2	63.1	4131	6	AR106659	Sequence
18	198.2	63.1	4131	10	RATADCYB	Sequence
19	196.6	62.6	6036	10	RATADC	Sequence
20	196.6	62.6	151706	2	AC129405	Rattus norv
c 21	186.2	59.3	108689	2	AC096835	Rattus no
22	178	56.7	3465	10	MUSADNLCYC	Mus musculu
23	57.8	18.4	61901	5	U72484	Fugu rubrip
c 24	46.6	14.8	125020	9	AF429315	Homo sapi
25	43.4	13.8	151605	9	AC011995	Homo sapi
c 26	43.2	13.8	139513	2	AP005659	Oryza sat
27	43	13.7	318696	2	AC102955	Rattus no
28	42	13.4	74721	2	AC096161	Rattus no
29	41.8	13.3	158946	2	AC127964	Rattus no
30	41.8	13.3	167594	2	AC100791	Homo sapi
31	41.6	13.2	126868	2	AC128569	Rattus no
c 32	41.6	13.2	203042	2	AC068500	Mus muscu
c 33	41.4	13.2	35284	1	SCE19A	Streptomy
34	41.4	13.2	61617	2	AC120284	Rattus no
35	41.2	13.1	57221	2	AC113912	Rattus no
36	41	13.1	69282	2	AC040912	Homo sapi
37	41	13.1	186187	2	AC110369	Rattus no
38	41	13.1	187617	2	AC118993	Rattus no
c 39	40.8	13.0	157282	2	AC128294	Rattus no
c 40	40.8	13.0	169915	2	AC119440	Rattus no
c 41	40.6	12.9	155679	2	AC120273	Rattus no
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43	40.4	12.9	103190	5	AY016020	Gallus ga
44	40.4	12.9	135301	14	BHV1CGEN	Bovine he
c 45	40.4	12.9	135301	14	BHV1CGEN	Bovine he

ALIGNMENTS

RESULT 1  
AR174471  
LOCUS AR174471  
DEFINITION Sequence 1 from patent US 6306830.  
ACCESSION AR174471  
VERSION AR174471.1 GI:17914791  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 314)  
AUTHORS Hammond,H.Kirk., Insel,P.A., Ping,P., Post,S.R. and Gao,M.  
TITLE Gene therapy for congestive heart failure  
JOURNAL Patent: US 6306830-A 1 23-OCT-2001;  
FEATURES Location/Qualifiers

QY	181	CCTCGGTGCCCCCTGGCAGGATGACGCCCTTCATCCGAGGGCGGCCANGCAAGGGCAAG	240																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
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REFERENCE 1 (bases 1 to 3549)  
AUTHORS Hammond, H.K. and Gao, M.  
TITLE Gene therapy for congestive heart failure  
JOURNAL Patent: WO 0148164-A 5 05-JUL-2001;  
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)  
FEATURES Location/Qualifiers  
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QY 301 GCGGGACCG 309  
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DEFINITION Sequence 10 from Patent WO0148164.  
ACCESSION AXI89766  
VERSION AXI89766.1 GI:15143139  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 3552)  
AUTHORS Hammond, H.K. and Gao, M.  
TITLE Gene therapy for congestive heart failure  
JOURNAL Patent: WO 0148164-A 10 05-JUL-2001;  
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)  
FEATURES Location/Qualifiers  
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Db 61 GAACGCAATGGCAGAGCGTTCCGGCGCGCTTCCGGCTCGGCACTCGGCGAGTGGCTTCTGCACG 120  
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QY 181 CCTCGTGGCTCGGGCAGTACGCTTCATCCGAGGGGGCCGCCANGCAAGGCAAG 240  
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QY 241 GAACTGGGCTCGGGCAGTACGCTTCCGAGATACCGGAAGTGAACAGCAGACCG 300  
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Db 241 GAGCTGGGCTCGGGCAGTACGCTTCCGAGATACCGGAGGTGACACGACAGCG 300  
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QY 301 GCGGGACCG 309  
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Db 301 GCGGGACG 309  
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RESULT 6  
AXI89768  
LOCUS AXI89768 3582 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 12 from Patent WO0148164.  
ACCESSION AXI89768  
VERSION AXI89768.1 GI:15143140  
KEYWORDS synthetic construct.  
SOURCE synthetic construct.  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 3582)  
AUTHORS Hammond, H.K. and Gao, M.  
TITLE Gene therapy for congestive heart failure  
JOURNAL Patent: WO 0148164-A 12 05-JUL-2001;  
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)  
FEATURES Location/Qualifiers  
source 1..3582  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Modified AC-VI"  
BASE COUNT 703 a 1036 c 1067 g 776 t  
ORIGIN  
Query Match 94.0%; Score 295.2; DB 6; Length 3582;  
Best Local Similarity 97.1%; Pred. No. 4.8e-56;  
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
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Db 22 ATGTCATGTTTAGTGGCTCCTCGTCCCTAAAGTGGATGAACGGAACAGCCTGGGT 81  
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QY 61 GAACGCAATGGCAGAGCGTTCCGGCGCGCTTCCGGCTCGGCACTCGGCGAGTGGCTTCTGCACG 120  
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Db 82 GAACGCAATGGCAGAGCGTTCCGGCGCGCTTCCGGCTCGGCACTCGGCGAGTGGCTTCTGCACG 141  
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QY 121 CCCCCTATATAGCTGCCTCCGGGATGAGAGCCACCCAGCCCTCGGGCCCC 180  
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QY 181 CCTCGTGGCTCGGGCAGTACGCTTCCGAGGAGGGCGGCCANGCAAGGCAAG 240  
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Db 202 CCTCGTGGCTCGGGCAGTACGCTTCCGAGGAGGGCGGCCAGCAAGGGCAAG 261  
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QY 241 GAACTGGGCTCGGGCAGTACGCTTCCGAGATACCGGAAGTGAACAGCAGACCG 300  
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Db 262 GAGCTGGGCTCGGGCAGTACGCTTCCGAGGATACCGGAGGTGACACGACAGCG 321  
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QY 301 GCGGGACCG 309  
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Db 322 GCGGGACG 330  
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AB007882
LOCUS Homo sapiens KIAA0422 mRNA, partial cds.
ACCESSION AB007882
VERSION AB007882.2 GI:20521044
KEYWORDS KIAA0422.
SOURCE Homo sapiens male brain cDNA to mRNA, clone_lib:pbluescriptII SK
plus clone:hh01205s1.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1
Ishikawa,K., Nagase,T., Nakajima,D., Seki,N., Ohira,M.,
Miyaajima,N., Tanaka,A., Kotani,H., Nemura,N. and Ohara,O.
Prediction of the coding sequences of unidentified human genes.
VIII. 78 new cDNA clones from brain which code for large proteins
in vitro
DNA Res. 4 (5), 307-313 (1997)
98116655
9455477
2 (bases 1 to 5877)
Direct Submission
Submitted (06-OCT-1997) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba
292-0812, Japan (E-mail:cdna@kazusa.or.jp, Tel:+81-438-52-3913,
Fax:+81-438-52-3914)
On May 9, 2002 this sequence version replaced gi:2887418.
Sequence updated (05-Jan-1998).
Location/Qualifiers
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derived from pg00161 and 1353 - 5877 was derived from
hh01205)."
1..5877
/gene="KIAA0422"
<1..3484
/gene="KIAA0422"
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/db_xref="GI:20521045"
/translation="GRRTAGGTARTGLGGPRGPRGPRGRRGGPGQARSRAGS
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RSCRRVLVOVQSQFSAKLERLYQRFQMNQSSITLMAVLVLTAVLLAFAAP
ARPOPAVALLAACAAALFVGLMVCNRRHSFQDSMWVYVVLGILAAVQGGALAD
PRSPAGLWCVFVYIATLLPIRMAAVALSLGLSTLHLILAWNLNRGDAFLWKQL
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QHAVEMEKDINTKGLTMMHFHVIYQKHDNYSILFADTEGFTSLASCTAQELVMTLN
ELFARFDKLAENHCLRIKILGDCYCVSGIPEARADHACCVEMGDMLEAISLVE
VTGVNVMRVGHSRVCVGLRKKQFVDSNDVTLANHEAGGRAGRIHITRATL
QYLGNDIEVPRGGERNAYLKEHIFETLLILGASQKKEKAMKLQRTANSMEG
LMRWVDFRASFRTKDFKQMGIDDSKDNRTQDALNDEPDEFLSRAIDARS1
DQLRKSTVDLFRGDRLEKYSRVDFRFGAYVACALVFCFIQILLIFPST
LMLGIYASIFELLITVILICAVSGSLFPKALORLSRVSRAHSTGAFISVLV
FTSAIANMYIGNMLISILASSVFLHISSTICKLAMIIVGLIYLVLLLGGPPIFDN
YDLLGVHGLASSNETDGLDCAAGRVALKWYTPVILLVFALYLLHAQVVESTARL
DRLWKLQATGEKEEELQAYNRLLNLPKVAHFLAERNDLELYQSCVAV
MFASINFSFVLEENNEVECLRLNETIADFEIISERFPLEKTIKIGSTVM
AASGLNSTYDQVGRSHITALADYAMEOMKHINEHSFNFMKGLNNGPVVAGV
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BASE COUNT
ORIGIN
Query Match 94.0%; Score 295.2; DB 9; Length 5877;
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Db 137 ATGTCATGTTTACTGGCTCTCTGTCCCTAAAGTGGATGAACGGAACACACCTGGGGT 196
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QY 61 GAACCAATGGGACAGAGCGTTTCGGGGCGCGTGCACATCGGGCAGGTGGCTTCGACG 120
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Db 197 GAACCAATGGGACAGAGCGTTTCGGGGCGCGTGCACATCGGGCAGGTGGCTTCGACG 256
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QY 181 CCTCGGTCCTCGCAGGATGACGCTTCATCCGGAGGGGGCCCGCAGGAGGCAAG 240
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Db 437 GCGGGACG 445
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RESULT 8
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LOCUS Homo sapiens clone Rp11-422021, *** SEQUENCING IN PROGRESS ***, 20
UNORDERED PIECES.
ACCESSION AC117498
VERSION AC117498.4 GI:22002346
KEYWORDS HTG; HTGS_PHASE1.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (Bases 1 to 205248)
REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisil,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hoques,M., Holloway,C., Hollins,B.,
Homsif,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlssoon,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Lounsegh,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mei,G., Mettaker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogih,M., Okunou,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savary,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
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Sodergren, E., Sonaik, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Gibbs, R.

Direct Submission  
Unpublished  
2 (bases 1 to 205248)  
Worley, K.C.  
Direct Submission  
Submitted (10-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 205248)  
Worley, K.C.  
Direct Submission  
Submitted (31-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Jul 29, 2002 this sequence version replaced gi:21956504.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Drafting Center Code: WUGSC  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: HEAU  
Center clone name: RP11-422021  
----- Summary Statistics  
Sequencing vector: Plasmid;  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 216840 bases at least Q40  
Consensus quality: 220255 bases at least Q30  
Consensus quality: 222408 bases at least Q20  
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\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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\* 98057 115533: gap of unknown length  
\* 115534 139873: contig of 24240 bp in length  
\* 139874 139973: gap of unknown length  
\* 139974 175364: contig of 35391 bp in length  
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Query Match 94.0%; Score 295.2; DB 2; Length 205248;  
Best Local Similarity 97.1%; Pred. No. 2.6e-56;  
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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QY 241 GAACGCGGGTGGCGGCGAGTGGCCCTGCGGCTTCGAAGATACCAAGTGAACGACACCG 300  
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QY 301 GCGGGACCG 309  
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Db 168819 GCGGGACCG 168811

RESULT 9  
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LOCUS  
DEFINITION Homo sapiens chromosome 12 clone RP11-455122, WORKING DRAFT  
SEQUENCE, 8 unordered pieces.  
AC021647  
AC021647.18 GI:20335444  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 193283)  
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaraturge, H.C., Are, J.R., Ayale, M., Banks, T., Barbaria, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D., Bouay, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,

Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Hawlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogue, M., Hollaway, C., Hollins, B., Homi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulsegged, H., Lotado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Massey, E., Mawhney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rivers, M., Rojas, A., Rojubokan, I., Roife, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoostari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, K., Tang, H., Tansley, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Gibbs, R.

Direct Submission  
Unpublished  
2 (bases 1 to 193283)  
Worley, K.C.  
Direct Submission  
Submitted (19-JAN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 193283)  
Worley, K.C.  
Direct Submission  
Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Apr 28, 2002 this sequence version replaced gi:15809061.  
----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: HAAF  
Center clone name: RP11-455122  
----- Summary Statistics  
Sequencing vector: Plasmid;  
Sequencing vector: M13;  
Chemistry: Dye-terminator Big Dye; 2% of reads  
Chemistry: Dye-terminator Big Dye; 98% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 219180 bases at least Q40  
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Consensus quality: 243367 bases at least Q20  
Estimated insert size: 209025; sum-of-ctgts estimation  
Quality coverage: 10x in Q20 bases; sum-of-ctgts estimation  
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\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
consists of 8 contigs. The true order of the pieces  
is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence.  
\* as soon as it is available and the accession number will  
\* be preserved.

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\* 2134 2233: gap of unknown length  
\* 2234 5400: contig of 3167 bp in length  
\* 5401 5500: gap of unknown length  
\* 5501 7889: contig of 2389 bp in length  
\* 7890 7990: gap of unknown length  
\* 7991 35656: contig of 27667 bp in length  
\* 35657 65617: contig of 29861 bp in length  
\* 65618 65717: gap of unknown length  
\* 65718 104448: contig of 38731 bp in length  
\* 104449 104548: gap of unknown length  
\* 104549 145966: contig of 41418 bp in length  
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BASE COUNT 49273 a 48888 c 46863 g 47544 t 715 others  
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Query Match 93.5%; Score 293.6; DB 2; Length 193283;  
Best Local Similarity 96.8%; Pred. No. 6.1e-56;  
Matches 299; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ATGTCATGTTTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAACACACCTGGGGT 60  
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DB 74771 ATGTCATGTTTAGTGGCTCTCTGTCCTAAAGTGGATGAACGGAACACACCTGGGGT 74712  
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RESULT 10  
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VERSION AF250226.1 GI:9049782  
KEYWORDS  
SOURCE  
ORGANISM  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 6463)  
Wicker, R., Catalan, A.G., Caillieux, A., Starenki, D., Stengel, D.,  
Sarasin, A., and Suarez, H.G.  
Cloning and expression of human adenylyl cyclase type VI in normal

thyroid tissues  
Biochim. Biophys. Acta 1493 (1-2), 279-283 (2000)  
20435313  
PUBMED  
10978539  
2 (bases 1 to 6463)  
Wicker, R., Gascon Catalan, A., Calilleux, A.-F., Starenki, D.,  
Stengel, D., Sarasin, A. and Suarez, H.G.  
Direct Submission  
TITLE  
JOURNAL  
genetic et cancer - 2169, Institut de Recherches sur le Cancer  
CNS IFR 1221, 7 rue Guy Moquet, Villejuif 94801, France  
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GDMIEATSLVRETVGVNVMRVGTHSGRVHCVGLVLRKQFQVDMVNDVTLANHMEAG  
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AKLORANSMEGLMPRPVDRASFRTKDSKRAFQMGIDDSKQNRGQDQALNPEDEV  
DEFUSRAIDANSIDOLRKHVRFLLTFQREDLEKYSRKYDPFRGAYVACALLVFCF  
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BASE COUNT 1264 a 1795 c 1871 g 1533 t  
ORIGIN

Query Match 93.0%; Score 292; DB 9; Length 6463;  
Best Local Similarity 96.4%; Pred. No. 2.3e-55;  
Matches 298; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATGTGATGTTAGTGGCTCTGTGCTTAAAGTGGATGAACGGAACACACCCCTGGGGT 60  
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DB 695 ATGTGATGTTAGTGGCTCTGTGCTTAAAGTGGATGAACGGAACACACCCCTGGGGC 754  
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QY 61 GAACGCAATGGCAGAGGTTTCGGCGGCGCTGCACCTCGGGCAGGTGGCTTCGTCAGC 120  
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DB 755 GAACGCAATGGCAGAGGTTTCGGCGGCGCTGCACCTCGGGCAGGTGGCTTCGTCAGC 814  
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QY 121 CCCCCTATATAGCTGCTTCGGGATGCAGAGCCACCCAGCCACCCCTCGGGGCCCC 180  
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DB 815 CCCCCTATATAGCTGCTTCGGGATGCAGAGCCACCCAGCCACCCCTCGGGGCCCC 874  
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QY 181 CCTCGGTCCTCGCAGATGACGCTTCATCCGGAGGGGGGGCCCGCAGGCGCAG 240  
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DB 875 CCTCGGTCCTCGCAGATGACGCTTCATCCGGAGGGGGGGCCCGCAGGCGCAG 934  
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QY 241 GAACCTGGGCTGGGGCAGTGGCCCTGGCTTCCGAAGATACCGAAGTACACGACACG 300  
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DB 935 GAGCTGGGCTGGGGCAGTGGCCCTGGCTTCCGAAGATACCGAAGTACACGACACG 994  
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QY 301 GCGGGACCG 309  
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DB 995 GCGGGACG 1003  
| | | | |

RESULT 11  
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LOCUS  
DEFINITION  
AC025557  
AC025557.4 GI:7657832  
HTG: HTGS\_PHASE1; HTGS\_DRAFT.  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 171945)  
Waterston, R.H.  
The sequence of Homo sapiens clone  
Unpublished  
2 (bases 1 to 171945)  
Waterston, R.H.  
Direct Submission  
Submitted (10-MAR-2000) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
COMMENT  
On Apr 27, 2000 this sequence version replaced gi:7574970.  
----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu/gsc/index.shtml  
----- Project Information -----  
Center project name: H\_NH0579D07  
----- Summary Statistics -----  
Sequencing vector: M13; 100%  
Chemistry: Dye-terminator Big Dye; 0% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 166140 bases at least Q40  
Consensus quality: 167959 bases at least Q30  
Consensus quality: 168924 bases at least Q20  
Insert size: 177000; agarose-fp  
Insert size: 170345; sum-of-contigs  
Quality coverage: 5.62 in Q20 bases; agarose-fp  
Quality coverage: 5.86 in Q20 bases; sum-of-contigs  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 17 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 1862: contig of 1862 bp in length  
\* 1863 1962: gap of unknown length  
\* 1963 3736: contig of 1774 bp in length  
\* 3737 3836: gap of unknown length  
\* 3837 6925: contig of 3089 bp in length  
\* 6926 7025: gap of unknown length  
\* 7026 11773: contig of 4748 bp in length  
\* 11774 11874: gap of unknown length  
\* 11874 19405: contig of 7532 bp in length  
\* 19406 26329: contig of unknown length  
\* 19506 26429: gap of unknown length  
\* 26330

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* 26430 33594: contig of 7165 bp in length
* 33595 33694: gap of unknown length
* 33695 42148: contig of 8454 bp in length
* 42149 42248: gap of unknown length
* 42249 52390: contig of 10142 bp in length
* 52390 52490: gap of unknown length
* 52491 62388: contig of 9898 bp in length
* 62389 62488: gap of unknown length
* 62489 72508: contig of 9920 bp in length
* 72509 84743: contig of 12235 bp in length
* 84744 84844: gap of unknown length
* 84844 97523: contig of 12679 bp in length
* 97523 97623: gap of unknown length
* 97623 110884: contig of 13262 bp in length
* 110885 110984: gap of unknown length
* 110985 126977: contig of 15993 bp in length
* 126978 127078: gap of unknown length
* 127078 146137: contig of 19060 bp in length
* 146138 146238: gap of unknown length
* 146238 171945: contig of 25708 bp in length.
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## FEATURES

Location/Qualifiers

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Db 79500 GAACGCAATGGGAGAGAGCGTTCCGGGGCGGCTGGCACTCGGGAGGTGGCTTCTGCACG 79441
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Db 79381 CCTCGTCCCTCGGAGGATGACGCTTTCATCCGGAGGGCGGCCCGCCAGGCAAG 79322
Qy 241 GAACGCAATGGGAGAGAGCGTTCCGGGGCGGCTGGCACTCGGGAGGTGGCTTCTGCACG 300
Db 79321 GAACGCAATGGGAGAGAGCGTTCCGGGGCGGCTGGCACTCGGGAGGTGGCTTCTGCACG 79262
Qy 301 GCGGGACCG 309
Db 79261 GCGGGACCG 79253
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## RESULT 12

DOGADENCYC

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

FEATURES

Source

1. 4046

/organism="Canis familiaris"

/db\_xref="taxon:9615"

/tissue\_type="cardiac muscle"

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Length

DB 4;

Pred. No. 6.2e-41;

Score 72.48;

227.4;

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LOCUS I29958 4046 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 1 from patent US 5578481.  
ACCESSION I29958  
VERSION I29958.1 GI:1820749  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 4046)  
AUTHORS Ishikawa,Y.  
TITLE Cloning and characterization of a cardiac adenylyl cyclase  
JOURNAL Patent: US 5578481-A 1 26-NOV-1996;  
LOCATION/Qualifiers  
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BASE COUNT 743 a 1202 c 1257 g 844 t  
ORIGIN

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DB 191 GAACGCAATGGGCGAGAGCGT---CCACGCGCGGACTCGGACGAGTGGCTTCGACG 247  
QY 121 CCCCCGTATATGAGTGGCTCCGGGATGAGAGCCACCCAGCCCTCGGGGCCCC 180  
DB 248 CCCCCGTATATGAGTGGCTCCGGGATGAGAGCCACCCAGTCCCACTCGGGCTCCC 307  
QY 181 CCTCGTGCCCTGGCAGATGAGCGCTTCATCCGGAGGGGGGGCCCGAAGGCGCAAG 240  
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QY 241 GAAGTGGGCTGGGGCGTGGCCCTGGGCTTCGAGATACCGAAG 286  
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RESULT 14  
LOCUS AX305965 5841 bp DNA linear PAT 11-DEC-2001  
DEFINITION Sequence 716 from Patent WO0188188.  
ACCESSION AX305965  
VERSION AX305965.1 GI:17645322  
KEYWORDS house mouse.  
SOURCE Mus musculus  
ORGANISM Mus musculus  
REFERENCE 1  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Euthera; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
JOURNAL I  
SCHOOL Juridical Person Nihon University (JP)  
LOCATION/Qualifiers  
1..5841  
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Best Local Similarity 82.3%; Pred. No. 1.1e-34;  
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QY 61 GAACGCAATGGGCGAGAGCGTTCCGGCGCGCTGGGCACTCGGCGAGTGGCTTCGACG 120  
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QY 121 CCCCCGTATATGAGTGGCTCCGGGATGAGAGCCACCCAGCCCTCGGGGCCCC 180  
DB 213 CCTCGGTACATGAGTGGCTCAAGATGGGAGGCCACCCAGGCCACTCTCTGACGCTAC 272  
QY 181 CCTCGGTGGCTGGGCGAGTGGCTTCATCCGGAGGGGGGGCCCGAAGGCGCAAG 240  
DB 273 ACTCGGTGGCTGGGCGAGTGAAGCTTCATCAGAGAGGGGGGGCCCGGCGAGGGTGTG 332  
QY 241 GAAGTGGGCTGGGCGAGTGGCCCTGGGCTTCGAGATACCGAAGTGAACAAC 293  
DB 333 GAGCTGGGCTGGGCTGAGTGGCTGGGCTTCGAGGACACTGAGGTGACCAC 385

RESULT 15  
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DEFINITION Mouse adenylyl cyclase type VI mRNA, complete cds.  
ACCESSION M93422.1 GI:191690  
VERSION M93422.1  
KEYWORDS adenylyl cyclase; adenylyl cyclase type VI.  
SOURCE Mus musculus cDNA to mRNA.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 5841)  
AUTHORS Yoshimura,M. and Cooper,D.M.  
TITLE Cloning and expression of a Ca(2+)-inhibitable adenylyl cyclase  
from NCB-20 cells  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (15), 6716-6720 (1992)  
MEDLINE 92357702  
PUBMED 1379717  
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ORIGIN
Query Match      63.4%; Score 199.2; DB 10; Length 5841;
Best Local Similarity 82.3%; Pred. No. 1.le-34;
Matches 241; Conservative 0; Mismatches 49; Indels 3; Gaps 1;
QY 1 ATGTCATGCTTTAGTGGCTCCTGCTAAAGTGGATGACGGAACAGCCCTGGGGT 60
Db 96 ATGTCATGCTTTAGTGGCTCCTGCTCCAAAGTGGATGACGGAACAGCTTGGGGG 155
QY 61 GAACGCAATGGCGAGAGCGTTTCGGGGCCGCTGGCACTCGGGGAGTGGCTTCTGCACG 120
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Db 213 CCTCGCTACATGAGCTGCTCAAGAATCGGAGCCACGCCCCACTCCTGCAGCTCAC 272
QY 181 COTCGGTGCCCTGGCAGGATGACGCTTCATCCGGAGGGGGCGCCANGCAAGGGCAAG 240
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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-09-750-240-1

Perfect score: 314

Sequence: 1 atgtcatgttttagtgccct.....acacggcgaggaccgtgaa 314

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Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA.\*

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- 6: /cgn2.6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	295.2	94.0	3549	US-09-008-097-5	Sequence 5, Appl
3	295.2	94.0	4942	US-09-474-076-1	Sequence 1, Appl
4	227.4	72.4	4046	US-07-793-961A-1	Sequence 1, Appl
5	227.4	72.4	4046	US-08-240-357-1	Sequence 1, Appl
6	198.2	63.1	4131	US-08-726-214-11	Sequence 11, Appl
7	38.6	12.3	6503	US-09-404-650-12	Sequence 12, Appl
8	37.6	12.0	4046	US-07-793-961A-1	Sequence 1, Appl
9	37.6	12.0	4046	US-08-240-357-1	Sequence 1, Appl
10	37.2	11.8	668	5498529-5	Patent No. 5498529
11	37.2	11.8	1438	US-08-928-069-5	Sequence 5, Appl
12	37.2	11.8	1438	US-08-828-683A-5	Sequence 5, Appl
13	36.6	11.7	3243	US-08-231-193A-44	Sequence 44, Appl
14	36.6	11.7	3243	US-08-486-273A-44	Sequence 44, Appl
15	36.6	11.7	3243	US-08-480-474-44	Sequence 44, Appl
16	36.6	11.7	3243	US-08-940-086A-44	Sequence 44, Appl
17	36.6	11.7	3243	US-08-940-035A-44	Sequence 44, Appl
18	36.6	11.7	3243	US-08-935-105A-44	Sequence 44, Appl
19	36.6	11.7	3243	US-09-648-797-44	Sequence 44, Appl
20	36.6	11.7	3698	US-08-231-193A-43	Sequence 43, Appl
21	36.6	11.7	3698	US-08-486-273A-43	Sequence 43, Appl
22	36.6	11.7	3698	US-08-480-474-43	Sequence 43, Appl
23	36.6	11.7	3698	US-08-940-086A-43	Sequence 43, Appl
24	36.6	11.7	3698	US-08-940-035A-43	Sequence 43, Appl
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C 40	36.6	11.7	4017	4	US-09-648-797-49	Sequence 49, Appl
C 41	36.6	11.7	4053	2	US-08-231-193A-47	Sequence 47, Appl
C 42	36.6	11.7	4053	2	US-08-486-273A-47	Sequence 47, Appl
C 43	36.6	11.7	4053	3	US-08-480-474-47	Sequence 47, Appl
C 44	36.6	11.7	4053	3	US-08-940-086A-47	Sequence 47, Appl
C 45	36.6	11.7	4053	4	US-08-940-035A-47	Sequence 47, Appl

## ALIGNMENTS

RESULT 1  
US-09-008-097-1  
; Sequence 1, Application US/09008097  
; Patent No. 6306830  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, H. Kirk  
; APPLICANT: Insel, Paul A.  
; APPLICANT: Ping, Peipei  
; APPLICANT: Post, Steven R.  
; APPLICANT: Gao, Meihua  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE  
; TITLE OF INVENTION: HEART FAILURE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FORSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/008,097  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dylan, Tyler M  
; REGISTRATION NUMBER: 37,612  
; REFERENCE/DOCKET NUMBER: 22000-20567.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 314 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 1...312  
; OTHER INFORMATION:

US-09-008-097-1

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Query Match          99.7%; Score 313; DB 4; Length 314;
Best Local Similarity 100.0%; Pred. No. 7.1e-71;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCATGTTTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAAACAGCCTGGGT 60
   |||||||
Db 1 ATGTCATGTTTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAAACAGCCTGGGT 60

QY 61 GAACGCAATGGGAGAGGCTTCGGCGGCGCTGGGACCTCGGACAGTGGCTTCTGCACG 120
   |||||||
Db 61 GAACGCAATGGGAGAGGCTTCGGCGGCGCTGGGACCTCGGACAGTGGCTTCTGCACG 120

QY 121 CCCCCTATATGAGCTTCCTCGGGATGAGAGCCACCCAGCCCTCGGGGCCCC 180
   |||||||
Db 121 CCCCCTATATGAGCTTCCTCGGGATGAGAGCCACCCAGCCCTCGGGGCCCC 180

QY 181 CTTGCGTGGCCCTGGCAGGATGACGCTTCATCCGAGGGGGGCCCAAGGCAAG 240
   |||||||
Db 181 CTTGCGTGGCCCTGGCAGGATGACGCTTCATCCGAGGGGGGCCCAAGGCAAG 240

QY 241 GAACCTGGGCTGGGCGAGTGGCCCTCGGCTTCGAGATACCGAAGTGCACACCG 300
   |||||||
Db 241 GAACCTGGGCTGGGCGAGTGGCCCTCGGCTTCGAGATACCGAAGTGCACACCG 300

QY 301 GCGGGACCGTGAA 314
   |||||||
Db 301 GCGGGACCGTGAA 314
```

RESULT 2

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US-09-008-097-5
; Sequence 5, Application US/09008097
; Patent No. 6306830
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. Kirz
; APPLICANT: Insel, Paul A.
; APPLICANT: Ping, Peipei
; APPLICANT: Post, Steven R.
; APPLICANT: Gao, Melhua
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,097
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dylan, Tyler M
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 22000-20567.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 3549 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...3501
; OTHER INFORMATION:
US-09-008-097-5
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Query Match          94.0%; Score 295.2; DB 4; Length 3549;
Best Local Similarity 97.1%; Pred. No. 3.4e-66;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGTTTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAAACAGCCTGGGT 60
   |||||||
Db 1 ATGTCATGTTTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAAACAGCCTGGGT 60

QY 61 GAACGCAATGGGAGAGGCTTCGGCGGCGCTGGGACCTCGGACAGTGGCTTCTGCACG 120
   |||||||
Db 61 GAACGCAATGGGAGAGGCTTCGGCGGCGCTGGGACCTCGGACAGTGGCTTCTGCACG 120

QY 121 CCCCCTATATGAGCTTCCTCGGGATGAGAGCCACCCAGCCCTCGGGGCCCC 180
   |||||||
Db 121 CCCCCTATATGAGCTTCCTCGGGATGAGAGCCACCCAGCCCTCGGGGCCCC 180

QY 181 CTTGCGTGGCCCTGGCAGGATGACGCTTCATCCGAGGGGGGCCCAAGGCAAG 240
   |||||||
Db 181 CTTGCGTGGCCCTGGCAGGATGACGCTTCATCCGAGGGGGGCCCAAGGCAAG 240

QY 241 GAACCTGGGCTGGGCGAGTGGCCCTCGGCTTCGAGATACCGAAGTGCACACCG 300
   |||||||
Db 241 GAACCTGGGCTGGGCGAGTGGCCCTCGGCTTCGAGATACCGAAGTGCACACCG 300

QY 301 GCGGGACCG 309
   || || ||
Db 301 GCGGGACG 309
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RESULT 3

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US-09-474-076-1
; Sequence 1, Application US/09474076
; Patent No. 6465237
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; TITLE OF INVENTION: CYCLASE
; FILE REFERENCE: 44481-5028-01-US
; CURRENT APPLICATION NUMBER: US/09/474,076
; CURRENT FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4942
; TYPE: DNA
; ORGANISM: human type VI adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(3648)
US-09-474-076-1
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Query Match          94.0%; Score 295.2; DB 4; Length 4942;
Best Local Similarity 97.1%; Pred. No. 3.5e-66;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGTTTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAAACAGCCTGGGT 60
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|||||  
Db 145 ATGTCATGTTTGTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAAAAACAGCTGGGGT 204  
QY 61 GAACGCAATGGGCGAGAGCGTTTCGGCGCGCCGTGGGACACCTGGGACGTGGCTTCTGCACG 120  
Db 205 GAACGCAATGGGCGAGAGCGTTTCGGCGCGCCGTGGGACACCTGGGACGTGGCTTCTGCACG 264  
QY 121 CCCCCTATATAGCTGCTCCGGGATGAGAGCCACCCAGCCACCCCTGGGGGCCCC 180  
Db 265 CCCCCTATATAGCTGCTCCGGGATGAGAGCCACCCAGCCACCCCTGGGGGCCCC 324  
QY 181 CTTCTGGTGGCCCTGGCAGGATGAGCGCTTCATCCGAGGGGGGCCCAAGGCGCAAG 240  
Db 325 CTTCTGGTGGCCCTGGCAGGATGAGCGCTTCATCCGAGGGGGGCCCAAGGCGCAAG 384  
QY 241 GAACCTGGGCTGGGGCAGTGGCCCTGGGCTTCGAGATACCAAGTGAACAGCACCG 300  
Db 385 GAGCTGGGGCTGGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAGGACGCG 444  
QY 301 GCGGGACCG 309  
Db 445 GCGGGACG 453

RESULT 4  
US-07-793-961A-1  
; Sequence 1, Application US/07793961A  
; Patent No. 5334521  
; GENERAL INFORMATION:  
; APPLICANT: Yoshihiro Ishikawa  
; TITLE OF INVENTION: Cloning and Character-  
; TITLE OF INVENTION: ization of a Cardiac Adenylyl Cyclase  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Alan M. Gordon  
; ADDRESSEE: American Cyanamid Company  
; STREET: 1937 West Main Street,  
; CITY: Stamford  
; STATE: Connecticut  
; COUNTRY: USA  
; ZIP: 06904  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC AT  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: ASCII from DW4  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/793,961A  
; FILING DATE: 19911118  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gordon, Alan M.  
; REGISTRATION NUMBER: 30,637  
; REFERENCE/DOCKET NUMBER: 31,705  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 203 321 2719  
; TELEFAX: 203 321 2971  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4046 base pairs listed  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-07-793-961A-1  
Query Match 72.4%; Score 227.4; DB 1; Length 4046;  
Best Local Similarity 89.5%; Pred. No. 4.9e-49;  
Matches 256; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Matches 256; Conservative 0; Mismatches 27; Indels 3; Gaps 1;  
QY 1 ATGTCATGTTTGTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAAAAACAGCTGGGGT 60  
Db 131 ATGTCGTTGTTTGTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAAAAACAGCTGGGGT 190  
QY 61 GAACGCAATGGGCGAGAGCGTTTCGGCGCGCCGTGGGACACCTGGGACGTGGCTTCTGCACG 120  
Db 191 GAACGCAATGGGCGAGAGCGT---CCACGCGCGGGACTCGGACCACTGGCTTCTGCACG 247  
QY 121 CCCCCTATATAGCTGCTCCGGGATGAGAGCCACCCAGCCACCCCTGGGGGCCCC 180  
Db 248 CCCCCTATATAGCTGCTCCGGGATGAGAGCCACCCAGCCACCCCTGGGGGCCCC 307  
QY 181 CTTCTGGTGGCCCTGGCAGGATGAGCGCTTCATCCGAGGGGGGCCCAAGGCGCAAG 240  
Db 308 CTTCTGGTGGCCCTGGCAGGATGAGCGCTTCATCCGAGGGGGGCCCAAGGCGCAAG 367  
QY 241 GAACCTGGGCTGGGGCAGTGGCCCTGGGCTTCGAGATACCAAGTGAACAGCACCG 286  
Db 368 GAGCTGGGGCTGGGGCAGTGGCCCTGGGCTTCGAGGACACTGAGG 413

RESULT 5  
US-08-240-357-1  
; Sequence 1, Application US/08240357  
; Patent No. 5578481  
; GENERAL INFORMATION:  
; APPLICANT: Ishikawa, Yoshihiro  
; TITLE OF INVENTION: Cloning and Characterization of a  
; TITLE OF INVENTION: Cardiac Adenylyl Cyclase  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Cyanamid Company  
; STREET: One Cyanamid Plaza  
; CITY: Wayne  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07470-8426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/240,357  
; FILING DATE: 10-MAY-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gordon, Alan M.  
; REGISTRATION NUMBER: 30,637  
; REFERENCE/DOCKET NUMBER: 31,705-01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-831-3244  
; TELEFAX: 201-831-3305  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4046 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 131...3625  
US-08-240-357-1  
Query Match 72.4%; Score 227.4; DB 1; Length 4046;  
Best Local Similarity 89.5%; Pred. No. 4.9e-49;  
Matches 256; Conservative 0; Mismatches 27; Indels 3; Gaps 1;  
QY 1 ATGTCATGTTTGTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAAAAACAGCTGGGGT 60  
|||||



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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII from DW4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/793,961A
; FILING DATE: 19911118
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,705
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203 321 2719
; TELEFAX: 203 321 2971
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4046 base pairs listed
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-07-793-961A-1

```

```

Query Match 12.0%; Score 37.6; DB 1; Length 4046;
Best Local Similarity 49.2%; Pred. No. 0.52;
Matches 97; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 90 CCGTGGCACTCGGCGAGTGGCTTCTGACAGCCCGCTATATGAGCTGCTCGGGGATGC 149
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 462 CCGGGGGTCCAGTCCAGGGCCACCTCCAGTGCCTCCCAACCGCTGACATGGCTCAGTGTCC 403

QY 150 AGAGCCACCCAGCCCGCCCTCGGGGCGCCCTCGGTGCGCCCTGGCAGGATGACGCCCTT 209
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 402 TCGAGCCCGAGGGCCCGCCGACGCGCCAGCTCGTCCCTTGGCCGGGCGCTCTC 343

QY 210 CATCCGGAGGGCGGGCCCGCCAGCAAGGAAGTGGGGCTGCGGGCAGTGGCCCTGGG 269
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 342 CGGATGAAGGCGCTCATCTCTGCCAGGGGCGCCAGGGGGGAGCCGCGAGGCTGGG 283

QY 270 CTTGGAAGATACCGAG 286
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 282 GGCTGGCATCCGGAG 266

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RESULT 9
US-08-240-357-1/c
; Sequence 1, Application US/08240357
; Patent No. 5578481
; GENERAL INFORMATION:
; APPLICANT: Ishikawa, Yoshihiro
; TITLE OF INVENTION: Cloning and Characterization of a
; TITLE OF INVENTION: Cardiac Adenyllyl Cyclase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/240,357
; FILING DATE: 10-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,705-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4046 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 131..3625
; US-08-240-357-1

```

```

Query Match 12.0%; Score 37.6; DB 1; Length 4046;
Best Local Similarity 49.2%; Pred. No. 0.52;
Matches 97; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 90 CCGTGGCACTCGGCGAGTGGCTTCTGACAGCCCGCTATATGAGCTGCTCGGGGATGC 149
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 462 CCGGGGGTCCAGTCCAGGGCCACCTCCAGTGCCTCCCAACCGCTGACATGGCTCAGTGTCC 403

QY 150 AGAGCCACCCAGCCCGCCCTCGGGGCGCCCTCGGTGCGCCCTGGCAGGATGACGCCCTT 209
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 402 TCGAGCCCGAGGGCCCGCCGACGCGCCAGCTCGTCCCTTGGCCGGGCGCTCTC 343

QY 210 CATCCGGAGGGCGGGCCCGCCAGCAAGGAAGTGGGGCTGCGGGCAGTGGCCCTGGG 269
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 342 CGGATGAAGGCGCTCATCTCTGCCAGGGGCGCCAGGGGGGAGCCGCGAGGCTGGG 283

QY 270 CTTGGAAGATACCGAG 286
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 282 GGCTGGCATCCGGAG 266

```

```

RESULT 10
5498529-5
; Patent No. 5498529
; APPLICANT: BERKA, THOMAS R.; FERNWALD, JAMES A.; GORNIAK,
; JOSEFINA G.; ROSENBERG, MARTIN; STRICKLER, JAMES E.; TAYLOR, DEAN P.
; TITLE OF INVENTION: PROTEIN PROTEASE INHIBITORS FROM
; STREPTOMYCES
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,506
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 894,167
; FILING DATE: 03-JUN-1992
; APPLICATION NUMBER: 346,119
; FILING DATE: 16-FEB-1989
; APPLICATION NUMBER: 897,245
; FILING DATE: 18-AUG-1986
; SEQ ID NO: 5
; LENGTH: 668
5498529-5

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Query Match 11.8%; Score 37.2; DB 6; Length 668;
Best Local Similarity 49.4%; Pred. No. 0.49;
Matches 126; Conservative 0; Mismatches 121; Indels 8; Gaps 1;

QY 57 GGGTGAACCAATGGCGAAGCGTTTCGGGGCGCCGCTGGCAGTTCGGGCGAGGTGCTTCG 116
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 130 GGATGACACAATGGCGAAGCGCGCTGGGCGAGCCACCTCGCCCTCAGGCGCACGG 189

```

QY 117 CAGCGCCCGCTATATGAGTGGCTCCGGGATGAGAGCCACCCAGCCCGCTCGCGG 176  
Db 190 CGGTCTGCG-----GACCCCTCACCAGGCGCGCTCGCCACCCCGCGCTGCTGG 241  
QY 177 CCCCCCTGGTGGCCCTGGCAGGATGAGCCCTTCATCCGGAGGGGCGGCCAAGG 236  
Db 242 GGCCTCGCTCTACGCCCTCGGCCCTGGCCCTGGTGTCACTCCGTCGCGCCACGCGCAAGCGCGC 301  
QY 237 CAAGGAACCTGGGCTCGGGGAGTGGCCCTGGCTTCGAAGTACCGAAGTGCACAAACG 296  
Db 302 CCCCCCGCGCTCGCGGCGGTCACTTGAAGTGCAGCGCGCGCTCGCGGCGCTCGCGGAAACCA 361  
QY 297 ACCGGCGGACCGCT 311  
Db 362 TCCGGCCGCGNCCT 376

## RESULT 11

US-08-928-069-5/c  
; Sequence 5, Application US/08928069  
; Patent No. 6462176  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: Apo-3 POLYPEPTIDE  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/928,069  
; FILING DATE: 11-Sep-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/026943  
; FILING DATE: 09/23/1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P1052R1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/952-9881  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1438 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
US-08-928-069-5

Query Match 11.8%; Score 37.2; DB 4; Length 1438;  
Best Local Similarity 47.6%; Pred. No. 0.55;  
Matches 108; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 78 CGCTTCGGCGCGCTGACCTCGGCAGTGGCTTCGACGCGCCCGCTATATGAGCTG 137  
Db 392 CGCGCGCTGCTCCATAGCCCTCCGACGGGCGCCAGGGGCTCCCGGCTCCGCTCTC 333  
QY 138 CTTCCGGGATGACAGAGCCAGCCACCCCTCGGGCGCCCTCGGTGCCCTGCA 197  
Db 332 TGCCGCTGCTGCTTCAGCCCTTCAGCCCGCGCGCGCGCGCGCGCTCGAGA 273  
QY 198 GGATGACGCTTCATCCGAGGGGGCGCCANGCAAGGCAAGTGGGTGCGGGC 257  
Db 272 AGGGCCCGCTTCGGGGCGGGGAGGCGGCGCGCGCGCGCGCGCTAGCTAGCT 213  
QY 258 AGTGGCCCTGGCTTCGAGATACCGAAGTGACACGACACCGCGG 304  
Db 212 GTGCCCCCTCTGCTCGGCTAGACCTGAGCTCATTAGCGCGCAGCGG 166

Db 272 AGGCGCCCGCTGGCGGGGAGGGGCGCGCGCGCGCGCGCGCGCGCGCGCG 213  
QY 258 AGTGGCCCTGGCTTCGAGATACCGAAGTGACACGACACCGCGGG 304  
Db 212 GTGCCCCCTCTGCTCGGCTAGACCTGAGCTCATTAGCGCGCAGCGG 166

## RESULT 12

US-08-828-683A-5/c  
; Sequence 5, Application US/08828683A  
; Patent No. 6469144  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/828,683A  
; FILING DATE: 31-Mar-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/625328  
; FILING DATE: 1-Apr-1996  
; APPLICATION NUMBER: 08/710802  
; FILING DATE: 23-Sep-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P1007P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1438 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-08-828-683A-5

Query Match 11.8%; Score 37.2; DB 4; Length 1438;  
Best Local Similarity 47.6%; Pred. No. 0.55;  
Matches 108; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 78 CGCTTCGGCGCGCTGACCTCGGCAGTGGCTTCGACGCGCCCGCTATATGAGCTG 137  
Db 392 CGCGCGCTGCTCCATAGCCCTCCGACGGGCGCCAGGGGCTCCCGGCTCCGCTCTC 333  
QY 138 CTTCCGGGATGACAGAGCCAGCCACCCCTCGGGCGCCCTCGGTGCCCTGCA 197  
Db 332 TGCCGCTGCTGCTTCAGCCCTTCAGCCCGCGCGCGCGCGCGCTCGAGA 273  
QY 198 GGATGACGCTTCATCCGAGGGGGCGCCANGCAAGGCAAGTGGGTGCGGGC 257  
Db 272 AGGGCCCGCTTCGGGGCGGGGAGGCGGCGCGCGCGCGCGCTAGCTAGCT 213  
QY 258 AGTGGCCCTGGCTTCGAGATACCGAAGTGACACGACACCGCGG 304  
Db 212 GTGCCCCCTCTGCTCGGCTAGACCTGAGCTCATTAGCGCGCAGCGG 166



Db 2686 CAGCGGGGCCGTGCAACCCAGCGGCGACGAGCTG 2651

RESULT 14  
US-08-486-273A-44/C  
; Sequence 44, Application US/08486273A  
; Patent No. 5985586  
; GENERAL INFORMATION:  
; APPLICANT: Daggett, Lorrie P.  
; APPLICANT: Ellis, Steven B.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lu, Chin-Chun  
; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA  
; TITLE OF INVENTION: ENCODING SAME AND USES THEREFOR  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,273A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/231,193  
; FILING DATE: 20-APR-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 6362-9383B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-238-0999  
; TELEFAX: 619-238-0062  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3243 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 1...3243  
US-08-486-273A-44

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	Matches 126;	Conservative 0;	Mismatches 150;	Indels 0;	Gaps 0;
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Db	2866	CAGACAGCCCCCAGCACAAATGGCAGTGGCGGTGGCGCTGCAGGCAGACGTGCTGCTG	2807		
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Db	2806	TGCTGCCAGGGGGGGGCCCTCGCTGTCTGCGCCCTCTCGGAGGGCCTCCCCGATAGTCGG	2747		
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; Sequence 44, Application US/08480474  
; Patent No. 6033865  
; GENERAL INFORMATION:  
; APPLICANT: Daggett, Lorrie P.  
; APPLICANT: Ellis, Steven B.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lu, Chin-Chun  
; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, DNA ENCODING  
; TITLE OF INVENTION: SAME AND USES THEREFOR  
; NUMBER OF SEQUENCES: 54  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,474  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 6362-9382B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-238-0999  
; TELEFAX: 619-238-0062  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3243 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 1...3243  
US-08-480-474-44

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Best Local Similarity 45.7%; Pred. No. 0.89;  
Matches 126; Conservative 0; Mismatches 150; Indels 0; Gaps 0;  
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| | | | | | | | | | | | | | | | | | | | | |

QY 253 CGGGCAGTGGCCCTGGCTTCGAAGATACCGAAGTG 288  
| | | | | | | | | | | | | | | | | | | | | |  
Db 2686 CAGGGGGGCCGGTGCACCCAGCGGCGAGAGCTG 2651

Search completed: March 1, 2003, 04:04:35  
Job time : 18.6909 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 1, 2003, 02:24:48 ; Search time 12.892 Seconds  
(without alignments)  
15188.998 Million cell updates/sec

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Title: US-09-750-240-1
Perfect score: 314
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 460893 seqs, 311809382 residues  
Total number of hits satisfying chosen parameters: 921786

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

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4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:**
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:**
6: /cgn2_6/ptodata/2/pubpna/PCRT05_PUBCOMB.seq:**
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:**
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9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:**
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:**
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:**
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:**
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:**
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:**
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## SUMMARIES

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		Match	Length	DB		
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2	295.2	94.0	3549	10	US-09-750-240-5	Sequence 5, Appli
3	295.2	94.0	3552	10	US-09-750-240-10	Sequence 10, Appli
4	295.2	94.0	3582	10	US-09-750-240-12	Sequence 12, Appli
5	295.2	94.0	4942	9	US-10-201-000-1	Sequence 1, Appli
6	163.4	52.0	358	9	US-09-933-797-165	Sequence 165, App
7	94.6	30.1	220	10	US-09-728-445-487	Sequence 487, App
C 8	38.6	12.3	6503	10	US-09-935-541-12	Sequence 12, Appli
C 9	37.2	11.8	1438	9	US-10-081-180-5	Sequence 5, Appli
C 10	37.2	11.8	1438	9	US-10-112-793-5	Sequence 5, Appli
C 11	37.2	11.8	1438	9	US-10-112-193-5	Sequence 5, Appli
C 12	37.2	11.8	1438	10	US-09-884-733-5	Sequence 5, Appli
C 13	37.2	11.8	1438	10	US-09-993-234-5	Sequence 5, Appli
C 14	36.6	11.7	3243	9	US-09-945-901-44	Sequence 44, Appli
C 15	36.6	11.7	3243	9	US-10-007-747-44	Sequence 44, Appli
C 16	36.6	11.7	3243	9	US-10-038-937-44	Sequence 44, Appli
C 17	36.6	11.7	3698	9	US-09-945-901-43	Sequence 43, Appli
C 18	36.6	11.7	3698	9	US-10-007-747-43	Sequence 43, Appli
C 19	36.6	11.7	3698	9	US-10-038-937-43	Sequence 43, Appli

## ALIGNMENTS

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RESULT 1
US-09-750-240-1
; Sequence 1, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 314
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(314)
; OTHER INFORMATION: n = A,T,C or G
US-09-750-240-1

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Query Match 99.7%; Score 313; DB 10; Length 314;  
Best Local Similarity 100.0%; Pred. No. 2.2e-73;  
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 61 GAACGCAATGGCAGAGCGTTCCGGCGCGTGGCACTCGGCAGGTGGCTTCTGCACG 120
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Qy 121 CCCGCTATATAGTGGCTCCGGGATGCAGAGCCACCCAGCCACCCCTGCGGGCCCC 180
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Db 121 CCCGCTATATAGTGGCTCCGGGATGCAGAGCCACCCAGCCACCCCTGCGGGCCCC 180
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Qy 181 CCTCGGTGCCCTGGCAGATGACGCCCTTTCATCCGGAGGGCGCCCGCCANGCAAGGCAAG 240
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## RESULT 2

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US-09-750-240-5
; Sequence 5, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3549
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-240-5
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Query Match 94.0%; Score 295.2; DB 10; Length 3549;  
Best Local Similarity 97.1%; Pred. No. 1.6e-68;  
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy 61 GAACGCAATGGCAGAGCGTTCCGGCGCGTGGCACTCGGCAGGTGGCTTCTGCACG 120
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Db 301 GCGGGACG 309
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RESULT 3
US-09-750-240-10
; Sequence 10, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 3552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-240-10
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Query Match 94.0%; Score 295.2; DB 10; Length 3552;  
Best Local Similarity 97.1%; Pred. No. 1.6e-68;  
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy 61 GAACGCAATGGCAGAGCGTTCCGGCGCGTGGCACTCGGCAGGTGGCTTCTGCACG 120
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Db 61 GAACGCAATGGCAGAGCGTTCCGGCGCGTGGCACTCGGCAGGTGGCTTCTGCACG 120
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Qy 121 CCCGCTATATAGTGGCTCCGGGATGCAGAGCCACCCAGCCACCCCTGCGGGCCCC 180
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Db 121 CCCGCTATATAGTGGCTCCGGGATGCAGAGCCACCCAGCCACCCCTGCGGGCCCC 180
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Qy 181 CCTCGGTGCCCTGGCAGATGACGCCCTTTCATCCGGAGGGCGCCCGCCANGCAAGGCAAG 240
|||
Db 181 CCTCGGTGCCCTGGCAGATGACGCCCTTTCATCCGGAGGGCGCCCGCCANGCAAGGCAAG 240
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Qy 241 GAACCTGGGGCTCGGGCAGTGGCCCTGGCTTCGAAGATACCGAGTGCACACGACACCG 300
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Db 241 GAGCTGGGGCTCGGGCAGTGGCCCTGGCTTCGAGGATACCGAGTGCACACGACACCG 300
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Qy 301 GCGGGACCG 309
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Db 301 GCGGGACG 309
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RESULT 4
US-09-750-240-12
; Sequence 12, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P. A.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 3582
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified AC-VI
US-09-750-240-12

Query Match          94.0%; Score 295.2; DB 10; Length 3582;
Best Local Similarity 97.1%; Pred. No. 1.6e-68;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGTTTAGTGGCTCTCGTCCCTAAAGTGGATGAACGGAACACGCTGGGGT 60
Db 22 ATGTCATGTTTAGTGGCTCTCGTCCCTAAAGTGGATGAACGGAACACGCTGGGGT 81

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Db 142 CCCCCTATATAGCTGCTCCGGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 201

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Db 202 CTTGGTGGCTTGGCAGGATGACGCTTTCATCCGGAGGGGGGCCCCANGCAAGGCAAG 261

QY 241 GACTGGGGCTCGGGCAGTGGCCCTTTCGAGATACCGAAGTACACGACGACGCG 300
Db 262 GACTGGGGCTCGGGCAGTGGCCCTTTCGAGATACCGAAGTACACGACGACGCG 321

QY 301 GCGGGACCG 309
Db 322 GCGGGACG 330

RESULT 5
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; Sequence 1, Application US/10201000
; Publication No. US20020187540A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; APPLICANT: COR Therapeutics, Inc.
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; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; TITLE OF INVENTION: CYCLASE
; FILE REFERENCE: 44481-5028-01-US
; CURRENT APPLICATION NUMBER: US/10/201,000
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US/09/474,076
; PRIOR FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 607830,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/866,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4942
; TYPE: DNA
; ORGANISM: human type VI adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(3648)
US-10-201-000-1

Query Match          94.0%; Score 295.2; DB 9; Length 4942;
Best Local Similarity 97.1%; Pred. No. 1.7e-68;
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGTCATGTTTAGTGGCTCTCGTCCCTAAAGTGGATGAACGGAACACGCTGGGGT 60
Db 145 ATGTCATGTTTAGTGGCTCTCGTCCCTAAAGTGGATGAACGGAACACGCTGGGGT 204

QY 61 GAACGCAATGGGCAAGCGTTTCGGGGCCGCTGGCACTCGGGCAGGTGGCTTCGCACG 120
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QY 121 CCCCCTATATAGCTGCTCCGGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 180
Db 265 CCCCCTATATAGCTGCTCCGGGATGCAGAGCCACCCAGCCCTCGGGGCCCC 324

QY 181 CTTGGTGGCTTGGCAGGATGACGCTTTCATCCGGAGGGGGGCCCCANGCAAGGCAAG 240
Db 325 CTTGGTGGCTTGGCAGGATGACGCTTTCATCCGGAGGGGGGCCCCANGCAAGGCAAG 384

QY 241 GACTGGGGCTCGGGCAGTGGCCCTTTCGAGATACCGAAGTACACGACGACGCG 300
Db 385 GACTGGGGCTCGGGCAGTGGCCCTTTCGAGATACCGAAGTACACGACGACGCG 444

QY 301 GCGGGACCG 309
Db 445 GCGGGACG 453

RESULT 6
US-09-933-797-165
; Sequence 165, Application US/09933797
; Patent No. US20020155119A1
; GENERAL INFORMATION:
; APPLICANT: Robert A. Sikes et al.
; TITLE OF INVENTION: Isolation and Use of Fetal Urogenital
; TITLE OF INVENTION: Sinus Expressed Sequences
; FILE REFERENCE: 9901-007-999
; CURRENT APPLICATION NUMBER: US/09/933,797
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US/09/482,933
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: PCT/US99/10746
; PRIOR FILING DATE: 1999-05/14
; PRIOR APPLICATION NUMBER: 60/085,383
; PRIOR FILING DATE: 1998-05-14
; NUMBER OF SEQ ID NOS: 811
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 165
```

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; LENGTH: 358
; TYPE: DNA
; ORGANISM: Murine
US-09-933-797-165

Query Match      52.0%; Score 163.4; DB 9; Length 358;
Best Local Similarity 83.1%; Pred. No. 3.7e-34;
Matches 196; Conservative 2; Mismatches 35; Indels 3; Gaps 1;

Qy 1 ATGTCATGTTTAGTGGCTCTCTGTCCTAAAGTGGATGAACGAAACAGCCTGGGGT 60
    |||||
Db 123 ATGTCATGTTTAGTGGCTCTCTGTCCTAAAGTGGATGAACGAAACAGCCTGGGG 182
    |||||

Qy 61 GAACCAATGGGAGAACGCTTCGGCGCGTGGCACTCGGCGAGGTGGCTTCTGCACG 120
    |||||
Db 183 GAACCAATGGGAGAACG--CCACGCCACGGAATCAGCAGTGGCTTCTGCVCAC 239
    |||||

Qy 121 CCCGCTATATGAGTGGCTCTCGGGATGCAGAGCCACCCAGCCACCCCTGGGGCCCC 180
    |||||
Db 240 CTTGCTATATGAGTGGCTCTCAAGAAATCGGAGGCCACCCAGCCCACTCTCTGCAGCTCAC 299
    |||||

Qy 181 CTTGCTGTCCTCGGAGATGAGCCTTCATCCGGAGGGCGGCCCAAGCAAGGG 236
    |||||
Db 300 ACTCGTGTCCTCGAGATGAAGCCTTCATCAGGAGGGCGGCCCGGCGAGGG 355

RESULT 7
US-09-728-445-487
; Sequence 487, Application US/09728445
; Patent No. US20020102543A1
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020102543alel Mutated Mammalian Cells and
; TITLE OF INVENTION: Animals
; FILE REFERENCE: LEX-0102-USA
; CURRENT APPLICATION NUMBER: US/09/728,445
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/168,358
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 891
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 487
; LENGTH: 220
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-728-445-487

Query Match      30.1%; Score 94.6; DB 10; Length 220;
Best Local Similarity 84.4%; Pred. No. 3.6e-16;
Matches 119; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

Qy 1 ATGTCATGTTTAGTGGCTCTCTGTCCTAAAGTGGATGAACGAAACAGCCTGGGGT 60
    |||||
Db 67 ATGTCATGTTTAGTGGCTCTCTGTCCTCCCAAGTGGATGAACGAAACAGCCTGGGG 126
    |||||

Qy 61 GAACCAATGGGAGAACGCTTCGGCGCGTGGCACTCGGCGAGGTGGCTTCTGCACG 120
    |||||
Db 127 GAACCAATGGGAGAACG--CCACGCCACGGAATCAGCAGTGGCTTCTGCACG 183
    |||||

Qy 121 CCCGCTATATGAGTGGCTC 141
    |||||
Db 184 CTTGCTATATGAGTGGCTC 204
    |||||

RESULT 8
US-09-935-541-12/c
; Sequence 12, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
```

```
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 6503
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-935-541-12

Query Match      12.3%; Score 38.6; DB 10; Length 6503;
Best Local Similarity 55.2%; Pred. No. 0.31;
Matches 74; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 141 CCGGGATGCAGAGCCACCCAGCCGCCCTGCGGGGCCCTCGGTGCGCCCTGGCAGGA 200
    |||||
Db 173 CCGCGCTGGAGAGGACCCCGCGCCCGCCGCGCCCTCGGATTCGGGATCCGGGATCAGCT 114
    |||||

Qy 201 TGACGCTTATCCGAGGCGCGCCGCGCCANGCAAGGCAAGAACTGGGGCTGCGGGCAGT 260
    |||||
Db 113 GCGCCCGCGGGGAGGGGAGCGGCGATGCAAGGCGCGGCCCGCGGGCGCGGCCAT 54
    |||||

Qy 261 GGCCTGGGCTTCG 274
    |||||
Db 53 GCGGGCGGGTCCG 40
    |||||

RESULT 9
US-10-081-280-5/c
; Sequence 5, Application US/10081280
; Patent No. US20020165157A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/081,280
; FILING DATE: 21-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,270
; FILING DATE: 31-Mar-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: PI007R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1438 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
```

```
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-081-280-5

Query Match      11.8%; Score 37.2; DB 9; Length 1438;
Best Local Similarity 47.6%; Pred. No. 0.55;
Matches 108; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 78 GCGTTCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACGCCCGCGCTATATGAGCTG 137
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 392 GCGGCGCTGCTCCATAGCCCTCCGACGGGCGCCAGGGGCTTCCCGGCTCCGTGCTCTC 333
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 138 CTTCCGGGATGACAGACCCACCCAGCCCTGCGGGCGCCCTGCGGTGCGCCCTGGCA 197
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 332 TGCCCGCTCGTGGTTCGCTTACAGCCCGCGGCGCCGAGGCGCCCGCGCGCTCGAGA 273
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 198 GGATGACGCTTATCCGAGGGGCGGCCANGCAGGCAAGAACTGGGCTGCGGGC 257
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 272 AGGGCGCGCTGCGGGCGGGGAGGCGGGCGCCGAGCCGCGCGCGCGTCCGAGA 213
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 258 AGTGGCCCTGCGGTTCGAAGATACCAAGTGACAACGACACCGCGG 304
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 212 GTGCCCTCTGCTCGGCTAGACCTGAGCTCATTTAGGCGGACGCG 166
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 10
US-10-112-793-5/c
; Sequence 5, Application US/10112793
; Publication NO. US20020192729A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,793
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,683A
; FILING DATE: 31-Mar-1997
; APPLICATION NUMBER: 08/625328
; FILING DATE: 1-Apr-1996
; APPLICATION NUMBER: 08/710802
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1438 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-112-793-5

Query Match      11.8%; Score 37.2; DB 9; Length 1438;
Best Local Similarity 47.6%; Pred. No. 0.55;
```

```
Matches 108; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 78 GCGTTCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACGCCCGCGCTATATGAGCTG 137
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 392 GCGGCGCTGCTCCATAGCCCTCCGACGGGCGCCAGGGGCTTCCCGGCTCCGTGCTCTC 333
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 138 CTTCCGGGATGACAGACCCACCCAGCCCTGCGGGCGCCCTGCGGTGCGCCCTGGCA 197
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 332 TGCCCGCTCGTGGTTCGCTTACAGCCCGCGGCGCCGAGGCGCCCGCGCGCTCGAGA 273
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 198 GGATGACGCTTATCCGAGGGGCGGCCANGCAGGCAAGAACTGGGCTGCGGGC 257
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 272 AGGGCGCGCTGCGGGCGGGGAGGCGGGCGCCGAGCCGCGCGCGTCCGAGA 213
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 258 AGTGGCCCTGCGGTTCGAAGATACCAAGTGACAACGACACCGCGG 304
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 212 GTGCCCTCTGCTCGGCTAGACCTGAGCTCATTTAGGCGGACGCG 166
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
US-10-112-193-5/c
; Sequence 5, Application US/10112193
; Publication NO. US20030004313A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-3 POLYPEPTIDE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,193
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/928,069
; FILING DATE: 11-Sep-1997
; APPLICATION NUMBER: 60/026943
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1052R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1438 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-112-193-5

Query Match      11.8%; Score 37.2; DB 9; Length 1438;
Best Local Similarity 47.6%; Pred. No. 0.55;
Matches 108; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 78 GCGTTCGGCGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACGCCCGCGCTATATGAGCTG 137
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 392 GCGGCGCTGCTCCATAGCCCTCCGACGGGCGCCAGGGGCTTCCCGGCTCCGTGCTCTC 333
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 138 CTTCCGGGATGACAGACCCACCCAGCCCTGCGGGCGCCCTGCGGTGCGCCCTGGCA 197
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 392 GCGGCGCTGCTCCATAGCCCTCCGACGGGCGCCAGGGGCTTCCCGGCTCCGTGCTCTC 333
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 138 CTTCCGGGATGACAGACCCACCCAGCCCTGCGGGCGCCCTGCGGTGCGCCCTGGCA 197
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```





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RESULT 15
US-10-007-747-44/c
; Sequence 44, Application US/10007747
; Patent No. US20020161193A1
; GENERAL INFORMATION:
; APPLICANT: Daggett, Lorrie P.
; Ellis, Steven B.
; Liaw, Chen W.
; Lu, Chin-Chun
; TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/007,747
; FILING DATE: 07-Dec-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/648,797
; FILING DATE: 28-Aug-2000
; APPLICATION NUMBER: US/08/940,086A
; FILING DATE: 29-SEPT-97
; APPLICATION NUMBER: US 08/231,193
; FILING DATE: 20-APR-1994
; APPLICATION NUMBER: US 08/052,449
; FILING DATE: 20-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9383C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 450-8400
; TELEFAX: (619) 450-8499
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3243 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...3243
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-007-747-44

Query Match      11.7%; Score 36.6; DB 9; Length 3243;
Best Local Similarity 45.7%; Pred. No. 0.92;
Matches 126; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY   13 AGTGGCTTCCTGTTCCCTAAAGTGATGAACGSAACAACAGCGCTGGGTGCAACCAATGGG 72
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   2926 AGAGCCCCCAGGCCGCCGAGGAGCGAGCGAGCGCGTGTCTCACAGGGTGAAGGTGAGGA 2867
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY   73 CAGAAGCGTTCGCGGCCTGCTACTCGGCGAGGTGGCTTCTGTACGCGCCCCCATATG 132
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   2866 CAGACAGCCCCCAGCACAAATGGCAGGTGGCGTGGCGTGCAGGCAGACGCTCTGCTG 2807
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY   133 AGCTGCTTCGGGATGACAGACCACCCAGCCCCCCCCTGCGGGCCCCCTCGGTGCCCC 192
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   2806 TGCTGCCAGGCGGGGGCCCCCTGCTGCTCGCCCTCTTGGCAGGCGCTCCCGGTAGATCGGC 2747
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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```
Qy 193 TGGCAGGATGACGCTTTCATCCGGAGGGGGGCCCCANGCAAGGGCAAGGAACTGGGGCTG 252
    ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2746 AAGCACATCGACTGGGCTGGCCCAAGGCCTGCAAGGCCGAGTGGCCGTCGGGGCGGGCG 2687
    ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 253 CGGCAGTGGCCCTGGGGCTTCGAAGATACCGAAGTG 288
    { ||| | | | | | | | | | | | | | | | | |
Db 2686 CAGGGGGGGCGGTGCACCCAGCGGGCAGCGAGCTG 2651
    { ||| | | | | | | | | | | | | | | | | |
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Search completed: March 1, 2003, 09:03:39  
Job time : 19.892 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 23:39:42 ; Search time 46.5329 Seconds  
(without alignments)  
11498.584 Million cell updates/sec

Title: US-09-750-240-1

Perfect score: 314

Sequence: 1 atgtcatgttttagtgccct.....acacggcgggaccgctgaa 314

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3936061 seqs, 852009584 residues

Total number of hits satisfying chosen parameters: 7872122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_NA\_New.\*  
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2: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq.\*  
3: /cgn2\_6/ptodata/2/pna/US07\_NEW\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/pna/US08\_NEW\_COMB.seq.\*  
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6: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq.\*  
7: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	295.2	94.0	1386	1	PCT-US02-36759-83
2	199.2	63.4	5826	6	US-10-144-771-5921
3	39.8	12.7	36303	6	US-10-152-724-24
4	39.8	12.7	36303	6	US-10-152-724A-24
5	38.2	12.2	1878	5	US-09-724-676-33617
6	38.2	12.2	1878	5	US-09-724-676A-33617
7	38.2	12.2	3174	6	US-10-218-140-5849
8	38.2	12.2	3182	5	US-09-724-676-33618
9	38.2	12.2	3182	5	US-09-724-676A-33618
10	36.6	11.7	1542	1	PCT-US02-38526-349
11	36.6	11.7	2216	1	PCT-US02-38526-347
12	36.4	11.6	485	5	US-09-585-645A-59
13	36	11.5	22118	6	US-10-287-313-16
14	35.8	11.4	1824	5	US-09-724-676-45770
15	35.8	11.4	1824	5	US-09-724-676A-45770
16	35.2	11.2	2883	6	US-10-125-923A-157
17	35.2	11.2	2883	6	US-10-205-892-157
18	35.2	11.2	2883	6	US-10-174-575-157
19	35.2	11.2	2883	6	US-10-174-575A-157
20	35.2	11.2	2883	6	US-10-015-610A-23
21	35.2	11.2	2883	6	US-10-226-254A-23
22	35.2	11.2	2883	6	US-10-187-755-157
23	35.2	11.2	2883	6	US-10-187-749-157
24	35.2	11.2	2883	6	US-10-017-253A-23
25	35.2	11.2	2883	6	US-10-199-672-157
26	35.2	11.2	2883	6	US-10-194-486-157

Sequence 3, Appli  
Sequence 3, Appli  
Sequence 65, Appli  
Sequence 21648, A  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 23402, A  
Sequence 319, App  
Sequence 179, App  
Sequence 179, App  
Sequence 66, Appli  
Sequence 17257, A  
Sequence 26872, A  
Sequence 143, App  
Sequence 143, App  
Sequence 1374, Ap  
Sequence 14604, A  
Sequence 14604, A

#### ALIGNMENTS

#### RESULT 1

PCT-US02-36759-83

; Sequence 83, Application PC/TUS0236759

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: DUGGAN, Brendan M.

; APPLICANT: YANG, Junming

; APPLICANT: GIETZEN, Kimberly J.

; APPLICANT: LEE, Soo Yeun

; APPLICANT: TANG, Y. Tom

; APPLICANT: AZIMZAI, Yalda

; APPLICANT: WALIA, Narinder K.

; APPLICANT: WARREN, Bridget A.

; APPLICANT: BARROSO, Ines

; APPLICANT: BECHA, Shanya D.

; APPLICANT: YUE, Henry

; APPLICANT: LEHR-MASON, Patricia M.

; APPLICANT: THANGAVELU, Kavitha

; APPLICANT: LEE, Sally

; APPLICANT: EMERLING, Brooke M.

; APPLICANT: KABLE, Amy E.

; APPLICANT: KHARE, Reena

; APPLICANT: BAUGHN, Mariah R.

; APPLICANT: GANDHI, Ameena R.

; APPLICANT: TRAN, Uyen K.

; APPLICANT: RICHARDSON, Thomas W.

; APPLICANT: MARQUIS, Joseph P.

; APPLICANT: LAL, Preeti G.

; APPLICANT: FORSYTHE, Ian J.

; APPLICANT: LEE, Ernestine A.

; APPLICANT: SWARNAKAR, Anita.

; APPLICANT: KALLICK, Deborah A.

; APPLICANT: GRIFFIN, Jennifer A.

; APPLICANT: ELLIOTT, Vicki S.

; APPLICANT: GORVAD, Ann E.

; APPLICANT: HAFALIA, April J.A.

; APPLICANT: ISON, Craig H.

; APPLICANT: JIN, Pei

; APPLICANT: JIANG, Xin

; APPLICANT: JACKSON, Alan

; APPLICANT: BHATIA, Umesh

; APPLICANT: BURRILL, John D.

; APPLICANT: BLAKE, Julie J.

; APPLICANT: HO, Ann

; APPLICANT: ZHENG, Wenjin

; APPLICANT: GAO, Jing

; TITLE OF INVENTION: RECEPTORS AND MEMBRANE-ASSOCIATED PROTEINS

; FILE REFERENCE: PF-1279 PCT

; CURRENT APPLICATION NUMBER: PCT/US02/36759

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; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 60/333,097
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,274
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/340,542
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/342,166
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/347,580
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: US 60/348,687
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PERL Program
; SEQ ID NO 83
; LENGTH: 1386
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 7506194CB1
PCT-US02-36759-83

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Best Local Similarity 97.1%; Pred. No. 1.6e-65;
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Qy 1 ATGTCATGTTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAACACACCCCTGGGGT 60
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Qy 61 GAACCAATGGGCAAGCGTTCCGGCGCCGCTGCGCACTCGGGCAGGTGGCTTCTGCACG 120
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Db 85 GAACCAATGGGCAAGCGTTCCGGCGCCGCTGCGCACTCGGGCAGGTGGCTTCTGCACG 144
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Qy 121 CCCCGCTATATAGTGGCTCGGGATCGAGAGCCACCCAGCCCTCGGGCCCCC 180
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Db 145 CCCCGCTATATAGTGGCTCGGGATCGAGAGCCACCCAGCCCTCGGGCCCCC 204
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Qy 181 CCTCGGTGCCCTGCGAGTACGCTTCAATCCGAGGGGGGCCCAAGGGAAG 240
    |||||
Db 205 CCTCGGTGCCCTGCGAGTACGCTTCAATCCGAGGGGGGCCCAAGGGAAG 264
    |||||

Qy 241 GAACCTGGGCTCGGCGAGTGGCTTCTGCAAGTTCGAGTACACACACCG 300
    |||||
Db 265 GAGCTGGGGCTCGGGCAGTGGCTTCTGAGGATACGAGGTGACACACGACG 324
    |||||

Qy 301 GCGGGACCG 309
    |||||
Db 325 GCGGGACG 333

RESULT 2
US-10-144-771-5921
; Sequence 5921, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 5921
; LENGTH: 5826
; TYPE: DNA
; ORGANISM: HUMAN
US-10-144-771-5921

Query Match          63.4%; Score 199.2; DB 6; Length 5826;
Best Local Similarity 82.3%; Pred. No. 4.3e-41;
Matches 241; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

Qy 1 ATGTCATGTTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAACACACCCCTGGGGT 60
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Db 25 ATGTCATGTTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAACACACCCCTGGGGT 84
    |||||

Qy 61 GAACCAATGGGCAAGCGTTCCGGCGCCGCTGCGCACTCGGGCAGGTGGCTTCTGCACG 120
    |||||
Db 85 GAACCAATGGGCAAGCGTTCCGGCGCCGCTGCGCACTCGGGCAGGTGGCTTCTGCACG 144
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Qy 121 CCCCGCTATATAGTGGCTCGGGATCGAGAGCCACCCAGCCCTCGGGCCCCC 180
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Db 145 CCCCGCTATATAGTGGCTCGGGATCGAGAGCCACCCAGCCCTCGGGCCCCC 204
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Qy 181 CCTCGGTGCCCTGCGAGTACGCTTCAATCCGAGGGGGGCCCAAGGGAAG 240
    |||||
Db 205 CCTCGGTGCCCTGCGAGTACGCTTCAATCCGAGGGGGGCCCAAGGGAAG 264
    |||||

Qy 241 GAACCTGGGCTCGGCGAGTGGCTTCTGCAAGTTCGAGTACACACACCG 300
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Db 265 GAGCTGGGGCTCGGGCAGTGGCTTCTGAGGATACGAGGTGACACACGACG 324
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Qy 301 GCGGGACCG 309
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Db 325 GCGGGACG 333

RESULT 3
US-10-152-724-24/c
; Sequence 24, Application US/10152724
; GENERAL INFORMATION:
; APPLICANT: LITTLE, Melissa
; APPLICANT: HOLMES, Gregory
; APPLICANT: KOLLE, Gabriel
; APPLICANT: YAMADA, Toshiya
; APPLICANT: GEORGAS, Kylie
; APPLICANT: WILKINSON, Lorine
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptide
; FILE REFERENCE: P22378
; CURRENT APPLICATION NUMBER: US/10/152,724
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: Australian App No PQ 4348
; PRIOR FILING DATE: 1999-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 36303
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-152-724-24

Query Match          12.7%; Score 39.8; DB 6; Length 36303;
Best Local Similarity 55.4%; Pred. No. 1.4;
Matches 77; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 78 GCGTTCGGCGCGCTGCGCACTCGGGCAGGTGGCTTCTGCAAGTTCGAGTACACACCG 137
    |||||
Db 34505 GAGTCCGGGGCCCCGGCGGGAGTGGCGGGAGCTCCCTACCCCTCGCCGACCGGAG 34446
    |||||

Qy 138 CCTCGGGATGACAGAGCCACCCAGCCCTCGGGGGCCCCCTCGGTGGCTTCTGCAAG 197
    |||||
Db 34445 CCTACGCGCGCAGCTCTCTCCCTGCGCCCTCTCTCCGCGGACGCGGAGTCCCGCCG 34386
    |||||

Qy 198 GGATGACGCTTCTATCCGG 216
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Db 34385 TCTCGCTCTCTTCTCCGG 34367
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RESULT 4
US-10-152-724A-24/c
; Sequence 24, Application US/10152724A
; GENERAL INFORMATION:
; APPLICANT: LITTLE, Melissa
; APPLICANT: HOLMES, Gregory
; APPLICANT: KOLLE, Gabriel
; APPLICANT: YAMADA, Toshiya
; APPLICANT: GEORGAS, Kylie
; APPLICANT: WILKINSON, Lorine
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptide
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; FILE REFERENCE: P22378
; CURRENT APPLICATION NUMBER: US/10/152,724A
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: Australian App No PQ 4348
; PRIOR FILING DATE: 1999-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 36303
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-152-724A-24

Query Match      12.7%; Score 39.8; DB 6; Length 36303;
Best Local Similarity 55.4%; Pred. No. 1.4;
Matches 77; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 78 GCCTTCGGCGCGCGTGGCACTCGGCGAGGTGGCTTCTGCACGCCCGCTATATAGACTG 137
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Db 34505 GAGTGGCGGCGCGCGGAGTGGCGGAGCCTCCCTATCCCTCGCCGACCGGCAG 34446

QY 138 CTTCCGGGATGACAGACCCAGCCACCCCTCGGGGCCCCCTCGGTCGCCCTGGCA 197
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Db 34445 CCTACGGCGCGAGCTCTCCTCTGCGCCCTCTTCTGCGCGGACGGGGAGTCCCGGCC 34386

QY 198 GGATGACGCTTCATCCGG 216
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Db 34385 TCTCGCTCTCTCTCCCG 34367

RESULT 5
US-09-724-676-33617/c
; Sequence 33617, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33617
; LENGTH: 1878
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-33617

Query Match      12.2%; Score 38.2; DB 5; Length 1878;
Best Local Similarity 46.0%; Pred. No. 1.9;
Matches 127; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

QY 13 AGTGGCTCTCTGTCTCCTAAAGTGGATGAACGGAACACGCCTGGGGTGAACGCAATGGG 72
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Db 1319 AGAGGCCCCCAGCCCCCGAGAGCCGAGAGCCGCTGCTGCGCCCTCTCTGGCAGCCTCCCGGTAGATCGGC 1140

QY 193 TGGCAGGATGACCCCTTCATCCGAGGGGGGGGCCCAAGGCAAGGAACTGGGGCTG 252
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Db 1139 AAGCATCATGACTGCGCCTGCGCAAGCGCTGCAGCCGAGTGGCGCTCGGGCGGGCG 1080

QY 253 CGGCGAGTGGCCCTGGGCTTCGAAGATACCGAAGTG 288
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Db 1079 CAGCGGGGCGGTGCACCCAGCGGCGAGCTG 1044

RESULT 6
US-10-218-140-5849
; Sequence 5849, Application US/10218140
; GENERAL INFORMATION:
; APPLICANT: Shinkets, Richard A.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES
; FILE REFERENCE: 15966-543 CON
; CURRENT APPLICATION NUMBER: US/10/218,140
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/340,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/127,728
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/127,636
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/127,607
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 6322
; SOFTWARE: Curanator Version 1.0
; SEQ ID NO 5849
; LENGTH: 3174
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (1870)..(2332)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1)
; OTHER INFORMATION: "n" = "a", "c", "t" or "g"
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US-09-724-676A-33617/c
; Sequence 33617, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33617
; LENGTH: 1878
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-33617

Query Match      12.2%; Score 38.2; DB 5; Length 1878;
Best Local Similarity 46.0%; Pred. No. 1.9;
Matches 127; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

QY 13 AGTGGCTCTCTGTCTCCTAAAGTGGATGAACGGAACACGCCTGGGGTGAACGCAATGGG 72
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Db 1319 AGAGGCCCCCAGCCCCCGAGAGCCGAGAGCCGCTGCTGCGCCCTCTCTGGCAGCCTCCCGGTAGATCGGC 1260

QY 73 CAGAAGCGTTTCGGCGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACGCCCGCTATATG 132
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Db 1259 CAGACAGCCCCCAGCAAAATGCGAGTGGCGCTGCGAGGACAGCTGCTGTCTG 1200

QY 133 AGTCTCGTCCGGATGACAGCCACCCAGCCCTCGGGGCCCCCTCGGTGGCCCC 192
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1199 TGCTGCCAGCGGGGCGCCCTGCTGCTGCGCCCTCTCTGGCAGCCTCCCGGTAGATCGGC 1140

QY 193 TGGCAGGATGACCCCTTCATCCGAGGGGGGGGCCCAAGGCAAGGAACTGGGGCTG 252
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1139 AAGCATCATGACTGCGCCTGCGCAAGCGCTGCAGCCGAGTGGCGCTCGGGCGGGCG 1080

QY 253 CGGCGAGTGGCCCTGGGCTTCGAAGATACCGAAGTG 288
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1079 CAGCGGGGCGGTGCACCCAGCGGCGAGCTG 1044

RESULT 7
US-10-218-140-5849
; Sequence 5849, Application US/10218140
; GENERAL INFORMATION:
; APPLICANT: Shinkets, Richard A.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES
; FILE REFERENCE: 15966-543 CON
; CURRENT APPLICATION NUMBER: US/10/218,140
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/340,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/127,728
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/127,636
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/127,607
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 6322
; SOFTWARE: Curanator Version 1.0
; SEQ ID NO 5849
; LENGTH: 3174
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (1870)..(2332)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1)
; OTHER INFORMATION: "n" = "a", "c", "t" or "g"
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; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 45770  
; LENGTH: 1824  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
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; NAME/KEY: misc\_feature  
; LOCATION: (1515)..(1516)  
; OTHER INFORMATION: n is a,c,g, or t  
; FEATURE:  
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; US-09-724-676A-45770

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Best Local Similarity 47.3%; Pred. No. 7.6;  
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Db 1574 AGCACCAGCGGCTCTCTGCTCAGCCCTCTGACGAGGAGCGAGNCCNGNAAAGNN 1515  
QY 224 GCCCANGCAGGGAAGAACTGGGCTGGGGCAGTGGCCCTGGGCTTGAAGATACCG 283  
Db 1514 CCCCCCAAAAGCAGGACCGCTGGGGCGGTGGGACGTCAACCACCGCAGGAAATCGCG 1455  
QY 284 AAGTGACACGACACCGGGGACC 308  
Db 1454 AATGAATCCAGAGCTTGTGACC 1430

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Job time : 68.5329 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 21:14:01 ; Search time 301.551 Seconds  
(without alignments)  
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Searched: 16154066 seqs, 8097743376 residues  
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Listing first 45 summaries

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8: em\_htc:\*  
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12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
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26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 21	40.4	12.9	894	17	CNS0159I
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c 23	40.2	12.8	1101	17	CNS0150D
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ALIGNMENTS

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DEFINITION  
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VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

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EST.  
house mouse.  
Mus musculus  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 618)

618 bp  
mRNA  
linear  
EST 27-NOV-2001

GI:17112730

Unpublished (2001)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Akimura, T., Furuno, M., Hanagaki, T., Hayashi, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imocani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., et al.  
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al. 2001)

TITLE  
JOURNAL  
COMMENT

Tel: 81-45-503-9222  
Fax: 81-45-503-9216

Email: genome-res@gsr.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh

M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,

Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura

S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and

Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara

Y., and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp) for

further details.

e mouse tissues.

Location/Qualifiers

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/db\_xref="taxon:10090"

/clone\_lib="RIKEN full-length enriched, colon RCB-0549

Cle-H3 cDNA"

/tissue\_type="colon"

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/note="pooled cell lines ; (cell\_line=RCB-1751 WEHI 164),

(cell\_line=RCB-2116 JC), (cell\_line=RCB-0035 WEHI-3),

(cell\_line=RCB-0464 Meth-A), (cell\_line=RCB-0545 OHTA),

(cell\_line=RCB-0559 K-1 .F1), (cell\_line=RCB-1283 B16

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), (cell\_type=Leydig cells, cell\_line=RCB-2065 MLTC-1),

(cell\_type=Nullipotent stem cell, cell\_line=RCB-2070 NE),

(tissue\_type=bladder, cell\_line=RCB-0544 MBT-2),

(tissue\_type=bone marrow, cell\_type=stroma cell,

cell\_line=RCB-2028 SR-4987), (tissue\_type=colon,

cell\_line=RCB-0549 Cle-H3), (tissue\_type=kidney,

cell\_line=CCL-142 RAG), (tissue\_type=submandibular gland,

cell\_line=CRU-1734 SCA-9 clone 15), (strain=BALEB/C,

cell\_type=B cells, cell\_line=RCB-1669 BCL1 Clone 13.20-3B3

), (strain=C3H, tissue\_type=brain, cell\_line=RCB-1443

BC3H1")

BASE COUNT 105 a 189 c 196 g 127 t 1 others

ORIGIN

Query Match 63.4%; Score 199.2; DB 10; Length 618;

Best Local Similarity 82.3%; Pred. No. 3.4e-39;

Matches 241; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

Qy 1 ATGTCATGTTAGTGGCTCTCTGCTCCCTAAAGTGATGAACGAAACACGCTGGGGT 60

Db 37 ATGTCATGTTAGTGGCTCTCTGCTCCCTAAAGTGATGAACGAAACACGCTGGGG 96

Qy 61 GAACCAATGGGAGAGCGTTTCGGCGCGCGTGGCACTCGGCGAGGTGCTTTCGACG 120

Db 97 GAACCAATGGGAGAGCG---CCCACGCCACGGATCGACGAGTCTTCGCGCA 153

Qy 121 CCCCGTATATAGTGGCTCGGGATCGAGGATCGAGCCACCCAGCCACCCCTGGGGCCCC 180

Db 154 CTTCCCTACATGAGTGGCTCTCAAGAAATCGGAGCGCACCCAGCCACCCCTCGACTCAC 213

Qy 181 CTTGGTCCCTTGGCAGATGACGCTTCATCGGAGGCGGCGCCCAAGCAAGGCGCAAG 240

Db 214 ACTGGTGGCCCTGGCAGATGAGCCCTTCATCAGGAGGGCGGGCCCGGCGGGGTGTG 273

Qy 241 GAACCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAAC 293

Db 274 GAGCTGGGGCTGCGGCTAGTGGCTTGGGGTTTGACGACACTGAGGTGACCAAC 326

RESULT 2

BB866451

LOCUS

DEFINITION

musculus cDNA clone G431005J18 5', mRNA sequence.

BB866451

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsr.riken.go.jp,

URL: http://genome.gsc.riken.go.jp/

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh

M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,

Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura

S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and

Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara

Y., and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp) for

further details.

e mouse tissues.

Location/Qualifiers

1. 631

/organism="Mus musculus"

/db\_xref="taxon:10090"

/clone\_lib="RIKEN full-length enriched, colon RCB-0549

Cle-H3 cDNA"

/tissue\_type="colon"

/cell\_line="RCB-0549 Cle-H3"

/note="pooled cell lines ; (cell\_line=RCB-1751 WEHI 164),

(cell\_line=RCB-2116 JC), (cell\_line=RCB-0035 WEHI-3),

(cell\_line=RCB-0464 Meth-A), (cell\_line=RCB-0545 OHTA),

(cell\_line=RCB-0559 K-1 .F1), (cell\_line=RCB-1283 B16

melanoma), (cell\_type=B cells, cell\_line=RCB-1702 WEHI 231

), (cell\_type=Leydig cells, cell\_line=RCB-2065 MLTC-1),

(cell\_type=Nullipotent stem cell, cell\_line=RCB-2070 NE),

(tissue\_type=bladder, cell\_line=RCB-0544 MBT-2),

(tissue\_type=bone marrow, cell\_type=stroma cell,

cell\_line=RCB-2028 SR-4987), (tissue\_type=colon,

cell\_line=RCB-0549 Cle-H3), (tissue\_type=kidney,

cell\_line=CCL-142 RAG), (tissue\_type=submandibular gland,

cell\_line=CRU-1734 SCA-9 clone 15), (strain=BALEB/C,

cell\_type=B cells, cell\_line=RCB-1669 BCL1 Clone 13.20-3B3

), (strain=C3H, tissue\_type=brain, cell\_line=RCB-1443

BC3H1")

BASE COUNT 105 a 189 c 196 g 127 t 1 others

ORIGIN

(tissue\_type=bladder, cell\_line=RCB-0544 MBT-2),  
(tissue\_type=bone marrow, cell\_type=stroma cell,  
cell\_line=CRL-2028 SR-4987), (tissue\_type=colon,  
cell\_line=RCB-0549 CLE-H3), (tissue\_type=kidney,  
cell\_line=CCL-142 RAG), (tissue\_type=submandibular gland,  
cell\_line=CRL-1734 SCA-9 clone 15), (strain=BALB/C,  
cell\_type=B cells, cell\_line=CRL-1669 BCL1 Clone 13.20-3B3  
, (strain=C3H, tissue\_type=brain, cell\_line=CRL-1443  
BC3H1)"

BASE COUNT 90 a 217 c 174 g 150 t  
ORIGIN

Query Match 57.3%; Score 180; DB 10; Length 631;  
Best Local Similarity 78.2%; Pred. No. 1.9e-34;  
Matches 229; Conservative 0; Mismatches 61; Indels 3; Gaps 1;

QY 1 ATGTCATGTTTGTAGTGGCTTCTGCTCCCTAAAGTGGATGAACGGAACAGCCTGGGT 60  
|||||  
Db 37 ATGTCATGTTTGTAGTGGCTTCTGCTCCACAGTGGATGAACGGAACAGCCTGGGG 96  
|||||  
QY 61 GAACGCAATGGGCGAGAGGTTTCGGCGCGCGTGGCACTCGGCGAGTGGCTTCTGCACG 120  
|||||  
Db 97 GAACCTTTGGGCGAAGCG---CCACGCCAGCGCTAATCGACCGAGTGGCTTCTGCGG 153  
|||||  
QY 121 CCCCCTATATAGTGCCTTCGCGGATGAGAGCCACCAGCCCCCACCCTCGCGGCCCC 180  
|||||  
Db 154 CTTGCTACTTGTAGTGCCTTCGCGAGTGGGAGGCCACCAGCCCCCCTCTGCTGCTTAC 213  
|||||  
QY 181 CPTCGTGGCCCTGGCAGATGACGCTTCATCCGAGGGGGCGGCCCAAGCGGCAAG 240  
|||||  
Db 214 ACTTGGTGCCCTTGGCAGATGAAGCTTCATCAAGAGGGGCCCGCCCGGGGGGTGTG 273  
|||||  
QY 241 GAACCTGGGCTGGGCGAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAAC 293  
|||||  
Db 274 GATCTGGGCTGGGCGAGTGGCCCTCGGCTTCGACGACACTGTGCTGAGCAC 326  
|||||

RESULT 3  
CNS02STX/C  
LOCUS  
DEFINITION  
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone  
162f16 of library G from Tetraodon nigroviridis, genomic survey  
sequence.

ACCESSION  
AL212334  
VERSION  
AL212334.1 GI:7871153  
KEYWORDS  
GSS; genome survey sequence.  
SOURCE  
Tetraodon nigroviridis.  
ORGANISM  
Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodon.  
REFERENCE  
1 (bases 1 to 1011)  
Roest-Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,  
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,  
Saurin,W. and Weissenbach,J.  
Human gene number estimate provided by genome wide analysis using  
Tetraodon nigroviridis DNA sequence  
Unpublished

JOURNAL  
2 (bases 1 to 1011)  
Roest-Crolius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,  
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and  
Weissenbach,J.  
Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis  
Unpublished

JOURNAL  
3 (bases 1 to 1011)  
Roest-Crolius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,  
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and  
Weissenbach,J.  
Direct Submission  
Submitted (12-APR-2000)  
Genoscope.  
TITLE  
This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at

http://www.genoscope.cns.fr/Tetraodon.  
Location/Qualifiers  
1..1011  
/organism="Tetraodon nigroviridis"  
/db\_xref="taxon:99883"  
/clone="162F16"  
/clone\_lib="G"  
/note="Genoscope sequence ID : C0AG162BC08SP1-end ;  
PUC-Ori"  
BASE COUNT 191 a 297 c 324 g 175 t 24 others  
ORIGIN

Query Match 19.2%; Score 60.2; DB 17; Length 1011;  
Best Local Similarity 63.1%; Pred. No. 9.1e-05;  
Matches 128; Conservative 1; Mismatches 64; Indels 10; Gaps 2;

QY 1 ATGTCATGTTTGTAGTGGCTTCTGCTCCCTAAAGTGGATGAACGGAACAGCCTGGGT 60  
|||||  
Db 283 ATGTCCTGTTTCAGTGGTTTCTCTAGTGGCAGAGTGGACGACGAAAGAGCGCTGGGG 224  
|||||  
QY 61 GAACGCAATGGGCGAGAGGTTTCGGCGCGCGTGGCACTCGGCGAGTGGCTTCTGCACG 120  
|||||  
Db 223 GACGCGAATGGCGAAGAGCCCAACCGAAGGAGGCTCGTCTC-----TCTGCAAC 173  
|||||  
QY 121 CCCCCTATATAGTGCCTTCGCGGATGAGAG--GCCACCAGCCCCCACCCTCGCGGCCCC 179  
|||||  
Db 172 CCCCCTWACATGAGTGCCTTCGCGGACCGCGACGCGCATGGAGCCCCCTCCGAGGCCCC 113  
|||||  
QY 180 CCCTCGGTGCCCTGCGCAGATG 202  
|||||  
Db 112 CTCCATCAGCACCAACCGCGGAGG 90  
|||||

RESULT 4  
BG916212  
LOCUS  
DEFINITION  
BG916212  
VERSION  
BG916212.1 GI:14296688  
KEYWORDS  
EST.  
SOURCE  
house mouse.  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 941)  
NIH-MGC http://mgc.nci.nih.gov/.  
AUTHORS  
National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE  
Unpublished (1999)  
JOURNAL  
Contact: Robert Strausberg, Ph.D.  
COMMENT  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth  
Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM10870 row: f column: 08  
High quality sequence stop: 151.  
Location/Qualifiers  
1..941  
/organism="Mus musculus"  
/strain="NMRI"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4937095"  
/clone\_lib="NCI\_CGAP\_Mam4"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="5 months"  
/lab\_host="DH10B"

FEATURES  
source  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt.









NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

source

1. .925  
/organism="Drosophila melanogaster"  
/db\_xref="taxon:7227"  
/clone="BACR19D16"  
/clone\_lib="RPCI-98"  
/note="end : TET3"

BASE COUNT 120 a 61 c 61 g 172 t 511 others

## ORIGIN

Query Match 13.5%; Score 42.4; DB 17; Length 925;

Best Local Similarity 10.4%; Pred. No. 2.2;

Matches 31; Conservative 146; Mismatches 120; Indels 0; Gaps 0;

QY 14 GTGGCTCTCGTCCCTAAAGTCGATGACGGAACAGCCTGGGTGACGCAATGGGC 73

Db 628 GTSCSSSSSSSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSS 687

QY 74 AGAAGCGTTTCGGCGCGCTGACCTCGGCAGGTGGCTTCTGCACGCCCGCTATATGA 133

Db 688 GSGTGSTSSSSSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSS 747

QY 134 GTGCTCTCGGGATGACGACCCACCCAGCCCTCGGCGCCCGCTCGGTGCCCT 193

Db 748 SSSSYSSSTSCCTCCSYSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSSTSSST 807

QY 194 GCAGATGACGCTTCATCCGAGGGGGCCCGCCGACGAGCAGGAACTGGGCTGC 253

Db 808 CTTCTCCSTTBMCTTSTSCGSSSSSGKGVTKCGCGSSSTNGMBGTSSACSSS 867

QY 254 GGCAGTGGCCCTGGGCTTGAAGTACCAAGTACACACACCGCGGCGGACCG 310

Db 868 SSCSS 924

## RESULT 12

CNS0108S/c

## LOCUS

Drosophila melanogaster genome survey sequence T7 end of BAC  
BACN03J03 of DrosBAC library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.

## ACCESSION

AL098662

## VERSION

AL098662.1

## KEYWORDS

GSS.

## SOURCE

Drosophila melanogaster.

## ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1065)

## REFERENCE

Genoscope.

## AUTHORS

Direct Submission

## TITLE

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr))- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a

collaboration with the European Drosophila Genome Project (EDGP) -

<http://www.edgp.ebi.ac.uk> . This Drosophila melanogaster BAC

library (Dros BAC) was made by Alain Billaud at CEPH (Centre

d'Etude du Polymorphisme Humain) with funding provided by a MRC

project grant. The DNA was prepared from embryos by Alain Bucheton

and Genevieve Payan. It has been constructed in the vector

pBelOBAC11.

Location/Qualifiers

1. .1065

/organism="Drosophila melanogaster"

## FEATURES

source

/db\_xref="taxon:7227"  
/clone="BACN03J03"  
/clone\_lib="DrosBAC"  
/plasmid="pBelOBAC11"  
/note="end : T7"

BASE COUNT 121 a 225 c 252 g 313 t 154 others

## ORIGIN

Query Match 13.5%; Score 42.4; DB 17; Length 1065;

Best Local Similarity 30.7%; Pred. No. 2.3;

Matches 73; Conservative 58; Mismatches 107; Indels 0; Gaps 0;

QY 75 GAAGCGTTTCGGCGCGCTGCGCAGTGGCTTCTGCACGCCCGCTATATGAG 134

Db 1028 GRCCSRGGSAGKVCAGACCGGGGRCCTCCSMSAGACMCSCSCCCACAC 969

QY 135 CTGCTTCGGGATGACAGCCACCCAGCCCGCCCTGCGGGCCCGCTCGGTGCCCTG 194

Db 968 AAKGVCCSMCYCSGCCCGCCACSCGSCCMGTMBCMAGCSCSSSCSSSCSCAMSG 909

QY 195 GCAGGATGAGCCCTTCATCGGAGGGCGGCCGANGCAAGGCAAGAACTGGGCTGCG 254

Db 908 MGAGGSS 849

QY 255 GGCAGTGGCGCTGGGCTTGAAGTACCAAGTACCAACACACCGCGGCGGCGCTG 312

Db 848 GGGGRRGCCCGGGAACMACVAAAGGTGACMCCSCSMVSSCVMSSSSCMCGG 791

## RESULT 13

CNS006XK

## LOCUS

Drosophila melanogaster genome survey sequence T7 end of BAC #  
BACR14N09 of RPCI-98 library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.

## ACCESSION

AL066051

## VERSION

AL066051.1

## KEYWORDS

GSS.

## SOURCE

Drosophila melanogaster.

## ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 935)

## REFERENCE

Genoscope.

## AUTHORS

Direct Submission

## TITLE

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr))- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegawa and

Aaron Mamoser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

EcoRI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain y2; cn bw sp, the same strain used for the BDGP's

p1 and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

Location/Qualifiers

1. .935

/organism="Drosophila melanogaster"

/db\_xref="taxon:7227"

/clone="BACR14N09"

/clone\_lib="RPCI-98"

/note="end : T7"

## BASE COUNT

257 a 170 c 162 g 96 t 250 others

## ORIGIN



[illegible]

Search completed: March 1, 2003, 03:51:56  
Job time : 307.884 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model  
Run On: March 1, 2003, 04:06:12 ; Search time 2156 Seconds  
(without alignments)  
1403.846 Million cell updates/sec

Title: US-09-750-240-2  
Perfect score: 570  
Sequence: 1 MSWFGSLVPRKDKTAWG.....RAVALGFEDTEVTTTPAGPL 104

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters: -DEV=xlh  
-Q/cgn2\_1/USPTO.spool/US09750240/runat\_25022003\_103941\_24963/app\_query.fasta\_1.263  
-DB-GenEmbl -QFAST=fastap -SUFFIX=rg -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09750240.@Cn\_1\_1.1616@runat\_25022003\_103941\_24963 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:\*  
1: gb.ba:\*  
2: gb.htg:\*  
3: gb.in:\*  
4: gb.om:\*  
5: gb.ov:\*  
6: gb.pat:\*  
7: gb.ph:\*  
8: gb.pl:\*  
9: gb.pr:\*  
10: gb.ro:\*  
11: gb.sts:\*  
12: gb.sy:\*  
13: gb.un:\*  
14: gb.vi:\*  
15: em.ba:\*  
16: em.fun:\*  
17: em.hum:\*  
18: em.in:\*  
19: em.mu:\*  
20: em.om:\*  
21: em.or:\*  
22: em.ov:\*  
23: em.pat:\*  
24: em.ph:\*  
25: em.pl:\*  
26: em.ro:\*  
27: em.sts:\*  
28: em.un:\*

29: em.vi:\*  
30: em.htg\_hum:\*  
31: em.htg\_inv:\*  
32: em.htg\_other:\*  
33: em.htg\_mus:\*  
34: em.htg\_pln:\*  
35: em.htg\_rtd:\*  
36: em.htg\_mam:\*  
37: em.htg\_vrt:\*  
38: em\_sy:\*  
39: em.htgo\_hum:\*  
40: em.htgo\_mus:\*  
41: em.htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	568	99.6	314	6	ARI174471 Sequence
2	568	99.6	314	6	AX189757 Sequence
3	545	95.6	3549	6	ARI174473 Sequence
4	545	95.6	3549	6	AX189761 Sequence
5	545	95.6	3552	6	AX189766 Sequence
6	545	95.6	3582	6	AX189768 Sequence
7	545	95.6	5877	9	AB007882 Homo sapi
8	545	95.6	6463	9	AF250226 Homo sapi
9	545	95.6	193283	2	AC021647 Homo sapi
10	545	95.6	205248	2	AC117498 Homo sapi
11	518	90.9	171345	2	AC025557 Homo sapi
12	472.5	82.9	4046	4	DOGADENCYC
13	472.5	82.9	4046	6	I29958 Sequence 1
14	432	75.8	4131	6	ARI06659 Sequence
15	432	75.8	4131	10	RATADCYB
16	432	75.8	5841	6	AX305965 Sequence
17	432	75.8	5841	10	MUSADCYC
18	428	75.1	6036	10	AC074028 Mouse adeny
19	428	75.1	6036	10	L0115 Rattus norv
20	426	74.7	151706	2	AC129405 Rattus no
21	402	70.5	108689	2	AC096835 Rattus no
22	395	69.3	3465	10	MUSADNLCYC
23	258	45.3	61901	5	U72484 Fugu rubrip
24	109	19.1	206934	2	AC126672 Mus muscu
25	105.5	18.5	110000	2	AC098456 Rattus no
26	103.5	18.2	8366	1	AF072709 Streptomy
27	103.5	18.2	17228	1	SC3F60 Streptomy
28	103.5	18.2	210215	2	AC097157 Rattus no
29	103	18.1	6536	10	MUSALCR01
30	103	18.1	179362	10	AC115355 Mus muscu
31	100.5	17.6	129778	8	AC091123 Oryza sat
32	100	17.5	148102	8	AP003328 Oryza sat
33	100	17.5	148762	8	AP002843 Oryza sat
34	99.5	17.5	14676	1	AE006014 Caulobact
35	99	17.4	431	14	HEHS03 V00462 Herpes simp
36	99	17.4	2391	1	AF288483 Azospirill
37	99	17.4	2560	14	HS1IEM5G J02220 Herpes simp
38	99	17.4	13037	1	AF157643 Mycobacte
39	99	17.4	98092	2	AC099455 Rattus no
40	99	17.4	148120	9	AC090051 Homo sapi
41	98.5	17.3	65190	2	B1011H02 AL442109 Oryza sat
42	98.5	17.3	139807	8	OSUN00183 AL662984 Oryza sat
43	98.5	17.3	171557	8	OSUN00177 AL662976 Oryza sat
44	98	17.2	13036	1	AE005839 Caulobact
45	98	17.2	201050	1	AL646064 Ralstonia

## ALIGNMENTS

RESULT 1

ARI174471 ARI174471 314 bp DNA linear PAT 17-DEC-2001  
LOCUS Sequence 1 from patent US 6306830.  
ACCESSION ARI174471  
VERSION ARI174471.1 GI:17914791  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 314)  
AUTHORS Hammond,H.Kirk., Insel,P.A., Ping,P., Post,S.R. and Gao,M.  
TITLE Gene therapy for congestive heart failure  
JOURNAL Patent: US 6306830-A 1 23-OCT-2001;  
FEATURES Location/Qualifiers  
source 1..314  
BASE COUNT 60 a 98 c 108 g 47 t 1 others  
ORIGIN  
Alignment Scores:  
Pred. No.: 3.27e-29 Length: 314  
Score: 568.00 Matches: 104  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.65% Indels: 0  
DB: 6 Gaps: 0  
US-09-750-240-2 (1-104) x ARI174471 (1-314)  
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Db 1 ATGTCATGGTTAGTGGCTCCTCGGTCCCTAAAGTGGATGAACGGAACACACCGCTGGGGT 60  
Qy 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
Db 61 GAACCAATGGCAGAGCGTTCCGGCGCGTGGCACTCGGAGAGTGGCTTCTGCACG 120  
Qy 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
Db 121 CCCGCTATATAGCTGCTCCGGGATGCAGAGCCACCCGCCCTCGGGGCCCC 180  
Qy 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro\*\*LysGlyLys 80  
Db 181 CCTCGTCCCTGGCAGGATGACGCTTCATCCGGAGGGGGCCCAAGGCGCAAG 240  
Qy 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
Db 241 GAACCTGGGGCTCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAACGACACCG 300  
Qy 101 AlaGlyProLeu 104  
Db 301 GCGGACCGCTG 312  
RESULT 3  
ARI174473 ARI174473 3549 bp DNA linear PAT 17-DEC-2001  
LOCUS Sequence 5 from patent US 6306830.  
DEFINITION ARI174473  
ACCESSION ARI174473  
VERSION ARI174473.1 GI:17914793  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3549)  
AUTHORS Hammond,H.Kirk., Insel,P.A., Ping,P., Post,S.R. and Gao,M.  
TITLE Gene therapy for congestive heart failure  
JOURNAL Patent: US 6306830-A 5 23-OCT-2001;  
FEATURES Location/Qualifiers  
source 1..3549  
BASE COUNT 699 a 1025 c 1061 g 764 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 8.64e-27 Length: 3549  
Score: 545.00 Matches: 99  
Percent Similarity: 97.06% Conservative: 0  
Best Local Similarity: 97.06% Mismatches: 3  
Query Match: 95.61% Indels: 0  
DB: 6 Gaps: 0  
US-09-750-240-2 (1-104) x ARI174473 (1-3549)  
Qy 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
Db 1 ATGTCATGGTTAGTGGCTCCTCGGTCCCTAAAGTGGATGAACGGAACACACCGCTGGGGT 60  
Qy 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40

ARI174471 ARI174471 314 bp DNA linear PAT 17-DEC-2001  
LOCUS Sequence 1 from patent US 6306830.  
ACCESSION ARI174471  
VERSION ARI174471.1 GI:17914791  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 314)  
AUTHORS Hammond,H.Kirk., Insel,P.A., Ping,P., Post,S.R. and Gao,M.  
TITLE Gene therapy for congestive heart failure  
JOURNAL Patent: US 6306830-A 1 23-OCT-2001;  
FEATURES Location/Qualifiers  
source 1..314  
BASE COUNT 60 a 98 c 108 g 47 t 1 others  
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Score: 568.00 Matches: 104  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.65% Indels: 0  
DB: 6 Gaps: 0  
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Db 1 ATGTCATGGTTAGTGGCTCCTCGGTCCCTAAAGTGGATGAACGGAACACACCGCTGGGGT 60  
Qy 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
Db 61 GAACCAATGGCAGAGCGTTCCGGCGCGTGGCACTCGGAGAGTGGCTTCTGCACG 120  
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Db 121 CCCGCTATATAGCTGCTCCGGGATGCAGAGCCACCCGCCCTCGGGGCCCC 180  
Qy 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro\*\*LysGlyLys 80  
Db 181 CCTCGTCCCTGGCAGGATGACGCTTCATCCGGAGGGGGCCCAAGGCGCAAG 240  
Qy 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
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Qy 101 AlaGlyProLeu 104  
Db 301 GCGGACCGCTG 312  
RESULT 2  
AXI189757 AXI189757 314 bp DNA linear PAT 08-AUG-2001  
LOCUS Sequence 1 from Patent WO0148164.  
DEFINITION AXI189757  
ACCESSION AXI189757  
VERSION AXI189757.1 GI:15143133  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 314)  
AUTHORS Hammond,H.K. and Gao,M.  
TITLE Gene therapy for congestive heart failure  
JOURNAL Patent: WO 0148164-A 1 05-JUL-2001;  
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)  
FEATURES Location/Qualifiers  
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/db\_xref="taxon:9606"

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QY 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro\*\*\*LysGlyLys 80  
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Db 181 CCTCGTGCCTTCGGCAGGATGACGCTTCATCCGAGGGGGGGCCAGGCAAGGCAAG 240

QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
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QY 101 AlaGly 102  
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Db 301 GCGGG 306

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DEFINITION Sequence 5 from Patent WO0148164.  
ACCESSION AXI89761  
VERSION AXI89761.1 GI:15143135  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE 1 (bases 1 to 3549)  
JOURNAL Hammond, H.K. and Gao, M.  
Gene therapy for congestive heart failure  
Patent: WO 0148164-A 5 05-JUL-2001;  
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)

FEATURES  
source Location/Qualifiers  
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BASE COUNT 699 a 1025 c 1061 g 764 t

ORIGIN

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Pred. No.: 8.64e-27 Length: 3549  
Score: 545.00 Matches: 99  
Percent Similarity: 97.06% Conservative: 3  
Best Local Similarity: 97.06% Mismatches: 0  
Query Match: 95.61% Indels: 0  
DB: 6

US-09-750-240-2 (1-104) x AXI89761 (1-3549)

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QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
|||||  
Db 61 GAACGCAATGGCGAGAGGCTTCGGCGCGCCCTGGGCACTGGGCGAGTGGCTTCTGCACG 120

QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
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QY 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro\*\*\*LysGlyLys 80  
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Db 181 CCTCGTGCCTTCGGCAGGATGACGCTTCATCCGAGGGGGGGCCAGGCAAGGCAAG 240

US-09-750-240-2 (1-104) x AXI89761 (1-3549)

QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
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QY 101 AlaGly 102  
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Db 301 GCGGG 306

RESULT 6  
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LOCUS AXI89768 3582 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 12 from Patent WO0148164.  
ACCESSION AXI89768  
VERSION AXI89768.1 GI:15143140  
KEYWORDS synthetic construct.  
SOURCE  
ORGANISM  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE 1 (bases 1 to 3582)  
JOURNAL Hammond, H.K. and Gao, M.  
Gene therapy for congestive heart failure  
Patent: WO 0148164-A 12 05-JUL-2001;

Db 301 GCGGG 306

RESULT 5  
AXI89766  
LOCUS AXI89766 3552 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 10 from Patent WO0148164.  
ACCESSION AXI89766  
VERSION AXI89766.1 GI:15143139  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE 1 (bases 1 to 3552)  
JOURNAL Hammond, H.K. and Gao, M.  
Gene therapy for congestive heart failure  
Patent: WO 0148164-A 10 05-JUL-2001;  
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FEATURES  
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BASE COUNT 686 a 1037 c 1068 g 761 t

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Score: 545.00 Matches: 99  
Percent Similarity: 97.06% Conservative: 0  
Best Local Similarity: 97.06% Mismatches: 3  
Query Match: 95.61% Indels: 0  
DB: 6

US-09-750-240-2 (1-104) x AXI89766 (1-3552)

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Db 61 GAACGCAATGGCGAGAGGCTTCGGCGCGCCCTGGGCACTGGGCGAGTGGCTTCTGCACG 120

QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
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Db 121 CCCCCTATATAGCTGCTCCGGGATGCAGACCAACCCAGCCCTCGGGGCCCC 180

QY 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro\*\*\*LysGlyLys 80  
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US-09-750-240-2 (1-104) x AXI89766 (1-3552)

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Db 241 GAGCTGGGCTGGGCGAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACGACAGCG 300

QY 101 AlaGly 102  
|||

Db 301 GCGGG 306

RESULT 6  
AXI89768  
LOCUS AXI89768 3582 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 12 from Patent WO0148164.  
ACCESSION AXI89768  
VERSION AXI89768.1 GI:15143140  
KEYWORDS synthetic construct.  
SOURCE  
ORGANISM  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE 1 (bases 1 to 3582)  
JOURNAL Hammond, H.K. and Gao, M.  
Gene therapy for congestive heart failure  
Patent: WO 0148164-A 12 05-JUL-2001;

## THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)

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  Qy 61 ProArgCysProTrpGlnAspAlaPheLeuArgGlyGlyPro**LysGlyLys 80
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  Db 322 GCGGG 327
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  ACCESSION  AB007882
  VERSION    AB007882.2 GI:20521044
  KEYWORDS   KIAA0422.
  SOURCE     Homo sapiens male brain cdna to mRNA, clone_lib:pBluescriptII SK
  ORGANISM   Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE  1
    AUTHORS  Ishikawa,K., Nagase,T., Nakajima,D., Seki,N., Ohira,M.,
    Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.
    TITLE    Prediction of the coding sequences of unidentified human genes.
    VILL-78 new-cDNA clones from brain which code for large proteins
    in vitro
    JOURNAL  DNA Res. 4 (5), 307-313 (1997)
    MEDLINE 98116655
    PUBMED  9455427
  REFERENCE  2 (bases 1 to 5877)
    AUTHORS  Ohara,O.
    TITLE    Direct Submission
    JOURNAL  Submitted (06-OCT-1997) Osamu Ohara, Kazusa DNA Research Institute,
    Laboratory of DNA Technology, Yana 1532-3, Kisarazu, Chiba
    292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel: +81-438-52-3913,
    Fax: +81-438-52-3914)
    On May 9, 2002 this sequence version replaced gi:2887418.
    Sequence updated (05-Jan-1998).
  COMMENT
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## FEATURES

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    DB:              9          Gaps:          0
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QY 101 AlaGly 102
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Db 437 GCGGG 442

RESULT 8
AF250226 AF250226 6463 bp mRNA linear PRI 15-SEP-2000
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DEFINITION Homo sapiens adenylyl cyclase type VI mRNA, complete cds.
ACCESSION AF250226
VERSION AF250226.1 GI:9049782
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 6463)
AUTHORS Wicker,R., Catalan,A.G., Cailleux,A., Starenki,D., Stengel,D.,
Sarasin,A. and Suarez,H.G.
TITLE Cloning and expression of human adenylyl cyclase type VI in normal
thyroid tissues
JOURNAL Biochim. Biophys. Acta 1493 (1-2), 279-283 (2000)
MEDLINE 20435313
PubMed 10978539
REFERENCE 2 (bases 1 to 6463)
AUTHORS Wicker,R., Gascon Catalan,A., Cailleux,A.-F., Starenki,D.,
Stengel,D., Sarasin,A. and Suarez,H.G.
TITLE Direct Submission
JOURNAL Submitted (28-MAR-2000) Lab Etude des Relations - Instabilite
genetique et Cancer UPR 2169, Institut de Recherches sur le Cancer
CNRS IFR 1221, 7 rue Guy Moquet, Villejuif 94801, France
FEATURES
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GYDMEATISLREVTVGNVMRVGTHSGRVHCVGLGRKQWQFVMSNVTLANHMEAG
GRAGHITRATLOVYNGDYVEVPGRGGERNAYLKEOHTETLILGASOKRKEEKAML
AKLQTRANSMGLPRWPVDRAFSTRKDSKAFROMGIDSSKDRNGTQDALNPEDEV
DEFLRAIDARSIDQLKDHVRLLITFORLEKRYSKRVDPFGVAYVACALLVFCF
ICFIQLLIPHSMTLGIYASIFLLITLVLCVYSCGSLFPKALQRLSRISVRSRA
HSTAVGIFSVLTFYSAINMFTCNHTPIRSCAARMNLTPADITACHLQNLVSLGL
DAPLCEGWTCSFFPYFTGNMLLSLASVFLHISISGLKAMIFVGLIYLVLLILG
PATIFDNYDLMLKQATGEKEMEELQAYNRLLHNLIPKDVAFHFLARERNDELYY
QVESTARLDFLKKQATGEKEMEELQAYNRLLHNLIPKDVAFHFLARERNDELYY
QSCCEAVNFASINFSEYVEANNEGVCEVRLNLEIIADFDEILSEERERQLEKI
KITGTYTMAAGSINATYDQVGRSHITALADYAMRLMEQMKHINSHSFNNFQMKIGLN
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GVVKKVGKGMTTYFLNGPSS"
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BASE COUNT 1264 a 1795 c 1871 g 1533 t  
ORIGIN

Alignment Scores:

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Pred. No.: 1.47e-26 Length: 6463
Score: 545.00 Matches: 99
Percent Similarity: 97.06% Conservative: 0
Best Local Similarity: 97.06% Mismatches: 3
Query Match: 95.61% Indels: 0
DB: 9 Gaps: 0

US-09-750-240-2 (1-104) x AF250226 (1-6463)
QY 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTgPly 20
    |||
Db 695 ATGTCATGTTTACTGTCCTCTGTCCTTAAAGTGTGATGAACGAAACAGCCTGGGGC 754
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QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
    |||
Db 755 GAACCAATGGGCGAGAGCGTTTCGCGCGCGCTGGCACTCGGCAGGTGCTTCTGCACG 814
    |||
QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
    |||
Db 815 CCCCGTATATGAGCTGCCTCCGGGATGCAGAGCCACCCAGCCCACTCCGCGCCCC 874
    |||
QY 61 ProArgCysProTrpGlnAspAspAlaPheIleArgArgGlyGlyPro**LysGlyLys 80
    |||
Db 875 CCTCGGTGCCCTGGCAGGATGACGCTTCATCCGAGGGCGGCCGCCAGGCGGCAAG 934
    |||
QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
    |||
Db 935 GACCTGGGCTGCGGGCAGTGGCCCTCGGCTTCGAGGATACCGAGGTGACACGACGCG 994
    |||
QY 101 AlaGly 102
    |||
Db 995 GCGGG 1000

RESULT 9
AC021647/c
LOCUS Homo sapiens chromosome 12 clone RP11-455I22, WORKING DRAFT
DEFINITION SEQUENCE, 8 unordered pieces.
ACCESSION AC021647
VERSION AC021647.18 GI:20335444
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 193283)
AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Adams,C., Ali-Osman,F.R., Allen,C.,
Muzny,D.M., Binkley,C., Binkley,C., Binkley,C., Binkley,C.,
Alsbrooks,S.L., Amaral, H.C., Are,J.R., Ayele,M., Banks,T.,
Barbata,J., Benton,J., Binkley,C., Binkley,C., Binkley,C.,
Bouck,J., Bowler,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carton,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davalila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabsi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
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Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,J., Kovar,C.,
Karlisson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kover,C.,
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Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseghe,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
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Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newtonson,N., Nguyen,A., Nguyen,N.,
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Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rivers, M., Rojas, A., Rojokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoostari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Woodson, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G., and Gibbs, R.

Direct Submission  
2 (bases 1 to 193283)  
Worley, K.C.

Direct Submission  
Submitted (19-JAN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 193283)  
Worley, K.C.

Direct Submission  
Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Apr 28, 2002 this sequence version replaced gi:15809061.

-----  
Center: Baylor College of Medicine  
Genome Center  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
-----  
Project Information  
Center project name: HAAF  
Center clone name: RP11-455122  
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Summary Statistics  
Sequencing vector: Plasmid;  
Chemistry: Dye-terminator  
Chemistry: Dye-terminator Big Dye; 2% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 219180 bases at least Q40  
Consensus quality: 233400 bases at least Q30  
Consensus quality: 243367 bases at least Q20  
Estimated insert size: 209025; sum-of-contigs estimation  
Quality coverage: 10x in Q20 bases; sum-of-contigs estimation  
-----

\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).

\* NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 2133: contig of 2133 bp in length  
2134 2233: gap of unknown length  
2234 5400: contig of 3167 bp in length  
5401 5500: gap of unknown length  
5501 7889: contig of 2389 bp in length  
7890 7990: gap of unknown length  
7990 35656: contig of 27667 bp in length  
35657 65617: contig of 29861 bp in length  
65618 65717: gap of unknown length  
65718 104448: contig of 38731 bp in length  
104449 104548: gap of unknown length  
104549 145966: contig of 41418 bp in length  
145967 146066: gap of unknown length  
146067 193283: contig of 47217 bp in length.

FEATURES  
source 1. 193283  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="12"  
/clone="RP11-455122"  
BASE COUNT 49273 a 48888 c 46863 g 47544 t 715 others  
ORIGIN  
Alignment Scores: 3.01e-25 Length: 193283  
Pred. No.: 545.00 Matches: 99  
Score: 97.06% Conservative: 0  
Percent Similarity: 97.06% Mismatches: 3  
Best Local Similarity: 95.61% Indels: 0  
Query Match: 2 Gaps: 0  
DB: 2  
US-09-750-240-2 (1-104) x AC021647 (1-193283)  
QY 1 MetSerTTPpHeSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTTPGly 20  
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Db 74771 ATGTCATGGTTTAGTGGCTCTCTGCTCTTAAAGTGGATGACGGAACACACCTGGGGT 74712  
QY 21 GluArgASngLgLnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
|||||  
Db 74711 GAACGCAATGGGACAGCGTTTCGGCGCGCTGGCACTCGGGCGGTGCTTCGCACG 74652  
QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
|||||  
Db 74651 CCCCGTATATAGCTGCTCGGGATGCGAGCCACCCAGCCCTCGGGGCCCC 74592  
QY 61 ProArgCysProTTPGlnAspAspAlaPheIleArgArgGlyGlyPro\*\*LysGlyLys 80  
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Db 74591 CTTGGTGGCCCTGGCAGGATGACGCTTCATCCGGAGGGGGCGCCAGGCAAGGCAAG 74532  
QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
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Db 74531 GAGCTGGGGCTCGGGCAGTGGCCCTGGGCTTCGAGATACCGAGGTGACACAGCAGCG 74472  
QY 101 AlaGly 102  
Db 74471 GCGGG 74466  
RESULT 10  
AC117498/C  
LOCUS AC117498 205248 bp DNA linear HTG 31-JUL-2002  
DEFINITION Homo sapiens clone RP11-422021, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 20  
unordered pieces.  
ACCESSION AC117498  
VERSION AC117498.4 GI:22002346  
KEYWORDS HTG; HTGS\_PHASE1.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 205248)  
AUTHORS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amarantunga, H.C., Are, J.R., Ayale, M., Banks, T., Barbara, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brileva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleaveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Din, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hoques, M., Holloway, C., Hollins, B.,

Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louise, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mahney, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mayhew, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., River, S., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shoostari, N., Sisson, I., Sodergren, E., Sonaite, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Gibbs, R.

Direct Submission  
 Unpublished  
 2 (bases 1 to 205248)  
 Worley, K.C.

Direct Submission  
 Submitted (10-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 205248)  
 Worley, K.C.

Direct Submission  
 Submitted (31-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 On Jul 29, 2002 this sequence version replaced gi:21956504.

----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Drafting Center Code: WUGSC  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Center project name: HEAU  
 Center clone name: RP11-422021  
 ----- Summary Statistics  
 Sequencing vector: Plasmid;  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 216840 bases at least Q40  
 Consensus quality: 220255 bases at least Q30  
 Consensus quality: 222408 bases at least Q20

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 \* NOTE: Estimated insert size may differ from sequence length  
 (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 20 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 2025: contig of 2025 bp in length  
 2026 2125: gap of unknown length  
 2126 4437: contig of 2312 bp in length  
 4438 4537: gap of unknown length  
 4538 6633: contig of 2096 bp in length  
 6634 6733: gap of unknown length  
 6734 9148: contig of 2415 bp in length  
 9149 9248: gap of unknown length

9249 11635: contig of 2387 bp in length  
 11636 11735: gap of unknown length  
 11736 13780: contig of 2045 bp in length  
 13781 13880: gap of unknown length  
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 16998 16997: gap of unknown length  
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 20090 20189: gap of unknown length  
 20190 23014: contig of 2825 bp in length  
 23015 23114: gap of unknown length  
 23115 25345: contig of 2231 bp in length  
 25346 25445: gap of unknown length  
 25446 31033: contig of 5588 bp in length  
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 31134 35863: contig of 4730 bp in length  
 35864 35963: gap of unknown length  
 35964 49814: contig of 13851 bp in length  
 49815 64385: contig of 14471 bp in length  
 64386 64485: gap of unknown length  
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 81201 97966: contig of 16766 bp in length  
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 115534 139873: contig of 24240 bp in length  
 139874 139973: gap of unknown length  
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BASE COUNT 51253 a 48444 c 48345 g 51200 t 6006 others  
 ORIGIN

Alignment Scores:  
 Pred. No.: 3.17e-25 Length: 205248  
 Score: 545.00 Matches: 99  
 Percent Similarity: 97.06% Conservatives: 0  
 Best Local Similarity: 97.06% Mismatches: 3  
 Query Match: 95.61% Indels: 0  
 DB: 2 Gaps: 0

US-09-750-240-2 (1-104) x AC117498 (1-205248)

QY 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
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 Db 168939 CCTCGTGGCCCTGGCAGGATGACGCTTCATCCGAGGGGGCGCCCGCAGGCGCAAG 168880  
 QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
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 Db 168879 GAGCTGGGCTGGGGGAGTGGGCCCTTCGAGGATACCGAGGTGACACAGCAGCG 168820  
 QY 101 AlaGly 102  
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 Db 168819 GCGGG 168814

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

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RESULT 11
AC025557/c
LOCUS      171945 bp      DNA      linear      HTG 07-JUL-2000
DEFINITION Homo sapiens chromosome 12 clone RP11-579D7, WORKING DRAFT
SEQUENCE, 17 unordered pieces.
ACCESSION AC025557
VERSION    4
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            Waterston,R.H.
            The sequence of Homo sapiens clone
            Unpublished
            2 (bases 1 to 171945)
            Waterston,R.H.
            Direct Submission
            Submitted (10-MAR-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
            On Apr 27, 2000 this sequence version replaced gi:7574970.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0579D07
----- Summary Statistics -----
Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 166140 bases at least Q40
Consensus quality: 167959 bases at least Q30
Consensus quality: 168924 bases at least Q20
Insert size: 177000; agarose-fp
Insert size: 170345; sum-of-ctnigs
Quality coverage: 5.62 in Q20 bases; agarose-fp
Quality coverage: 5.86 in Q20 bases; sum-of-ctnigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1863 1962: gap of unknown length
* 3736: contig of 1774 bp in length
* 3737 3836: gap of unknown length
* 3837 6925: contig of 3089 bp in length
* 6926 7025: gap of unknown length
* 7026 11773: contig of 4748 bp in length
* 11774 11873: gap of unknown length
* 11874 19405: contig of 7532 bp in length
* 19406 19505: gap of unknown length
* 19506 26329: contig of 6824 bp in length
* 26330 26429: gap of unknown length
* 26430 33594: contig of 7165 bp in length
* 33595 33694: gap of unknown length
* 33695 42148: contig of 8454 bp in length
* 42149 42249: gap of unknown length
* 42249 52391: contig of 10142 bp in length
* 52391 52491: gap of unknown length
* 52491 62388: contig of 9898 bp in length
* 62389 72408: gap of unknown length
* 72408 72408: contig of 9920 bp in length

* 72409 72508: gap of unknown length
* 72509 84743: contig of 12235 bp in length
* 84843 97522: contig of 12679 bp in length
* 97523 97622: gap of unknown length
* 97623 110884: contig of 13262 bp in length
* 110885 126977: contig of 15993 bp in length
* 126978 127077: gap of unknown length
* 127078 146137: contig of 19060 bp in length
* 146138 146237: gap of unknown length
* 146238 171945: contig of 25708 bp in length.
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             /db_xref="taxon:9606"
             /chromosome="12"
             /clone="RP11-579D7"
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         1863..3736
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         3837..6925
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         7026..11773
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         11874..19405
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         19506..26329
             /note="assembly_name:Contig10"
         26430..33594
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         clone_end:SP6
         vector_side:left
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             /note="assembly_name:Contig17"
         97623..110884
             /note="assembly_name:Contig18"
         110985..126977
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         127078..146137
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BASE COUNT  43195 a 42962 c 41369 g 42818 t 1601 others
ORIGIN
Alignment Scores:
Pred. No.:      1.51e-23      Length:      171945
Score:          518.00      Matches:      98
Percent Similarity: 96.08%      Conservative: 0
Best Local Similarity: 96.08%      Mismatches: 4
Query Match:     90.88%      Indels:      1
DB:              2          Gaps:      0
US-09-750-240-2 (1-104) x AC025557 (1-171945)
Qy      1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20
Db      79560 ATGTCATGGTTTACTGGCCCTCTGTCCTCTAAAGTGGATGAACGAAACACCTGGGGT 79501

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QY 21 GluArgAsnGlyClnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
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Db 79500 GAACGCAATGGCAGAGCGTTCCGCGCGCTGGGCACTCGGCAGTGGCTTCGCACG 79441

QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
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QY 61 ProArgCysProTrpClnAspAlaPheIleArgArgGlyGlyPro***LysGlyLys 80
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Db 79381 CTTGGTGGCCCTGGCAGGATGAGCGCTTCATCCGGAGGGGGCCAGGCAAGGGCAAG 79322

QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
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Db 79321 GAGCTGGGCTGGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACGACAGCG 79262

QY 101 AlaGly 102
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Db 79261 GCGGG 79256

RESULT 12
DOGADENCYC 4046 bp mRNA linear MAM 27-APR-1993
LOCUS Canis familiaris adenylyl cyclase type VI mRNA sequence.
DEFINITION M94968
ACCESSION M94968
VERSION M94968.1 GI:163896
KEYWORDS adenylyl cyclase type VI.
SOURCE Canis familiaris cardiac muscle cDNA to mRNA.
ORGANISM Canis familiaris
REFERENCE 1 (bases 1 to 4046)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
AUTHORS Katsushika, S., Chen, L., Kawabe, J., Nilakantan, R., Halnon, N.J.,
Honey, C.J. and Ishikawa, Y.
TITLE Cloning and characterization of a sixth adenylyl cyclase isoform:
types V and VI constitute a subgroup within the mammalian adenylyl
cyclase family
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (18), 8774-8778 (1992)
MEDLINE 92409599
PUBMED 1528892
FEATURES
source
location/Qualifiers
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Alignment Scores:
Pred. No.: 4.7e-22 Length: 4046
Score: 472.50 Matches: 89
Percent Similarity: 85.05% Conservative: 2
Best Local Similarity: 83.18% Mismatches: 11
Query Match: 82.89% Indels: 5
DB: 4 Gaps: 2
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QY 1 MetSerTrpPheSerClyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20
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QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
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US-09-750-240-2 (1-104) x DOGADENCYC (1-4046)
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QY 61 ProArgCysProTrpClnAspAlaPheIleArgArgGlyGlyPro***LysGlyLys 80
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QY 97 ThrThrThrProAlaGlyPro 103
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Db 428 GGGCAGCTGGAGGTGGCCCT 448

RESULT 13
LOCUS I29958
DEFINITION Sequence 1 from patent US 5578481.
ACCESSION I29958
VERSION I29958.1 GI:1820749
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4046)
AUTHORS Ishikawa, Y.
TITLE Cloning and characterization of a cardiac adenylyl cyclase
JOURNAL Patent: US 5578481-A 1 26-NOV-1996;
FEATURES
location/Qualifiers
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/organism="unknown"
BASE COUNT 743 a 1202 c 1257 g 844 t
ORIGIN
Alignment Scores:
Pred. No.: 4.7e-22 Length: 4046
Score: 472.50 Matches: 89
Percent Similarity: 85.05% Conservative: 2
Best Local Similarity: 83.18% Mismatches: 11
Query Match: 82.89% Indels: 5
DB: 6 Gaps: 2
US-09-750-240-2 (1-104) x I29958 (1-4046)
QY 1 MetSerTrpPheSerClyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20
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QY 21 GluArgAsnGlyClnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
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Db 191 GAACGCAATGGCAGAGCGTCCA---CGCCCGGGGACTCGGACCACTGGCTTCTGCACG 247

QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
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Db 248 CCCCCTATATAGTGCCTCCGGATGCAGAGCCACCCAGTCCACCCCTGGCGTCCC 307

QY 61 ProArgCysProTrpClnAspAlaPheIleArgArgGlyGlyPro***LysGlyLys 80
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Db 308 CCTCGTGGCCCTGGCAGGATGAGCGCTTCATCCGAGAGGGCGGCCGGAAGGGCAGC 367

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Db 368 GAGCTGGGCTGGCGGCGTGGCCCTGGGCTTCGAGGACACTGAGGCCCATGTCAGCGGTT 427

QY 97 ThrThrThrProAlaGlyPro 103
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Db 428 GGGCAGCTGGAGGTGGCCCT 448

RESULT 14
LOCUS AR106659
DEFINITION Sequence 11 from patent-US 6107076.
ACCESSION AR106659
VERSION AR106659.1 GI:12821189
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

```

REFERENCE 1 (bases 1 to 4131)  
AUTHORS Tang,W.-J. and Gilman,A.G.  
TITLE Soluble mammalian adenylyl cyclase and uses therefor  
JOURNAL Patent: US 6107076-A 11 22-AUG-2000;  
FEATURES Location/Qualifiers  
1. .4131  
/organism="unknown"

BASE COUNT 835 a 1190 c 1182 g 924 t  
ORIGIN

Alignment Scores:  
Pred. No.: 1.99e-19 Length: 4131  
Score: 432.00 Matches: 81  
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US-09-750-240-2 (1-104) x AR106659 (1-4131)

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RESULT 15  
RATADCYB 4131 bp mRNA linear ROD 27-APR-1993  
LOCUS  
DEFINITION Rattus norvegicus adenylyl cyclase type VI mRNA, complete cds.  
ACCESSION M96160  
VERSION M96160.1 GI:202718  
KEYWORDS adenylyl cyclase; adenylyl cyclase type VI.  
SOURCE Rattus norvegicus (strain Sprague-Dawley) adult liver, kidney, heart cDNA to mRNA.  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 4131)  
AUTHORS Premont,R.T.  
TITLE Multiple mechanisms underlying desensitization of the liver adenylyl cyclase system. Structure and cAMP regulation of liver adenylyl cyclases  
Thesis (1992)  
2 (bases 1 to 4131)  
AUTHORS Premont,R.T., Chen,J., Ma,H.W., Ponnappalli,M. and Iyengar,R.  
TITLE Two members of a widely expressed subfamily of hormone-stimulated adenylyl cyclases  
Proc. Natl. Acad. Sci. U.S.A. 89 (20), 9809-9813 (1992)  
JOURNAL MEDLINE 93028552  
PUBMED 1409703  
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BASE COUNT 835 a 1190 c 1182 g 924 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 1.99e-19 Length: 4131  
Score: 432.00 Matches: 81  
Percent Similarity: 86.27% Conservative: 7  
Best Local Similarity: 79.41% Mismatches: 12  
Query Match: 75.79% Indels: 2  
DB: 6 Gaps: 2  
US-09-750-240-2 (1-104) x RATADCYB (1-4131)

Qy 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
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Db 116 GAACGCAATGACAGACGCGCCCA---CGCCAGCGGACCCGCGGCTTCTGCGCG 172  
Qy 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
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Db 173 CCCCGCTACATGAGCTGCTCAAGAATGTGGAGCCACCCAGCCCACTCTGCGAGCTGCG 232  
Qy 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro\*\*LysGlyLys 80  
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Db 233 ACTGGTGGCCCTGGCAGGATGAGCCTTCATCAGGAGGCGTGGCCCGGAAGGGGTGTG 292  
Qy 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
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Db 293 GAGTGGGGCTGCGGTCACTAGTGGCTTGGGTTTGTATGACACTGAGGTG---ACCACACCG 349  
Qy 101 AlaGly 102  
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Db 350 ATGGGG 355

Search completed: March 1, 2003, 11:05:22







GenCore version 5.1.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 1, 2003, 03:53:43 ; Search time 219 Seconds  
(without alignments)  
1069.442 Million cell updates/sec

Title: US-09-750-240-2  
Perfect score: 570  
Sequence: 1 MSWFGSLVVKVDERKTAWG.....RAVALGFEDTEVTTPAGPL 104

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	568	99.6	314	22	Human partial card
2	568	99.6	2127	19	Human adenylyl cycl
3	545	95.6	3549	22	Human cardiac aden
4	545	95.6	3552	22	Human cardiac aden
5	545	95.6	3582	22	Human modified car
6	545	95.6	4942	20	Human type VI aden
7	472.5	82.9	4046	14	Cardiac adenylyl c
8	432	75.8	4131	21	Type VI adenylyl c
9	432	75.8	5841	24	Mouse ischaemic co
10	94	16.5	1533	23	Pseudomonas aerugi
11	94	16.5	2312	14	snmr coding sequen
12	92.5	16.2	2622	22	Human cDNA sequen
13	91.5	16.1	3474	9	Sequence of Herpes
14	91.5	16.1	4257	19	The nucleotide seq
15	91.5	16.1	4257	19	Infected cell prot
16	91.5	16.1	12001	16	HSV L/SF region.
17	90.5	15.9	1173	21	Maize cyclin delta
18	90.5	15.9	1932	20	Human cDNA clone (
19	90	15.8	777	22	Human cDNA sequen
20	90	15.8	2612	22	HSVgB gene. Herpe
21	90	15.8	3465	12	Streptomyces clavu
22	89.5	15.7	1182	19	Sequence encoding
23	89.5	15.7	1879	12	Streptomyces clavu
24	89.5	15.7	7193	19	DNA fragment encod
25	89	15.6	3642	6	Human prostate exp
26	88.5	15.5	1032	23	Human polynucleoti
27	88.5	15.5	3387	22	Human polynucleoti
28	88.5	15.5	3394	22	Fusion gene of tre
29	88.5	15.5	4098	23	Human Huntington's
30	88.5	15.5	12749	20	M. capsulatus gene
31	88	15.4	1974	24	Glycoprotein B (gB
32	88	15.4	3472	14	Herpes simplex vir
33	88	15.4	10862	22	Human nervous syst
34	88	15.4	10982	22	Human nervous syst
35	88	15.4	49634	24	Kidney cancer rela
36	88	15.4	49634	24	Amycolatopsis medi
37	88	15.4	53789	19	Thermus thermophil
38	87.5	15.4	2127	23	Human secreted pro
39	87	15.3	1544	20	Human EST-derived
40	87	15.3	1622	22	Vector pVGRXR enco
41	87	15.3	2241	21	Control vector pVg
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43	87	15.3	2301	21	DNA encoding novel
44	87	15.3	9110	24	
45	87	15.3	16489	22	

ALIGNMENTS

RESULT 1

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ID AAD08561 standard; cDNA; 314 BP.  
XX  
AC AAD08561;  
XX  
DT 04-SEP-2001 (first entry)  
XX

Human partial cardiac adenylylase VI (ACVI) isoform #1 cDNA.

Human; cardiant; beta-adrenergic signalling protein; beta-ASP;  
myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
adenylylase; adenylylase; cAMP synthetase;  
G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ss.  
Homo sapiens.  
XX  
OS

PH Key Location/Qualifiers  
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PN W0200148164-A2.  
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XX PD 05-JUL-2001.  
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XX 26-DEC-2000; 2000WO-US35411.  
XX PF  
XX 27-DEC-1999; 99US-0472667.  
XX PR  
XX (REGC ) UNIV CALIFORNIA.  
XX PA  
XX PI Hammond HK, Gao M;  
XX  
XX WPI: 2001-418260/44.  
XX P-PSDB; AAE04308.  
XX  
XX Novel polynucleotide encoding a modified adenylcyclase polypeptide  
XX useful for enhancing cardiac function in mammalian hearts, and for  
XX treating heart disease, especially congestive heart failure -  
XX  
XX Example 5; Page 114; 153pp; English.  
XX  
XX The present invention relates to methods and compositions for enhancing  
XX cardiac function in mammalian hearts by inserting transgenes encoding  
XX beta-adrenergic signalling proteins (beta-ASP) which increase  
XX beta-adrenergic responsiveness within the myocardium using in vivo  
XX gene therapy. The beta-ASPs of the invention include beta-adrenergic  
XX receptors (beta-AR), adenylcyclases (also referred as adenylcyclase,  
XX adenylylate cyclase and cAMP synthetase) and G-protein receptor kinase  
XX (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
XX in mammalian hearts and for treating heart disease, especially  
XX congestive heart failure. The present cDNA sequence encodes human  
XX partial cardiac adenylcyclase VI (ACVI) isoform which is used for  
XX generating a third beta-ASP transgene, used in the exemplification  
XX of the invention.  
XX  
SQ Sequence 314 BP; 60 A; 98 C; 108 G; 47 T; 1 other;

Alignment Scores:  
Pred. No.: 2.76e-36 Length: 314  
Score: 568.00 Matches: 104  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.65% Indels: 0  
DB: 22 Gaps: 0

US-09-750-240-2 (1-104) x AAD08561 (1-314)

Qy 1 MetSerTTPheSerGlyLeuLenValProLysValAspGluArgLysThrAlaTrpGly 20  
Db 1 AFGTCAGTGTATAGTGGCTCTGTGCTCCTAAGTGGATGAACGGAACACCTGGGGT 60  
Qy 21 GluArgAnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
Db 61 GAACGCAATGGCAGACGTCGGGGCGCGCTGGCACTCGGGCAGGTGCTTCGCACG 120  
Qy 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
Db 121 CCCCGCTATATAGTGGCTCGGGATGCAGAGCCACCCACCCCTCGGGCCCC 180  
Qy 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro\*\*IysGlyLys 80  
Db 181 CCTCGGTGCCCCCTGACAGATGACGCCCTCATCCGGAGGGGGCGGCCCAAGGCAAG 240  
Qy 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100

Db 241 GAACCTGGGGCTGCGGCGAGTGGCTGGCTCGAAGATACCGAAGTCAACACGACCG 300  
Qy 101 AlaGlyProLeu 104  
Db 301 GCGGACCGCTG 312  
RESULT 2  
AAV23246  
ID AAV23246 standard; cDNA; 2127 BP.  
XX  
XX AAV23246;  
XX  
XX 17-JUL-1998 (first entry)  
XX  
XX Human adenylcyclase isoform VI encoding cDNA.  
XX  
XX Human; adenylcyclase VI; AC-VI; beta-adrenergic signalling protein;  
XX transgene; gene therapy; congestive heart failure; cardiac function;  
XX adenovirus; ss.  
XX  
XX Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 1..2127  
FT /\*tag= a  
FT /product= "adenylcyclase isoform VI"  
FT /transl\_except= (pos:229..231,aa:xaa)  
FT /transl\_except= (pos:315..317,aa:xaa)  
FT /note= "no stop codon given; xaa = unknown"  
FT misc\_difference 315  
FT /\*tag= b  
FT /note= "n indicates a gap of about 0.5 kb"  
XX  
XX W09810085-A2.  
XX PD 12-MAR-1998.  
XX  
XX 05-SEP-1997; 97WO-US15610.  
XX  
XX 16-JUN-1997; 97US-0048933.  
XX PR 05-SEP-1996; 96US-0708661.  
XX  
XX (COLL-) COLLATERAL THERAPEUTICS.  
XX (REGC-) UNIV-CALIFORNIA.  
XX  
XX Gao M, Hammond HK, Insel PA, Ping P, Post SR;  
XX WPI: 1998-193633/17.  
XX P-PSDB; AAW53345.  
XX  
XX Vectors containing transgene(s) encoding beta-adrenergic signalling  
XX proteins - useful for gene therapy of congestive heart failure  
XX  
XX Claim 60; Fig 12A; 114pp; English.  
XX  
XX The present sequence encodes human adenylcyclase isoform VI (AC-VI)  
XX from the present invention. The present invention describes a  
XX recombinant replication-defective viral particle (I) comprising a gene  
XX encoding a beta-adrenergic signalling protein (beta-ASP) operably  
XX linked to a promoter. Also described are: (1) a recombinant pro-viral  
XX plasmid (Ia) comprising a gene encoding a beta-ASP, as above, operably  
XX linked to a promoter and further comprising a replication-defective  
XX viral genome; (2) a (mammalian) cell transfected with (1) or (Ia); (3)  
XX an isolated polynucleotide comprising a sequence encoding a human  
XX adenylcyclase isoform VI (AC-VI), or a variant having AC activity;  
XX (4) a human AC-VI encoded by (3); (5) an isolated polynucleotide  
XX sequence which hybridises at high stringency to (3); and (6) a vector  
XX comprising the polynucleotide of (3). (1) can be used to form a  
XX filtered adenovirus particle preparation. (1) is used to enhance  
XX cardiac function in mammals.  
XX  
XX Sequence 2127 BP; 421 A; 637 C; 615 G; 452 T; 2 other;

```

Alignment Scores:
Pred. No.: 1,86e-35 Length: 2127
Score: 568.00 Matches: 104
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.65% Indels: 0
DB: 19 Gaps: 0

US-09-750-240-2 (1-104) x AAV23246 (1-2127)

QY 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20
   |||||
Db 1 ATGTCATGGTTAGTGGCTCCTCGTCCCTAAAGTGGATGAACGGAACACAGCGCTGGGT 60

QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
   |||||
Db 61 GAACGCAATGGGCGAGAGCGTTCCGCGCGCCGCTGGCACTCGGCGAGGTGGCTTCTGCACG 120

QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
   |||||
Db 121 CCCCCTATATAGCTGCTCCGGGATGTCAGACCCACCGCCCTCGCGGGCCCC 180

QY 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro***LysGlyLys 80
   |||||
Db 181 CPTCGGTGCGCTCGCAGGATGACGCTTCATCCGGAGGGGGCGGCCANGCAGGCGCAAG 240

QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
   |||||
Db 241 GAACTGGGGTGGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACACAGCACCG 300

QY 101 AlaGlyProLeu 104
   |||||
Db 301 GCGGGACCGCTG 312

RESULT 3
ID AAD08563 standard; DNA; 3549 BP.
AC AAD08563;
XX
DT 04-SEP-2001 (first entry)
DE Human cardiac adenylylase VI (ACVI) isoform #1 DNA.
XX
KW Human; cardiant; beta-adrenergic signalling protein; beta-ASP;
KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;
KW adenylylase; adenylylase; adenylylase; adenylylase; adenylylase;
KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;
KW cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..3504
FT /*tag= a
FT /product= "Human cardiac adenylylase VI isoform #1"
FT /EC_number= "4.6.1.1"
XX
PN WO200148164-A2.
XX
PD 05-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US35411.
XX
PR 27-DEC-1999; 99US-0472667.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Hammond HK, Gao M;
XX
XX WPI; 2001-418260/44.
DR P-PSDB; AAE04310.

```

Novel polynucleotide encoding a modified adenylylase polypeptide useful for enhancing cardiac function in mammalian hearts, and for treating heart disease, especially congestive heart failure -

Example 5; Page 122-129; 153pp; English.

The present invention relates to methods and compositions for enhancing cardiac function in mammalian hearts by inserting transgenes encoding beta-adrenergic signalling proteins (beta-ASP) which increase beta-adrenergic responsiveness within the myocardium using in vivo gene therapy. The beta-ASPs of the invention include beta-adrenergic receptors (beta-AR), adenylylases (also referred to as adenylylase, adenylylase and cAMP synthetase) and G-protein receptor kinase (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function in mammalian hearts and for treating heart disease, especially congestive heart failure. The present DNA sequence encodes human cardiac adenylylase VI (ACVI) isoform which is used for generating a third beta-ASP transgene, used in the exemplification of the invention.

Sequence 3549 BP; 699 A; 1025 C; 1061 G; 764 T; 0 other;

Alignment Scores:

Pred. No.:	1-91e-33	Length:	3549
Score:	545.00	Matches:	99
Percent Similarity:	97.06%	Conservative:	0
Best Local Similarity:	97.06%	Mismatches:	3
Query Match:	95.61%	Indels:	0
DB:	22	Gaps:	0

US-09-750-240-2 (1-104) x AAD08563 (1-3549)

QY 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
 |||||  
 Db 1 ATGTCATGGTTAGTGGCTCCTCGTCCCTAAAGTGGATGAACGGAACACAGCGCTGGGT 60

QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
 |||||  
 Db 61 GAACGCAATGGGCGAGAGCGTTCCGCGCGCCGCTGGCACTCGGCGAGGTGGCTTCTGCACG 120

QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
 |||||  
 Db 121 CCCCCTATATAGCTGCTCCGGGATGTCAGACCCACCGCCCTCGCGGGCCCC 180

QY 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro\*\*\*LysGlyLys 80  
 |||||  
 Db 181 CPTCGGTGCGCTCGCAGGATGACGCTTCATCCGGAGGGGGCGGCCANGCAGGCGCAAG 240

QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
 |||||  
 Db 241 GAACTGGGGTGGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACACAGCACCG 300

QY 101 AlaGly 102  
 ||||  
 Db 301 GCGGG 306

RESULT 4  
 AAD08567  
 ID AAD08567 standard; DNA; 3552 BP.  
 XX  
 AC AAD08567;  
 XX  
 DT 04-SEP-2001 (first entry)  
 DE Human cardiac adenylylase VI (ACVI) isoform #2 DNA.  
 XX  
 KW Human; cardiant; beta-adrenergic signalling protein; beta-ASP;  
 KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
 KW adenylylase; adenylylase; adenylylase; adenylylase; adenylylase;  
 KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
 KW cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ds.  
 XX

OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT 1..3507  
FT /\*tag= a  
FT /product= "Human cardiac adenylylase VI isoform #2"  
FT /EC\_number= "4.6.1.1"  
XX  
PN WO200148164-A2.  
XX  
XX 05-JUL-2001.  
XX  
XX 26-DEC-2000; 2000WO-US35411.  
XX  
XX 27-DEC-1999; 99US-0472667.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Hammond HK, Gao M;  
XX WPI; 2001-418260/44.  
XX P-PSDB; AAE04311.  
XX  
XX Novel polynucleotide encoding a modified adenylylase polypeptide  
XX useful for enhancing cardiac function in mammalian hearts, and for  
XX treating heart disease, especially congestive heart failure -  
XX  
XX Claim 6; Page 134-140; 153pp; English.  
XX  
XX The present invention relates to methods and compositions for enhancing  
XX cardiac function in mammalian hearts by inserting transgenes encoding  
XX beta-adrenergic signalling proteins (beta-ASP) which increase  
XX beta-adrenergic responsiveness within the myocardium using in vivo  
XX gene therapy. The beta-ASPs of the invention include beta-adrenergic  
XX receptors (beta-AR), adenylylases (also referred as adenylylase,  
XX adenylylase cyclase and G-protein receptor kinase  
XX (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
XX in mammalian hearts and for treating heart disease, especially  
XX congestive heart failure. The present DNA sequence encodes human  
XX cardiac adenylylase VI (ACVI) isoform which is used for generating  
XX a fourth beta-ASP transgene, used in the exemplification  
XX of the invention.  
XX  
XX SQ Sequence 3552 BP; 686 A; 1037 C; 1068 G; 761 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 1.91e-33 Length: 3552  
Score: 545.00 Matches: 99  
Percent Similarity: 97.06% Conservative: 0  
Best Local Similarity: 97.06% Mismatches: 3  
Query Match: 95.61% Indels: 0  
DB: 22 Gaps: 0  
  
US-09-750-240-2 (1-104) x AAD08567 (1-3552)  
  
Qy 1 MetSerTrpPheSerGlyLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
-Db 1 ATGTGTCATGTTAGTGGCTCTCTGTCCTTAAGTGGATGAACGAAACAGCCCTGGGGT 60  
Qy 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
-Db 61 GAACGCAATGGGCAAGAACGTCGCGGGCGCGTGCGACTCGGCGAGGTGCTTGCACG 120  
Qy 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
-Db 121 CCCCGCTATATAGTCTCGGGATGCAGAGCCACCCACCCCTCGGGGCCCC 180  
Qy 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro\*\*\*LysGlyLys 80  
-Db 181 CCTCGGTCCCTGGCAGGATGACGCTTCATCCGGAGGGCGGCCACGAGGCAAGGCAAG 240  
Qy 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
-Db 100

Db 241 GAGCTGGGGTGGGGGCGAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACGACGCG 300  
Qy 101 AlaGly 102  
-Db 301 GCGGG 306  
RESULT 5  
AAD08568  
ID AAD08568 standard; cDNA: 3582 BP.  
XX  
XX AAD08568;  
XX  
XX 04-SEP-2001 (first entry)  
XX  
XX Human modified cardiac adenylylase VI (ACVI) isoform cDNA.  
XX  
XX Human; cardiant; beta-adrenergic signalling protein; beta-ASP;  
XX myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
XX adenylylase; adenylylase cyclase; CAMP synthetase;  
XX G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
XX cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ss.  
XX  
XX Homo sapiens.  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
XX CDS 22..3525  
XX /\*tag= a  
XX /product= "Human modified cardiac ACVI isoform"  
XX  
XX WO200148164-A2.  
XX  
XX 05-JUL-2001.  
XX  
XX 26-DEC-2000; 2000WO-US35411.  
XX  
XX 27-DEC-1999; 99US-0472667.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Hammond HK, Gao M;  
XX  
XX WPI; 2001-418260/44.  
XX P-PSDB; AAE04312.  
XX  
XX Novel polynucleotide encoding a modified adenylylase polypeptide  
XX useful for enhancing cardiac function in mammalian hearts, and for  
XX treating heart disease, especially congestive heart failure -  
XX  
XX Claim 4; Page 143-150; 153pp; English.  
XX  
XX The present invention relates to methods and compositions for enhancing  
XX cardiac function in mammalian hearts by inserting transgenes encoding  
XX beta-adrenergic signalling proteins (beta-ASP) which increase  
XX beta-adrenergic responsiveness within the myocardium using in vivo  
XX gene therapy. The beta-ASPs of the invention include beta-adrenergic  
XX receptors (beta-AR), adenylylases (also referred as adenylylase,  
XX adenylylase cyclase and CAMP synthetase) and G-protein receptor kinase  
XX (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
XX in mammalian hearts and for treating heart disease, especially  
XX congestive heart failure. The present cDNA sequence encodes human  
XX modified cardiac adenylylase VI (ACVI) isoform which is used for  
XX generating a beta-ASP transgene, used in the exemplification of the  
XX invention.  
XX  
XX SQ Sequence 3582 BP; 703 A; 1036 C; 1067 G; 776 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 1.93e-33 Length: 3582  
Score: 545.00 Matches: 99  
Percent Similarity: 97.06% Conservative: 0  
Best Local Similarity: 97.06% Mismatches: 3  
Query Match: 95.61% Indels: 0

```

DB:          22          Gaps:          0
US-09-750-240-2 (1-104) x AAD08568 (1-3582)
QY 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20
   |||
Db 22 ATGTCATGTTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAAACAGCGCTGGGT 81
QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
   |||
Db 82 GAACGCAATGGCGAAGCGCTTCGCGCGCCGCGGACATCGGCGCAGTGGCTTCTGCACG 141
QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
   |||
Db 142 CCCCGCTATATGAGTCCCTCCGGGATGCAGAGCCACCCAGCCCGCTGGGGGCC 201
QY 61 ProArgCysProTrpGlnAspAspAlaPheIleArgArgGlyGlyPro***LysGlyLys 80
   |||
Db 202 CCTCGGTGCCCTGGCAGGATGACGCTTCATCCGGAGGGCGCGCCCAAGGCAAGGCAAG 261
QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
   |||
Db 262 GAGCTGGGCTGGGGCAGTGGCCCTTCGAGGATACCGAGGTGACAGCAGCG 321
QY 101 AlaGly 102
   |||
Db 322 GCGGG 327

RESULT 6
AAX00461
ID AAX00461 standard; cDNA; 4942 BP.
XX
AC AAX00461;
XX
DT 21-MAY-1999 (first entry)
XX
DE Human type VI adenylyl cyclase cDNA.
XX
KW Adenylyl cyclase type VI; human; hAC6; therapy; diagnosis; ds.
XX
OS Homo sapiens.
XX
FH Key
FT CDS
FT Location/Qualifiers
   145..3651
   /*tag= a
XX
PN WO9901547-A1.
XX
PD 14-JAN-1999.
XX
XX 01-JUL-1998; 98WO-US13694.
XX
PR 01-JUL-1997; 97US-0886550.
PR 01-JUL-1997; 97US-0070904.
XX
PA (CORT-) COR THERAPEUTICS INC.
XX
PI Tomlinson JA;
XX
WPI: 1999-106049/09.
DR P-PSDB; AAW30599.
XX
PT Newly isolated and purified human type VI adenylyl cyclase (hAC6)
PT polypeptide - useful for identifying potential therapeutic agents
PT that modulate hAC6 activity, and for the diagnosis of
PT hAC6-associated diseases and disorders
XX
PS Claim 3; Fig 1A-I; 42pp; English.
XX
CC This DNA sequence encodes human type VI adenylyl cyclase (hAC6), see
CC AAW30599) that is expressed mainly in the heart and brain. hAC6 has
CC a similar putative structure to other adenylyl cyclase isoforms
CC but, like type V, is distinguishable in that it has a larger

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CC N-terminus and a relatively shorter C-terminus as it lacks the C2b
CC region. hAC6 cDNA was initially isolated from a human heart cDNA
CC library using an adenylyl cyclase PCR fragment as probe. It was
CC used to design primers that were used in a PCR-based RACE to obtain
CC the full-length cDNA sequence. The invention relates to the hAC6
CC gene, methods for the recombinant production of purified hAC6 and
CC the proteins made by these methods, antibodies against hAC6,
CC vectors, probes and host cells (especially HEK-293) transformed by
CC genes encoding polypeptides having hAC6 activity, along with
CC diagnostic and therapeutic uses for these various reagents. hAC6
CC can be used as a tool to screen for agonists and antagonists that
CC stimulate/inhibit hAC6. Such compounds have therapeutic utility
CC in treating diseases caused by aberrant activity of this enzyme.
CC and diseases whose symptoms can be ameliorated by stimulating or
CC inhibiting the activity of hAC6.
XX
SQ Sequence 4942 BP; 953 A; 1404 C; 1512 G; 1073 T; 0 other;

Alignment Scores:
Pred. No.:      2,66e-33      Length:      4942
Score:          545.00      Matches:      99
Percent Similarity: 97.06%      Conservative: 0
Best Local Similarity: 97.06%      Mismatches: 3
Query Match:      95.61%      Indels:      0
DB:              20          Gaps:          0

US-09-750-240-2 (1-104) x AAX00461 (1-4942)
QY 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20
   |||
Db 145 ATGTCATGTTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAAACAGCGCTGGGT 204
QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
   |||
Db 205 GAACGCAATGGCGAAGCGCTTCGCGCGCCGCGCCTTCGCGCAGTGGCTTCTGCACG 264
QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
   |||
Db 265 CCCCGCTATATGAGTCCCTCCGGGATGCAGAGCCACCCAGCCCGCTGGGGGCC 324
QY 61 ProArgCysProTrpGlnAspAspAlaPheIleArgArgGlyGlyPro***LysGlyLys 80
   |||
Db 325 CCTCGGTGCCCTGGCAGGATGACGCTTCATCCGGAGGGCGCGCCCAAGGCAAGGCAAG 384
QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
   |||
Db 385 GAGCTGGGCTGGGGCAGTGGCCCTTCGAGGATACCGAGGTGACAGCAGCG 444
QY 101 AlaGly 102
   |||
Db 445 GCGGG 450

RESULT 7
AAX042525
ID AAX042525 standard; DNA; 4046 BP.
XX
AC AAX042525;
XX
DT 14-SEP-1993 (first entry)
XX
DE Cardiac adenylyl cyclase gene.
XX
KW Regulation; cardiac function; heart; heart failure; ss.
XX
OS Canis familiaris.
XX
FH Key
FT CDS
FT Location/Qualifiers
   131..3627
   /*tag= a
XX
XX EP543137-A.
XX
XX 26-MAY-1993.

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XX PF 12-OCT-1992; 92EP-0117374.
XX XX
PR 18-NOV-1991; 91US-0793961.
XX XX
PA (AMCY ) AMERICAN CYANAMID CO.
XX XX
PI Ishikawa Y;
XX XX
DR WPI: 1993-168873/21.
DR P-PSDB; AAR37309.
XX XX
PT Purified DNA encoding cardiac adenyl cyclase - useful to screen
PT for cpds. which stimulate activity of the cyclase
XX
XX Claim 1; Fig 2; 34pp; English.
XX
CC A canine heart cDNA library was constructed in lambda gt10 and was
CC screened with a 970 bp AatI-HincII fragment from type I adenyl
CC cyclase cDNA probe (encodes the first cytoplasmic domain of adenyl
CC cyclase, which has significant homology to other previously known
CC types of adenyl cyclase). One positive clone, of 5.4 kb was obtd.
CC Positive colonies were subcloned into pUC18 and further subcloned
CC and sequenced bidirectionally. The 5.4 kb clone was used to
CC rescreen the library and on overlapping clone contg. the 5' end of
CC the gene was isolated. Together the two clones cover the complete
CC canine cardiac adenyl cyclase gene. The gene is suspected of
CC being involved in the regulation of cardiac function and it is thought
CC that decreased activity of adenyl cyclase in the heart may be a
CC major factor in the development of heart failure. Thus the adenyl
CC cyclase gene is useful to screen cpds. which stimulate the activity
CC of the cyclase.
XX
SQ Sequence 4046 BP; 743 A; 1206 C; 1254 G; 843 T; 0 other;

Alignment Scores:
Pred. No.: 9,62e-28 Length: 4046
Score: 472.50 Matches: 89
Percent Similarity: 85.05% Conservative: 2
Best Local Similarity: 83.18% Mismatches: 11
Query Match: 82.89% Indels: 5
DB: 14 Gaps: 2

US-09-750-240-2 (1-104) x AAQ42525 (1-4046)
QY 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20
Db 131 ATGTCGTGTTTAGTGGCCCTCTGTGCCCAAGTGGATGAACGGAACACAGCCCTGGGGT 190
QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
Db 191 GAACGCAATGGCAGACAGGGTCCA--CGCCGCGGAGCTCGACCATGGCTTCGTGCAGG 247
QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
Db 248 CCCCCTATATAGCTGCTCGGGATGGCAGCCCGCCAGTCCACCCCTCGCGCTCCC 307
QY 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro***LysGlyLys 80
Db 308 CCTCGGTGCCCTGGCAGATGAGGCTTCATCCGGAGAGCGGCCCGGCAAGGCGACG 367
QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGlu-----Val 96
Db 368 GAGCTGGGGCTCGGGCGGTGGCCCTTCGGCTTCGAGGACACTGAGCCCATGTCACGGGTT 427
QY 97 ThrThrThrProAlaGlyPro 103
Db 428 GGGGAGCTGGAGGTGGCCCT 448

RESULT 8
AAA53923
ID AAA53923 standard; cDNA; 4131 BP.
XX

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```

.AC AAA53923;
XX XX
DT 03-JAN-2001 (first entry)
XX XX
DE Type VI adenyl cyclase coding sequence.
XX XX
KW Adenyl cyclase; type I; type II; recombinant; enzyme; CAMP;
KW cyclic AMP; adenosine monophosphate; screening; stimulation;
KW inhibition; treatment; cholera; pituitary tumour; heart failure;
KW ischaemia; endocrine disorder; cell necrosis;
KW pseudohypoparathyroidism; endocrine deficiency; human; ss.
XX OS Homo sapiens.
XX XX
FH Key Location/Qualifiers
FT CDS 14..3536
FT /tag= a
FT /product= Type VI adenyl cyclase
XX
PN US6107076-A.
XX
PD 22-AUG-2000.
XX
PF 04-OCT-1996; 96US-0726214.
XX
PR 04-OCT-1995; 95US-0005498.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX Gilman AG, Tang W;
XX WPI: 2000-578539/54.
XX P-PSDB; AAB02010.
XX
PT Novel soluble mammalian polypeptide composition comprising adenyl
PT cyclase activity for screening stimulators and inhibitors of adenyl
PT cyclase, is activated by Gsalpha
XX
XX Disclosure; Columns 75-78; 73pp; English.
XX
XX A recombinant Adenyl cyclase is described which lacks membrane
XX bound domains. Separation and purification of the recombinant
XX enzyme is much easier compared with wild type enzymes and the
XX recombinant enzyme is more stable than the wild type enzyme which
XX allows easier screening of compounds that stimulate and inhibit
XX Adenyl cyclase activity. The recombinant adenyl cyclase comprises
XX a chimera of adenyl cyclase C_1 and C_2 domains linked covalently.
XX The domains may be linked by a linker peptide. The recombinant
XX adenyl cyclase is useful for screening inhibitors and stimulators
XX of adenyl cyclase activity. Inhibitors of the enzyme are useful for
XX treating cholera, pituitary tumors, heart failure, ischaemia,
XX endocrine disorders and cell necrosis. Stimulators of adenyl
XX cyclase are useful for treating pseudohypoparathyroidism and other
XX endocrine deficiencies.
XX
SQ Sequence 4131 BP; 835 A; 1190 C; 1182 G; 924 T; 0 other;

Alignment Scores:
Pred. No.: 1.4e-24 Length: 4131
Score: 432.00 Matches: 81
Percent Similarity: 86.27% Conservative: 7
Best Local Similarity: 79.41% Mismatches: 12
Query Match: 75.79% Indels: 2
DB: 21 Gaps: 2

US-09-750-240-2 (1-104) x AAA53923 (1-4131)
QY 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20
Db 56 ATGTCATGTTTAGCGGCTCTCTGTTCCTCCAAAGTGGATGAACGGAACACCCCTGGGCG 115
QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
Db 115 ATGTCATGTTTAGCGGCTCTCTGTTCCTCCAAAGTGGATGAACGGAACACCCCTGGGCG 115

```

```
Db 116 GAGCGCAATGGACAGAGCCGCCA---CGCCAGCGGACCGACCGCGTGGCTTCTCGCGG 172
QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
Db 173 CCCCGCTACATGAGCTGCCTCAGATGTGGACCCACCCAGCCCTCTCTGAGCTCGC 232
QY 61 ProArgCysProTrpGlnAspAlaPheIleArgGlyGlyPro***LysGlyLys 80
Db 233 ACTCGGTGCCCTGGCAGGATGAAGCTTCATCAGGAGGCTGCCCGGGAAGGGTGTG 292
QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
Db 293 GAGCTGGGGTGGCGTCAAGTGGCTTGGGTTTGTATGACACTGAGGTG---ACCACACCG 349
QY 101 AlaGly 102
Db 350 ATGGGG 355
RESULT 9
ABI99680
ID ABI99680 standard; cDNA; 5841 BP.
XX
AC ABI99680;
XX
DT 07-MAR-2002 (first entry)
XX
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:716.
XX
KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
XX
OS Mus musculus.
XX
PN WO200118188-A2.
XX
PD 22-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-JP041192.
XX
PR 18-MAY-2000; 2000JP-0145977.
XX
PA (UYN1-) UNIV NTHON SCHOOL JURIDICAL PERSON.
XX
PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX
WPI: 2002-034733/04.
XX
P-PSDB; ABB57257.
XX
PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or
PT by determining the expression profile of a gene group comprising these
PT genes -
XX
PS Claim 2; Page 1771-1780; 2690pp; English.
XX
CC The present invention describes a method for examining ischaemic
CC conditions, comprising measuring the expression levels of particular
CC genes (1) in a test sample or determining the expression profile of a
CC gene group in the sample comprising genes selected from (1). The method
CC is useful for examining the ischaemic condition (e.g. compressive
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC expression levels of particular genes (ABI99202 to ABI99912, encoding
CC the protein sequences in ABB57020 to ABB57374) or by determining the
CC expression profile of a gene group comprising these genes. The
CC expression levels or expression profiles produced by these genes are
CC used as an indicator when screening for ischaemic condition-improving
CC drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914
CC represent PCR primers for a mouse ischaemic condition related sequence,
CC which are used in the exemplification of the present invention.
XX
SQ Sequence 5841 BP; 1214 A; 1558 C; 1673 G; 1396 T; 0 other;
Alignment Scores:
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Pred. No.: 1.98e-24 Length: 5841
Score: 432.00 Matches: 81
Percent Similarity: 85.29% Conservative: 6
Best Local Similarity: 79.41% Mismatches: 13
Query Match: 75.79% Indels: 2
DB: Gaps: 2
US-09-750-240-2 (1-104) x ABI99680 (1-5841)
QY 1 MetSerTrpPheSerGlyLeuValProLysValAspGluArgLysThrAlaTrpGly 20
Db 96 ATGTCATGGTTAGTGGCCCTCGTTCCTCCAAAGTGGATGAACGAAACAGCTTGGGG 155
QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
Db 156 GAACGCAATGGCAGAGCGCCCA---CGCCACCGCAATCGACCGCTTCTCGGCA 212
QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
Db 213 CCTCGCTACATGAGCTGCCTCAAGAATGCGGAGCCACCCAGCCCTCTCTGAGCTCAC 272
QY 61 ProArgCysProTrpGlnAspAlaPheIleArgGlyGlyPro***LysGlyLys 80
Db 273 ACTCGGTGCCCTGGCAGGATGAAGCTTCATCAGGAGGCGCGCGGCGGGGTG 332
QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
Db 333 GAGCTGGGGTGGCGTCAAGTGGCTTGGGTTTGTACGACACTGAGGTG---ACCACACCG 389
QY 101 AlaGly 102
Db 390 ATGGGC 395
RESULT 10
AAS54118/c
ID AAS54118 standard; DNA; 1533 BP.
XX
AC AAS54118;
XX
DT 13-FEB-2002 (first entry)
XX
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #249.
XX
KW Antisense; ds; prokaryotic cellular proliferation gene;
KW antibiotic; antibacterial; drug design.
XX
OS Pseudomonas aeruginosa.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
WPI: 2001-611495/70.
XX
P-PSDB; AAU36259.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
```

PS Claim 27; Seq ID No 7755; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to

CC prokaryotic cellular proliferation, their use in identifying the

CC genes, their use in the discovery of novel antibiotics, the essential

CC genes themselves and the encoded proteins. The prokaryotes used are

CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*

CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The

CC invention is also useful for the identification of potential new targets

CC for antibiotic development. The antisense nucleic acids can also be used

CC to identify proteins used in proliferation, to express these proteins,

CC and to obtain antibodies capable of binding to the expressed proteins.

CC The proteins can be used to screen compounds in rational drug discovery

CC programmes. The antisense nucleic acid sequence is also useful to screen

CC for homologous nucleic acids which are required for cell proliferation in

CC a wide variety of organisms. The present sequence encodes an

CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic

CC format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences.

XX

SQ Sequence 1533 BP; 218 A; 515 C; 571 G; 229 T; 0 other;

Alignment Scores:

Pred. No.:	108	Length:	1533
Score:	94.00	Matches:	27
Percent Similarity:	43.48%	Conservative:	3
Best Local Similarity:	39.13%	Mismatches:	29
Query Match:	16.49%	Indels:	10
DB:	23	Gaps:	4

US-09-750-240-2 (1-104) x AAS54118 (1-1533)

QY 19 TrpGlyGluArgAsnGlyClnLysArgSerArgArgGly-----Thr 33

DB 514 TGGGTGCTGCGAGGATACAGCGGCAGTCGCCGATCAGGTGCGGGCGATCTCGACCA 455

QY 34 ArgAlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluPro--- 52

DB 454 TCTGCTGGTGGCGGATCGCGAGGTCCGCGACGAGGTGT---CGGGATCATCGCTCCA 398

QY 53 -----ProSerProThrProAlaGlyProProArgCysProTrpGlnAspAlaPhe 70

DB 397 GCGCGACCTGGCGCCATCGCTCGCGGCGCGCGCGCA---GGCGCGCAGCGTGCATCC 341

QY 71 IleArgArgGlyGlyPro\*\*LysGly 79

DB 340 AGCCGGCGCGCGGCGAGGTGCTGGA 314

RESULT 11

AAQ35141/c

ID AAQ35141 standard; DNA; 2312 BP.

XX

AC AAQ35141;

XX 24-MAY-1993 (first entry)

XX smR coding sequence.

KW Regulatory; activator; protein; smR; complementation experiment;

KW macrolide; biosynthetic; gene; transcription; S. ambifaciens;

KW biosynthesis; antibody; polyclonal; monoclonal; pathway; ss.

OS Streptomyces ambifaciens.

XX Key Location/Qualifiers

PH CDS 345..2312

FT

FT /tag= a

FT /note= "Claim 2"

FT misc\_feature 459..461

FT

FT /tag= b

FT /note= "Potential translation initiation codon"

FT misc\_feature 498..500

FT /tag= c

XX /note= "Potential translation initiation codon"

PN EP524832-A.

PD 27-JAN-1993.

XX

PF 24-JUL-1992; 92EP-0306792.

XX

PR 26-JUL-1991; 91US-0736178.

XX

PA (ELIL ) LILLY & CO ELI.

PI Rao RN, Turner JR;

XX WPI; 1993-028879/04.

DR P-PSDB; AAR31041.

XX

PT DNA encoding regulatory activator protein smR - for macrolide

PT biosynthesis to increase efficiency of antibiotic prodn.

XX

PS Disclosure; Page 3-4; 22pp; English.

XX

CC The sequence given encodes the regulatory (activator) protein smR.

CC This sequence has the ability in complementation experiments to

CC restore macrolide biosynthetic gene transcription in mutants having

CC defective smR genes due to insertional inactivation of that region

CC of the S. ambifaciens genome. The smR gene product activates

CC macrolide biosynthetic gene transcription and may be used to increase

CC the efficiency of macrolide biosynthesis. The translation product of

CC this gene is useful for the generation of antibodies (polyclonal or

CC monoclonal) which are useful in the detection of other macrolide

CC biosynthetic pathways.

XX

SQ Sequence 2312 BP; 342 A; 862 C; 782 G; 326 T; 0 other;

Alignment Scores:

Pred. No.:	163	Length:	2312
Score:	94.00	Matches:	36
Percent Similarity:	36.67%	Conservative:	8
Best Local Similarity:	30.00%	Mismatches:	38
Query Match:	16.49%	Indels:	38
DB:	14	Gaps:	9

US-09-750-240-2 (1-104) x AAQ35141 (1-2312)

QY 2 SerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThr----- 17

DB 1584 GCGTGGGTGAGCGGG-----GCGCCCGCATCAGGTCTCGAAGAACTCTCTGGTGGCTCT 1531

QY 18 ---AlaTrpGlyGluArgAsnGlyGlnLysArgSerArgArgGly----- 32

DB 1530 GCGCCTTGGGGAGTCTGCTGTCGACGCGAGGTGCGCGCGAGGGTGGGGCGACCA 1471

QY 33 ThrArgAlaGlyGly---PheCysThrProArg-----Tyr 43

DB 1470 TCGGGAGCAGGGGGACGCGGTGTGTCGCGTCCGCGACCGAGTCCGTCAGCAGGAAGC 1411

QY 44 MetSerCysLeuArgAspAla-----GluProProSerPro----- 55

DB 1410 CGGCGTTCCCGCGGGAAGCAGGGGCACGTCACACCCCGCGGCCACGAGGTGGGCC 1351

QY 56 -----ThrProAlaGlyProProArgCys---ProTrpGlnAspAlaPhe 70

DB 1350 GCGCGGTCTCGCGCGCGCGGCGCGCGCGCGCGCGTCTCGTGGGG----- 1303

QY 71 IleArgArgGlyGlyPro\*\*LysGlyLysGluLeuGlyLeuArgAlaValalaLeuGly 90

DB 1302 ---CGACGGGGCGCAGGTCCCGTACTCGGCGAGCGGGCGCGCGCGGTGCACAGGC 1246

RESULT 12

AAH16074







PS Disclosure; Fig 2; 63pp; English.

XX The herpes simplex virus (HSV) alpha-4 gene encodes infected cell protein  
 CC number 4 (ICP4). Both the alpha-4 gene and ICP4 can be used to block  
 CC cell apoptosis. Similarly the administration of an agent that inhibits  
 CC ICP4 or the alpha-4 gene can induce apoptosis in HSV infected cells.  
 CC This can be used for the immortalisation of cells, production of  
 CC proteins, gene therapy, or inhibition of cell death induced in vivo.  
 CC They can also be used for production of therapeutics comprising  
 CC inhibitors of HSV ICP4 function, useful for treating HSV function.  
 XX

SQ Sequence 4257 BP; 412 A; 1768 C; 1663 G; 414 T; 0 other;

Alignment Scores:

Pred. No.:	470	Length:	4257
Score:	91.50	Matches:	36
Percent Similarity:	42.86%	Conservative:	6
Best Local Similarity:	36.73%	Mismatches:	38
Query Match:	16.05%	Indels:	18
DB:	19	Gaps:	5

US-09-750-240-2 (1-104) x AAV10362 (1-4257)

QY	17	ThrAlaTrpGlyGluArgAsnGlyGlnLysArgSer-----ArgArg-ArgG1	32
DB	2786	ACCCCTGGGGGTGGCGCGCGAGCCCGGGCCAGCCACACGGCGCGCGCGCGG	2845
QY	32	yThrArgAlaGlyGly-PheCysThrProArgTyrMetSerCysLeuArgAspAlaGluP	52
DB	2846	CCGCGCCCTGGAGGCTACTGTCCCGCGCGCGCTGCGCGAGCTACGGAC---CACC	2902
QY	52	ro-ProSerProThrProAlaGlyProProArgCys-----ProTrpGlnAsp	67
DB	2903	CGCTGTTCCTCCCTGGCGACCGCCCTCATGTTTGACCCGGGGCCCTGGCCTCGA	2962
QY	68	AspAlaPheIleArgArgGlyGlyPro**LysGlyLysGluLeuGlyLeuArgAlaVal	87
DB	2963	TCGCGG-----CGCGGTGGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGG	3013
QY	88	AlaLeuGlyPheGluAspThrGluValThrThrProAlaGlyPro	103
DB	3014	GCG-----GCGAGGACGACGATAACCCACCCACCCCGCGCGGCGG	3052

Search completed: March 1, 2003, 09:07:43  
 Job time : 228 secs



GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 1, 2003, 09:01:49 ; Search time 44 Seconds  
(without alignments)  
724.872 Million cell updates/sec

Title: US-09-750-240-2

Perfect score: 570

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Scoring table: BLOSUM62

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
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-LIST=45 -DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09750240@cgn2.1.1.17@runat\_25022003\_103942\_24989 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
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-YGAPOP=10 -IGAPEXT=0.5 -DELOP=6 -DELEXT=7

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5: /cgn2.6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2.6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	545	95.6	3549	4	US-09-008-097-5
3	545	95.6	4942	4	US-09-474-076-1
4	472.5	82.9	4046	1	US-07-793-961A-1
5	472.5	82.9	4046	1	US-08-240-357-1
6	432	75.8	4131	3	US-07-726-214-11
7	94	16.5	2312	1	US-07-736-178C-1
8	91.5	16.1	4257	2	US-08-690-473-1
9	91.5	16.1	4257	4	US-09-259-821A-1
10	91.5	16.1	4257	4	US-08-843-659-1
11	91.5	16.1	12001	1	US-08-458-568A-11
12	89.5	15.7	1221	6	5212296-16

C 13	89.5	15.7	1879	6	5212296-5	Patent No. 5212296
C 14	88	15.4	3472	3	5244792-2	Patent No. 5244792
C 15	87	15.3	2241	3	US-09-144-759-17	Sequence 17, Appl
C 16	87	15.3	2295	3	US-09-144-759-19	Sequence 19, Appl
C 17	87	15.3	2301	3	US-09-144-759-21	Sequence 21, Appl
C 18	86.5	15.2	1078	4	US-09-452-239-41	Sequence 41, Appl
C 19	86	15.1	1108	5	PCT-US93-03035-1	Sequence 1, Appl
C 20	86	15.1	2368	3	US-09-032-365A-57	Sequence 57, Appl
C 21	85	14.9	4695	2	US-08-231-193A-57	Sequence 57, Appl
C 22	85	14.9	4695	2	US-08-486-272A-57	Sequence 57, Appl
C 23	85	14.9	4695	3	US-08-940-086A-57	Sequence 57, Appl
C 24	85	14.9	4695	4	US-08-940-035A-57	Sequence 57, Appl
C 25	85	14.9	4695	4	US-08-935-105A-57	Sequence 57, Appl
C 26	85	14.9	4695	4	US-09-648-797-57	Sequence 57, Appl
C 27	84.5	14.8	2728	3	US-09-188-930-213	Sequence 213, Appl
C 28	84	14.7	1656	3	US-08-659-188-17	Sequence 17, Appl
C 29	84	14.7	1656	3	US-08-655-227-17	Sequence 17, Appl
C 30	84	14.7	1656	3	US-08-655-241-17	Sequence 17, Appl
C 31	84	14.7	1656	4	US-09-398-326-17	Sequence 17, Appl
C 32	84	14.7	2970	5	PCT-US92-06391-1	Sequence 1, Appl
C 33	84	14.7	4800	3	US-09-106-638-1	Sequence 1, Appl
C 34	84	14.7	13953	4	US-09-738-884-3	Sequence 3, Appl
C 35	83	14.6	540	2	US-08-726-306A-182	Sequence 182, Appl
C 36	83	14.6	1430	4	US-09-492-985-1	Sequence 1, Appl
C 37	83	14.6	3624	1	US-07-951-715A-6	Sequence 6, Appl
C 38	83	14.6	3624	2	US-08-459-448A-6	Sequence 6, Appl
C 39	83	14.6	3624	3	US-08-459-595A-6	Sequence 6, Appl
C 40	83	14.6	3624	3	US-08-459-504B-6	Sequence 6, Appl
C 41	83	14.6	3624	3	US-08-459-444-6	Sequence 6, Appl
C 42	83	14.6	3624	3	US-09-053-549-7	Sequence 7, Appl
C 43	83	14.6	3624	4	US-09-547-422-6	Sequence 6, Appl
C 44	82.5	14.5	3060	1	US-08-714-991-26	Sequence 26, Appl
C 45	82.5	14.5	3090	1	US-08-102-942A-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1  
US-09-008-097-1  
; Sequence 1, Application US/09008097  
; Patent No. 6306830  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, H. Kirk  
; APPLICANT: Insel, Paul A.  
; APPLICANT: Ping, Peipei  
; APPLICANT: Post, Steven R.  
; APPLICANT: Gao, Meihua  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE  
; TITLE OF INVENTION: HEART FAILURE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/008,097  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dylan, Tyler M  
; REGISTRATION NUMBER: 37,612  
; REFERENCE/DOCKET NUMBER: 22000-20567.21

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..312
; OTHER INFORMATION:
US-09-008-097-1

Alignment Scores:
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.65% Indels: 0
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US-09-750-240-2 (1-104) x US-09-008-097-1 (1-314)
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Db 61 GAACGCAATGGCAGAACGCTTCGCGCGCGCTGCGCACTCGGCAGGTGGCTTCTGCACG 120
Qy 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
Db 121 CCCGCTATATGAGTCGCTCCGGGATGCAGAGCCACCCAGCCGCCCTCGGGGCCCC 180
Qy 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro**LysGlyLys 80
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Qy 101 AlaGlyProLeu 104
Db 301 GCGGACCGCGTG 312

RESULT 2
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; Sequence 5, Application US/09008097
; Patent No. 6306830
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. Kirk
; APPLICANT: Insel, Paul A.
; APPLICANT: Ping, Peipei
; APPLICANT: Post, Steven R.
; APPLICANT: Gao, Meihua
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
; TITLE OF INVENTION: HEART FAILURE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,097
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dylan, Tyler M
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 22000-20567.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3549 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...3501
; OTHER INFORMATION:
US-09-008-097-5

Alignment Scores:
Pred. No.: 4.58e-38 Length: 3549
Score: 545.00 Matches: 99
Percent Similarity: 97.06% Conservative: 0
Best Local Similarity: 97.06% Mismatches: 3
Query Match: 95.61% Indels: 0
DB: 4 Gaps: 0

US-09-750-240-2 (1-104) x US-09-008-097-5 (1-3549)
Qy 1 MetSerTrpPheSerGlyLeuValProLysValAspGluArgLysThrAlaTrpGly 20
Db 1 ATGTCATGTTTATGGCTCTCTGGTCCCTAAAGTGGATGAACGAAACAGCCTGGGGT 60
Qy 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
Db 61 GAACGCAATGGCAGAACGCTTCGCGCGCGCTGCGCACTCGGCAGGTGGCTTCTGCACG 120
Qy 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
Db 121 CCCGCTATATGAGTCGCTCCGGGATGCAGAGCCACCCAGCCGCCCTCGGGGCCCC 180
Qy 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro**LysGlyLys 80
Db 181 CCTCGGTGCCCCGGCAGGATGACGCTTCATCCGGAGGGCGGCCCAAGGCGCAAG 240
Qy 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
Db 241 GAGCTGGGCTGCGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACGCG 300
Qy 101 AlaGly 102
Db 301 GCGGCG 306

RESULT 3
US-09-474-076-1
; Sequence 1, Application US/09474076
; Patent No. 6465237
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYL
; TITLE OF INVENTION: CYCLASE
; FILE REFERENCE: 44481-5028-01-US
```

;/ CURRENT APPLICATION NUMBER: US/09/474,076  
;/ CURRENT FILING DATE: 1999-12-12  
;/ PRIOR APPLICATION NUMBER: PCT/US98/13694  
;/ PRIOR FILING DATE: 1998-07-01  
;/ PRIOR APPLICATION NUMBER: 60/070,904  
;/ PRIOR FILING DATE: 1997-07-01  
;/ PRIOR APPLICATION NUMBER: 08/886,550  
;/ PRIOR FILING DATE: 1997-07-01  
;/ NUMBER OF SEQ ID NOS: 2  
;/ SOFTWARE: PatentIn Ver. 2.0  
;/ SEQ ID NO 1  
;/ LENGTH: 4942  
;/ TYPE: DNA  
;/ ORGANISM: human type VI adenylyl cyclase  
;/ FEATURE:  
;/ NAME/KEY: CDS  
;/ LOCATION: (145)..(3648)  
US-09-474-076-1

Alignment Scores:  
Pred. No.: 6,66e-38 Length: 4942  
Score: 545.00 Matches: 99  
Percent Similarity: 97.06% Conservative: 0  
Best Local Similarity: 97.06% Mismatches: 3  
Query Match: 95.61% Indels: 0  
DB: 4 Gaps: 0

US-09-750-240-2 (1-104) x US-09-474-076-1 (1-4942)

QY 1 MetSerTrpPheSerGlyLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
|||||  
Db 145 ATGTCATGTTAGTGGCTCTCTGGTCCCTAAAGTGATGAACGGAAACAGCGCTGGGT 204  
QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
|||||  
Db 205 GAACGCAATGGGCGAAGGCTTTCGGCGCGCTGGCACTCGGCGAGGTGCTTCTGCACG 264  
QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
Db 265 CCCCCGTATAGTGGCTCTCGGGATGAGAGCCACCCAGCCCTCGCGGCCCC 324  
QY 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro\*\*\*LysGlyLys 80  
|||||  
Db 325 CCTCGTGGCTGGCGAGGATGAGCTTCATCCGAGGGGGCGGCCAGGCAAGGCAAG 384  
QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
|||||  
Db 385 GAGCTGGGCTGGCGCAGTGGCCCTTGGGCTTGGAGGATACCGAGGTGACACGACGCG 444  
QY 101 AlaGly 102  
|||  
Db 445 GCGGG 450

RESULT 4

US-07-793-961A-1  
; Sequence 1, Application US/07793961A  
; Patent No. 5334521

;/ GENERAL INFORMATION:  
;/ APPLICANT: Yoshihiro Ishikawa  
;/ TITLE OF INVENTION: Cloning and Character-  
;/ TITLE OF INVENTION: ization of a Cardiac Adenylyl Cyclase  
;/ NUMBER OF SEQUENCES: 1  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Alan M. Gordon  
;/ ADDRESSEE: American Cyanamid Company  
;/ STREET: 1937 West Main Street,  
;/ CITY: P.O. Box 60  
;/ STATE: Stamford  
;/ COUNTRY: Connecticut  
;/ ZIP: 06904  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy Disk

;/ COMPUTER: IBM PC AT  
;/ OPERATING SYSTEM: MS-DOS  
;/ SOFTWARE: ASCII from DW4  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/07/793,961A  
;/ FILING DATE: 19911118  
;/ CLASSIFICATION: 435  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER:  
;/ FILING DATE:  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Gordon, Alan M.  
;/ REGISTRATION NUMBER: 30,637  
;/ REFERENCE/DOCKET NUMBER: 31,705  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: 203 321 2719  
;/ TELEFAX: 203 321 2971  
;/ TELEX:

;/ INFORMATION FOR SEQ ID NO: 1:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 4046 base pairs listed  
;/ TYPE: NUCLEIC ACID  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: DNA (genomic)  
US-07-793-961A-1

Alignment Scores:  
Pred. No.: 8,9e-32 Length: 4046  
Score: 472.50 Matches: 89  
Percent Similarity: 85.05% Conservative: 2  
Best Local Similarity: 83.18% Mismatches: 11  
Query Match: 82.89% Indels: 5  
DB: 1 Gaps: 2

US-09-750-240-2 (1-104) x US-07-793-961A-1 (1-4046)

QY 1 MetSerTrpPheSerGlyLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
|||||  
Db 131 ATGTCGTGTTAGTGGCTCTCTGGTCCCAAGTGATGAACGGAAACAGCGCTGGGT 190  
QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
|||||  
Db 191 GAACGCAATGGGCGAAGGCTTCA---CGCCGGGACTCGGACCATGCTTCTGCACG 247  
QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
|||||  
Db 248 CCCCCGTATAGTGGCTCTCGGGATGAGAGCCACCCAGTCCACCCCTGGCGGTCCC 307  
QY 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro\*\*\*LysGlyLys 80  
|||||  
Db 308 CCTCGTGGCTGGCGCAGTGGCCCTTCATCCGAGAGGGCGGCCCGGCAAGGCGACG 367  
QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGlu-----Val 96  
|||||  
Db 368 GAGCTGGGCTGGCGCGGTGGCCCTTGGGCTTCCGAGGACACTCAGGCGCATGTCAGCGGTT 427  
QY 97 ThrThrThrProAlaGlyPro 103  
|||||  
Db 428 GGGCGAGCTGGAGGTGGCCCT 448

RESULT 5

US-08-240-357-1  
; Sequence 1, Application US/08240357  
; Patent No. 5578481

;/ GENERAL INFORMATION:  
;/ APPLICANT: Ishikawa, Yoshihiro  
;/ TITLE OF INVENTION: Cloning and Characterization of a  
;/ TITLE OF INVENTION: Cardiac Adenylyl Cyclase  
;/ NUMBER OF SEQUENCES: 2  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: American Cyanamid Company  
;/ STREET: One Cyanamid Plaza

;  
; CITY: Wayne  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07470-8426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/240,357  
; FILING DATE: 10-MAY-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gordon, Alan M.  
; REGISTRATION NUMBER: 30,637  
; REFERENCE/DOCKET NUMBER: 31,705-01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-831-3244  
; TELEFAX: 201-831-3305  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4046 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 131..3625  
; US-08-240-357-1

Alignment Scores:  
Pred. No.: 8.9e-32 Length: 4046  
Score: 472.50 Matches: 89  
Percent Similarity: 85.05% Conservative: 2  
Best Local Similarity: 83.18% Mismatches: 11  
Query Match: 82.89% Indels: 5  
DB: 1 Gaps: 2

US-09-750-240-2 (1-104) x US-08-240-357-1 (1-4046)

Qy 1 MetSerTrpPheSerGlyLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
Db 131 ATGTCGTGTTAGTGGCTCTGTCCTCCCAAGTGGATGAACGAGACAGCCTGGGTT 190  
Qy 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
Db 191 GAACGCAATGGCAGAACGTCCTCA--CGCCGGGACTCGGACAGTGGCTTCGACG 247  
Qy 41 ProArgTrpMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
Db 248 CCCGCTATAGTGGCTCTCGGATGCGAGTCCGCCGCCAGTCCACCCCTCGGCTCC 307  
Qy 61 ProArgCysProTrpGlnAspAlaPheleArgArgGlyGlyPro\*\*\*LysGlyLys 80  
Db 308 CTGCGTCCCTGCGAGGATGAGGCTTCATCGGAGAGCGCGCCGCGGAAGGGCAG 367  
Qy 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGlu-----Val 96  
Db 368 GAGCTGGGGCTCGGGCGGTGGCTTCGAGGACACTGAGGCCATGTCAGCGGTT 427  
Qy 97 ThrThrThrProAlaGlyPro 103  
Db 428 GGGCAGCTGGAGGTGGCCT 448  
RESULT 6  
US-08-726-214-11  
; Sequence 11, Application US/08726214  
; Patent No. 6107076  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Wei-Jen  
; APPLICANT: Gilman, Alfred G.

;  
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYL CYCLASE  
; TITLE OF INVENTION: AND USES THEREFOR  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/726,214  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/005,498  
; FILING DATE: 04-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L.  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: UTSD:450  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4131 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-726-214-11  
Alignment Scores:  
Pred. No.: 2.74e-28 Length: 4131  
Score: 432.00 Matches: 81  
Percent Similarity: 86.27% Conservative: 7  
Best Local Similarity: 79.41% Mismatches: 12  
Query Match: 75.79% Indels: 2  
DB: 3 Gaps: 2  
US-09-750-240-2 (1-104) x US-08-726-214-11 (1-4131)  
Qy 1 MetSerTrpPheSerGlyLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
Db 56 ATGTCATGTTTAGCGGCTCTGTTCCCAAGTGGATGAACGAAACAGCCTGGGGC 115  
Qy 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
Db 116 GAACGCAATGACAGAGAGCGCCCA--CGCCGGGACCCGAGCCCTCTGCGCG 172  
Qy 41 ProArgTrpMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
Db 173 CCCGCTATAGTGGCTCTCAAGAAATGTGGAGCACCCAGCCACCTCTGACGCTGC 232  
Qy 61 ProArgCysProTrpGlnAspAlaPheleArgArgGlyGlyPro\*\*\*LysGlyLys 80  
Db 233 ACTCGTCCCTGCGAGGATGAAGCCTTCATCAGGAGGCTGGCCCGGGAAGGGGTGTG 292  
Qy 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
Db 293 GAGCTGGGGCTGCGGTGCTGAGTGGCTTTGATGACTGAGGTG---ACCACACCG 349  
Qy 101 AlaGly 102  
Db 350 ATGGGG 355  
RESULT 7  
US-07-736-178C-1/c



```
; Sequence 1, Application US/07736178C
; Patent No. 5514544
; GENERAL INFORMATION:
; APPLICANT: Rao, Ramachandra N
; TITLE OF INVENTION: ACTIVATOR GENE FOR MACROLIDE
; TITLE OF INVENTION: BIOSYNTHESIS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly And Company
; STREET: Lilly corporate Center
; CITY: Indianapolis
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07736,178C
; FILING DATE: 19910726
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Conrad, Robert A
; REGISTRATION NUMBER: 32089
; REFERENCE/DOCKET NUMBER: X8144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-3334
; TELEFAX: 317-276-1294
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2312 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 345..2312
;
US-07-736-178C-1

Alignment Scores:
Pred. No.: 14.8 Length: 2312
Score: 94.00 Matches: 36
Percent Similarity: 36.67% Conservative: 8
Best Local Similarity: 30.00% Mismatches: 38
Query Match: 16.49% Indels: 38
DB: 1 Gaps: 9

US-09-750-240-2 (1-104) x US-07-736-178C-1 (1-2312)

QY 2 SerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThr----- 17
Db 1584 GCCTGGTGGAGTCTGCTGTGACGCGCAGGTCTCGAAGAACTCTCTGTGGCTCT 1531
QY 18 ---AlaTrpGlyGluArgAsnGlyGlnLysArgSerArgArgArgly----- 32
Db 1530 GCCTCTGGGGAGTCTGCTGTGACGCGCAGGTCTCGAAGAACTCTCTGTGGCTCT 1471
QY 33 ThrArgAlaGlyGly---PheCysThrProArg-----Tyr 43
Db 1470 TCGGAGACAGGGAGCGGGTGTGCTGCGTCCGCGTCCGACCGAGGTCTGTCAGGAGC 1411
QY 44 MetSerCysLeuArgAspAla-----GluProSerPro----- 55
Db 1410 CGCGCTTGGCCCGGGAAGCAGGGGACCGTCCAGACCCCGGGGCGCAGGAGTGGCC 1351
QY 56 -----ThrProAlaGlyProProArgCys---ProTrpGlnAspAlaPhe 70
Db 1350 GGCGGTCTGGCGGCGCGCGCAGCGCGCGCAGTTCCTGGGGG----- 1303

; Sequence 1, Application US/08690473
; Patent No. 5876923
; GENERAL INFORMATION:
; APPLICANT: Leopardi, Rosario
; TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 AS AN
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,473
; FILING DATE: 26-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD:239
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4257 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-690-473-1

Alignment Scores:
Pred. No.: 48.6 Length: 4257
Score: 91.50 Matches: 36
Percent Similarity: 42.86% Conservative: 6
Best Local Similarity: 36.73% Mismatches: 38
Query Match: 16.05% Indels: 18
DB: 2 Gaps: 5

US-09-750-240-2 (1-104) x US-08-690-473-1 (1-4257)

QY 17 ThrAlaTrpGlyGluArgAsnGlyGlnLysArgSer-----ArgArg-ArgG 32.
Db 2786 ACCCTCTGGCGGCTGGCGGCGCAGCCCGGCGCCACACACCGCGCGCGCGG 2845
QY 32 yThrArgAlaGlyGly-PheCysThrProArgTyrMetSerCysLeuArgAspAlaGluP 52
Db 2846 CGCGCGCCCTGGAGGCTACTGCTCCCGCGCGCGGCGCGGAGCTCAGCAGC---CAC 2902
QY 52 ro-ProSerProThrProAlaGlyProProArgCys-----ProTrpGlnAsp 67
Db 2903 CGCTGTTCCTCCCTCCCTGCGCAGCCGCGCTCATGTTTGACCGCGCGCGCTG 2962
QY 68 AspAlaPheIleArgArgGlyGlyPro**LysGlyLysGluLeuGlyLeuArgAlaVal 87
Db 2963 TCCTCG-----CGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3013
QY 88 AlaLeuGlyPheGluAspThrGluValThrThrProAlaGlyPro 103
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Db 3014 GCG-----GCGAGCAGCAGATACACCCACCCACCCACCGGGCGG 3052

## RESULT 9

US-09-259-821A-1  
; Sequence 1, Application US/09259821A  
; Patent No. 6210926  
; GENERAL INFORMATION:  
; APPLICANT: LEOPARDI, ROSARIO  
; APPLICANT: ROIZMAN, BERNARD  
; TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 IS AN INHIBITOR OF APOPTOSIS  
; FILE REFERENCE: ARCD:317  
; CURRENT APPLICATION NUMBER: US/09/259,821A  
; CURRENT FILING DATE: 1999-03-01  
; PRIOR APPLICATION NUMBER: 08/690,473  
; PRIOR FILING DATE: 1996-07-26  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4257  
; TYPE: DNA  
; ORGANISM: HERPES VIRUS, TYPE 1  
US-09-259-821A-1

Alignment Scores:  
Pred. No.: 48.6 Length: 4257  
Score: 91.50 Matches: 36  
Percent Similarity: 42.86% Conservative: 6  
Best Local Similarity: 36.73% Mismatches: 38  
Query Match: 16.05% Indels: 18  
DB: 4 Gaps: 5

US-09-750-240-2 (1-104) x US-09-259-821A-1 (1-4257)

QY 17 ThrAlaTrpGlyGluArgAsnGlyGlnLysArgSer-----ArgArg-ArgGl 32  
Db 2786 ACCCCCTGGCGGCGTGGCGGCGAGCCCCGGGGCCAGCCACACGCGCGCGCGCGG 2845  
QY 32 yThrArgAlaGlyGly-PheCysThrProArgTyrMetSerCysLysLeuArgAspAlaGluP 52  
Db 2846 CCGCGCGCCCTGGAGCGCTACTCTCCCGCGCGCGTGGCGGAGTCTACGGAC---CACC 2902  
QY 52 ro-ProSerProThrProAlaGlyProProArgCys-----ProTrpGlnAsp 67  
Db 2903 CGCTGTCCCGTCCCTGGCGGCGGCGCTCATGTTGACCCCGCGGCGCTGGCTCGA 2962  
QY 68 AspAlaPheIleArgArgGlyGlyPro\*\*\*LysGlyLysGluLeuGlyLeuArgAlaVal 87  
Db 2963 TCGCGG-----CGCGGTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3013  
QY 88 AlaLeuGlyPheGluAspThrGluValThrThrThrProAlaGlyPro 103  
Db 3014 GCG-----GCGAGCAGCAGATACACCCACCCACCGGGCGG 3052

## RESULT 10

US-08-843-659-1  
; Sequence 1, Application US/08843659  
; Patent No. 6218103  
; GENERAL INFORMATION:  
; APPLICANT: Leopardi, Rosario  
; APPLICANT: Roizman, Bernard  
; TITLE OF INVENTION: HERPES SIMPLEX VIRUS US3 AND ICP4 AS  
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/843,659  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L.  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: ARSB.519  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4257 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-843-659-1

Alignment Scores:  
Pred. No.: 48.6 Length: 4257  
Score: 91.50 Matches: 36  
Percent Similarity: 42.86% Conservative: 6  
Best Local Similarity: 36.73% Mismatches: 38  
Query Match: 16.05% Indels: 18  
DB: 4 Gaps: 5

US-09-750-240-2 (1-104) x US-08-843-659-1 (1-4257)

QY 17 ThrAlaTrpGlyGluArgAsnGlyGlnLysArgSer-----ArgArg-ArgGl 32  
Db 2786 ACCCCCTGGCGGCGTGGCGGCGAGCCCCGGGGCCAGCCACACGCGCGCGCGG 2845  
QY 32 yThrArgAlaGlyGly-PheCysThrProArgTyrMetSerCysLysLeuArgAspAlaGluP 52  
Db 2846 CCGCGCGCCCTGGAGCGCTACTCTCCCGCGCGCGTGGCGGAGTCTACGGAC---CACC 2902  
QY 52 ro-ProSerProThrProAlaGlyProProArgCys-----ProTrpGlnAsp 67  
Db 2903 CGCTGTCCCGTCCCTGGCGGCGGCGCTCATGTTGACCCCGCGGCGCTGGCTCGA 2962  
QY 68 AspAlaPheIleArgArgGlyGlyPro\*\*\*LysGlyLysGluLeuGlyLeuArgAlaVal 87  
Db 2963 TCGCGG-----CGCGGTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3013  
QY 88 AlaLeuGlyPheGluAspThrGluValThrThrThrProAlaGlyPro 103  
Db 3014 GCG-----GCGAGCAGCAGATACACCCACCCACCGGGCGG 3052

## RESULT 11

US-08-458-568A-11/c  
; Sequence 11, Application US/08458568A  
; Patent No. 5821339  
; GENERAL INFORMATION:  
; APPLICANT: Schaffer, Priscilla A.  
; APPLICANT: Yeh, Lily  
; TITLE OF INVENTION: Compositions and Methods for Treatment of Herpesvirus  
; TITLE OF INVENTION: Infections  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5821339rls  
; STREET: One Liberty place, 46th floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 5.1

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,568A
; FILING DATE: 02-JUNE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/065,146
; FILING DATE: 05-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary Ph.D., Kathryn R.
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: DFCI-0029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12001 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Herpes simplex virus
; STRAIN: Herpes Simplex Virus Type 1
; US-08-458-568A-11

Alignment Scores:
Pred. No.: 157 Length: 12001
Score: 91.50 Matches: 36
Percent Similarity: 42.86% Conservative: 6
Best Local Similarity: 36.73% Mismatches: 38
Query Match: 16.05% Indels: 18
DB: 1 Gaps: 5

US-09-750-240-2 (1-104) x US-08-458-568A-11 (1-12001)

QY 17 ThrAlaTrpGlyluArgAsnGlyLysArgSer-----ArgArg-ArgGl 32
Db 3888 ACCCTTGGGGCTGGCGCGCGACCCCGGGGCGCCAGCCACACGGCGCGCGCGG 3829

QY 32 yThrArgAlaGlyGly-PheCysThrProArgTyrMetSerCysLeuArgAspAlaGluP 52
Db 3828 CCGCCGCCCTGGAGGCTACTGTCCTCCCGCGCGCGCGCGCGCGCGCGCGGAC---CACC 3772

QY 52 ro-ProSerProThrProAlaGlyProProArgCys-----ProTrpGlnAsp 67
Db 3771 CGCTGTCCCGCTCCCTGGCGACCGCGCGCTCATGTTGACCGCGCGCGCGCGCGCTCGA 3712

QY 68 AspAlaPheIleArgArgGlyGlyPro**LysGlyLysGluLeuGlyLeuArgAlaVal 87
Db 3711 TCGCGG-----CGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 3661

QY 88 AlaLeuGlyPheGluAspThrGluValThrThrProAlaGlyPro 103
Db 3660 GCG-----CGCAGCAGCAGCAGTAAACCCACCCACCCACCGCGCGG 3622

RESULT 12
5212296-16/c
; Patent No. 5212296
; APPLICANT: DEAN, CAROLINE; HARDER, PATRICIA A.; LETO, KENNETH
; J.; O'KEEFE, DANIEL P.; OMER, CHARLES A.; ROMESSER, JAMES A.
; TEPPERMAN, JAMES M.
; TITLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING
; CYTOCHROMES
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/569,781
; FILING DATE: 23-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 464,499
; FILING DATE: 12-JAN-1990
; APPLICATION NUMBER: 405,605
; FILING DATE: 11-SEP-1989
; SEQ ID NO: 5:
; LENGTH: 1879
5212296-5

Alignment Scores:
Pred. No.: 28.5 Length: 1879
Score: 89.50 Matches: 30
Percent Similarity: 44.44% Conservative: 6
Best Local Similarity: 37.04% Mismatches: 26
Query Match: 15.70% Indels: 19
DB: 6 Gaps: 5

US-09-750-240-2 (1-104) x 5212296-5 (1-1879)

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Db 1199 GGCCCCAGGCACCTGGTCACGCCGAGCGGAGGTGGTGGCGCGCGCGGTGGA 1140

QY 38 Phe-----CysThrProArgTyrMetSerCysLeuArg 48
Db 1012 TGTCGAGGGCGTCGCGGTCTCTGTACACCGTCGCCGTTGGCTATCGAGTTGACGA 953

QY 49 AspAlaGluProProSerProThrProAlaGlyPro---ProArgCys---ProTrpGln 66
Db 952 CGATCACGCCCTCGCGCGCGCGATGAGTGCCCTCGACCTCGATCGCGCGTGG--- 896

QY 67 AspAlaPheIleArgArgGlyGlyPro**LysGlyLysGluLeuGlyLeuArgAla 86
Db 895 -----CGACGCGCGCGCGCGCGATGTCGCGGATGGCGGAGTAGCGGAGCA 851

QY 87 Val 87
Db 850 GTT 848

RESULT 13
5212296-5/c
; Patent No. 5212296
; APPLICANT: DEAN, CAROLINE; HARDER, PATRICIA A.; LETO, KENNETH
; J.; O'KEEFE, DANIEL P.; OMER, CHARLES A.; ROMESSER, JAMES A.
; TEPPERMAN, JAMES M.
; TITLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING
; CYTOCHROMES
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/569,781
; FILING DATE: 23-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 464,499
; FILING DATE: 12-JAN-1990
; APPLICATION NUMBER: 405,605
; FILING DATE: 11-SEP-1989
; SEQ ID NO: 5:
; LENGTH: 1879
5212296-5

Alignment Scores:
Pred. No.: 28.5 Length: 1879
Score: 89.50 Matches: 30
Percent Similarity: 44.44% Conservative: 6
Best Local Similarity: 37.04% Mismatches: 26
Query Match: 15.70% Indels: 19
DB: 6 Gaps: 5

US-09-750-240-2 (1-104) x 5212296-5 (1-1879)

QY 20 GlyluArgAsnGlyLysArgSerArgArg-----GlyThrArgAlaGlyGly 37
Db 1199 GGCCCCAGGCACCTGGTCACGCCGAGCGGAGGTGGTGGCGCGCGGTGGA 1140

QY 38 Phe-----CysThrProArgTyrMetSerCysLeuArg 48
Db 1012 TGTCGAGGGCGTCGCGGTCTCTGTACACCGTCGCCGTTGGCTATCGAGTTGACGA 953

QY 49 AspAlaGluProProSerProThrProAlaGlyPro---ProArgCys---ProTrpGln 66
Db 952 CGATCACGCCCTCGCGCGCGCGATGAGTGCCCTCGACCTCGATCGCGCGTGG--- 896

QY 67 AspAlaPheIleArgArgGlyGlyPro**LysGlyLysGluLeuGlyLeuArgAla 86
Db 895 -----CGACGCGCGCGCGCGCGATGTCGCGGATGGCGGAGTAGCGGAGCA 851

QY 87 Val 87
Db 850 GTT 848
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Qy 49 AspaLagluProSerProThrProAlaGlyPro---ProArgCys---ProTrpGln 66
Db 1079 CGATCAGCCCTCGCGCGCGGAGGTGAGGTGCGCTCGACCTCGATGTCGCGCGTGG--- 1023
Qy 67 AspaAlaPheIleArgArgGlyGlyPro***LysGlyLysGluLeuGlyLeuArgAla 86
Db 1022 -----CGACGCGCGCGCGCGATGTCGCGGATGTCGCGGATGTCGCGGAGCA 978
Qy 87 Val 87
Db 977 GTT 975

RESULT 14
5244792-2/c
; Patent No. 5244792
; APPLICANT: BURKE, RAE L.; PACHL, CAROL; VALENZUELA, PABLO D.T.
; TITLE OF INVENTION: EXPRESSION OF RECOMBINANT GLYOPROTEIN
; B FROM HERPES SIMPLEX VIRUS
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/587,179
; FILING DATE: 20-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 921,730
; FILING DATE: 20-OCT-1986
; APPLICATION NUMBER: 597,784
; FILING DATE: 06-APR-1984
; SEQ ID NO:2:
; LENGTH: 3472
5244792-2

Alignment Scores:
Pred. No.: 77 Length: 3472
Score: 88.00 Matches: 33
Percent Similarity: 39.45% Conservative: 10
Best Local Similarity: 30.28% Mismatches: 36
Query Match: 6 Indels: 30
DB: 6 Gaps: 6

US-09-750-240-2 (1-104) x 5244792-2 (1-3472)
Qy 20 GlyGluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCys 39
Db 495 GSGCGCGCCAGGCGCGCGCGCGCGCGGAGTGGCAGGCGCCCGTTCGCGCGCTGGTGC 436
Qy 40 ThrProArgTyrMetSerCysLeuArgAspAlaGluProProSerPro-----ThrPro 57
Db 435 CGGCGCGCACCCAGCGCGTGGCGGGAACTCGGAGCGCGCGACGCCACCGAGGCCCA 376
Qy 58 AlaGlyProProArgCysProTrpGlnAspAlaPheIleArg-----GlyGly 75
Db 375 GCGTCAACCCCAAGAGCGCCC-----ATACGACGAACCAACCGCGCAC 334
Qy 76 Pro***LysGlyLys----- 80
Db 333 CCCGCGCGGGGCGCGCTGCGGCATGCGGCGACTACGGGGCGCGCTGCGCCCCCGTCA 274
Qy 81 ---GluLeuGlyLeuArgAla-----ValAlaLeuGlyPheGluAspThrGluVal--- 96
Db 273 GGTAGCCTGGGGCGCGAGGTGTGGAGGACCGAGTAGAGGATCGAGAAAACGCTCTCGGTGC 214
Qy 97 ---ThrThrThrProAlaGlyProLeu 104
Db 213 TAGACCACGACCGCGGGGCGCGATA 187
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RESULT 15
US-09-144-759-17/c
; Sequence 17, Application US/09144759
; Patent No. 6117639
; GENERAL INFORMATION:
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; APPLICANT: HOOK, THOMAS
; APPLICANT: GERMAN, URSULA
; APPLICANT: KWONG, ANN
; TITLE OF INVENTION: FUSION PROTEINS, DNA MOLECULES, VECTORS, AND HOST CELLS
; FILE REFERENCE: VPI/98-08
; CURRENT APPLICATION NUMBER: US/09/144,759
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 2241
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: man-made
US-09-144-759-17

Alignment Scores:
Pred. No.: 57.1 Length: 2241
Score: 87.00 Matches: 38
Percent Similarity: 38.46% Conservative: 7
Best Local Similarity: 32.48% Mismatches: 41
Query Match: 15.26% Indels: 32
DB: 3 Gaps: 4

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Db 1575 TGGCGGATGGCATGACGTCCTCCAGATCTCTCGAGAACTTGGCAGTTTTCGCGTTTTT 1516
Qy 15 -----ArgLysThrAlaTrpGlyGlu 21
Db 1515 GAGCTTTAGTGAACACATCTCGGCGTTCGTGTTGCCAGCTACGAGCTCGGTGAG 1456
Qy 22 ArgAsnGlyGlnLysArgSerArgArgGlyThr-----ArgAlaGlyGly--- 37
Db 1455 GATCGAGAGCAGCT-TTGGGTAGAGACGAGGCTCATTGAGTCGCGCAGTGGCGGTTC 1397
Qy 38 -----PheCysThrProArgTyrMetSerCysLeuArgAspAlaGluPro 52
Db 1396 GTATATAAATCGTAGCGTGTGATGTAGTAGCTCTGGATCGCTTCGACTAGCT---GGG 1340
Qy 53 ProSerProThrProAlaGlyProProArgCysProTrpGlnAspAlaPheIleArg 72
Db 1339 CCTCTCCAGCGCGCGCGTCCGAGAAATCACAATGGCAGTGAAGAAGCGGTATTCCA 1280
Qy 73 ArgGlyGlyPro***LysGlyLysGluLeuGlyLeuArgAlaValAlaLeu 89
Db 1279 CGTTCTCCACCTTCATCCAGAACATTTGGCGGCAGAAATGCGAGCAGGCTTT 1229

Search completed: March 1, 2003, 12:17:18
Job time : 51 secs
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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 1, 2003, 11:05:29 ; Search time 61 Seconds  
(without alignments)  
1063.219 Million cell updates/sec

Title: US-09-750-240-2

Perfect score: 570

Sequence: 1 MSWESGLLVKPKDKRTANG.....RAVALGFEDTEVTTPAGPL 104

Scoring table: BLOSUM62

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 460893 seqs, 311809382 residues

Total number of hits satisfying chosen parameters: 921786

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-O=/cgn2.1/USPTO.spool/US09750240/runat\_25022003\_103943\_25085/app\_query.fasta\_1.263  
-DB=PublishedApplications\_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09750240.@CGN\_1.1.31.grunat\_25022003\_103943\_25085  
-NCPU=6 -ICPU=3 -NO\_XLPXY -NO\_MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=10 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cgn2.6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	568	99.6	314	10	US-09-750-240-1
2	545	95.6	3549	10	US-09-750-240-5
3	545	95.6	3552	10	US-09-750-240-10
4	545	95.6	3582	10	US-09-750-240-12
					-----
					Sequence 1, Appli
					Sequence 5, Appli
					Sequence 10, Appl
					Sequence 12, Appl

5	545	95.6	4942	9	US-10-201-000-1	Sequence 1, Appli
6	338.5	59.4	358	9	US-09-933-797-165	Sequence 165, App
7	212.5	37.3	220	10	US-09-728-445-487	Sequence 487, App
c 8	94	16.5	1533	10	US-09-815-242-7755	Sequence 7755, Ap
9	91.5	16.1	4257	9	US-09-825-288A-1	Sequence 1, Appli
c 10	89.5	15.7	1182	9	US-10-071-338-6	Sequence 6, Appli
c 11	89.5	15.7	7193	9	US-10-071-338-1	Sequence 1, Appli
c 12	87.5	15.4	618	10	US-09-833-381-1050	Sequence 1050, Ap
c 13	87	15.3	280	9	US-09-796-692-6321	Sequence 6321, Ap
c 14	87	15.3	16489	9	US-09-764-868-1483	Sequence 1483, Ap
c 15	86.5	15.2	398	10	US-09-925-299-608	Sequence 608, App
c 16	86.5	15.2	1038	10	US-09-917-800A-1479	Sequence 1479, Ap
c 17	86.5	15.2	1078	10	US-09-452-239-41	Sequence 41, Appl
c 18	86	15.1	485	9	US-10-004-717-59	Sequence 59, Appl
c 19	85	14.9	240	10	US-09-923-876-2469	Sequence 2469, Ap
c 20	85	14.9	4695	9	US-09-945-901-57	Sequence 57, Appl
c 21	85	14.9	4695	9	US-10-007-747-57	Sequence 57, Appl
c 22	85	14.9	4695	9	US-10-038-937-57	Sequence 57, Appl
c 23	84.5	14.8	2728	9	US-10-152-661-213	Sequence 213, App
c 24	84	14.7	969	10	US-09-965-703-10	Sequence 10, Appl
c 25	84	14.7	1338	10	US-09-965-703-9	Sequence 9, Appli
c 26	84	14.7	1850	10	US-09-965-703-8	Sequence 8, Appli
c 27	84	14.7	1856	9	US-09-853-450-17	Sequence 17, Appl
c 28	84	14.7	1752	10	US-09-965-703-7	Sequence 7, Appli
c 29	84	14.7	1878	10	US-09-965-697-1	Sequence 1, Appli
c 30	84	14.7	1878	10	US-09-965-703-6	Sequence 6, Appli
c 31	84	14.7	2241	9	US-09-042-4888-4	Sequence 4, Appli
c 32	84	14.7	2241	9	US-09-042-4888-6	Sequence 6, Appli
c 33	84	14.7	3126	9	US-09-042-4888-8	Sequence 8, Appli
c 34	84	14.7	13953	9	US-10-096-961-3	Sequence 3, Appli
c 35	83	14.6	4682	10	US-09-962-832-243	Sequence 243, App
c 36	83	14.6	65464	9	US-09-859-888-3	Sequence 3, Appli
c 37	82.5	14.5	597	10	US-09-864-761-31718	Sequence 31718, A
c 38	82.5	14.5	1680	10	US-09-815-242-7988	Sequence 7988, Ap
c 39	82.5	14.5	1372	10	US-09-864-761-15194	Sequence 15194, A
c 40	82.5	14.5	3090	10	US-09-929-315-3	Sequence 3, Appli
c 41	82.5	14.5	3090	10	US-09-993-215-3	Sequence 3, Appli
c 42	82	14.4	1683	9	US-09-712-363-113	Sequence 113, Appl
c 43	81.5	14.3	1026	9	US-09-894-844-113	Sequence 113, App
c 44	81.5	14.3	1029	9	US-09-712-363-64	Sequence 64, Appl
c 45	81.5	14.3	18596	9	US-09-954-531-124	Sequence 124, App

ALIGNMENTS

RESULT 1  
US-09-750-240-1  
; Sequence 1, Application US/09750240  
; Patent No. US20020103147A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammon, H. K.  
; APPLICANT: Insel, P. A.  
; APPLICANT: Ping, P. A.  
; APPLICANT: Post, S. R.  
; APPLICANT: Gao, M.  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART FAILURE  
; FILE REFERENCE: 220002056723  
; CURRENT APPLICATION NUMBER: US/09/750,240  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/472,667  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: US 09/008,097  
; PRIOR FILING DATE: 1998-01-16  
; PRIOR APPLICATION NUMBER: US 08/924,757  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/048,933  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: US 08/708,661  
; PRIOR FILING DATE: 1996-09-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1

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; LENGTH: 314
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(314)
; OTHER INFORMATION: n = A,T,C or G
US-09-750-240-1
Alignment Scores:
Pred. No.: 2,33e-43 Length: 314
Score: 568.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.65% Indels: 0
DB: 10 Gaps: 0

US-09-750-240-2 (1-104) x US-09-750-240-1 (1-314)
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Db 1 ATGTCATGTTTAGTGGCTCTCGTCCCTAAAGTGGATGAACGGAACACGCTGGGGT 60
Qy 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyPheCysThr 40
Db 61 GAACGCAATGGCGACAAGCGTTCCGGCGCCGTCGCACTCGGGCAGGTGGCTTCTGCACG 120
Qy 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
Db 121 CCCCCTATATAGTGGCTCGGGATGCAGAGCCACCCAGCCCGCCCGGGCCCC 180
Qy 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro**LysGlyLys 80
Db 181 CCTCGTGGCCCTGGCAGATGACGCTTCATCCGGAGGGGGCCCAAGGCGCAAG 240
Qy 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
Db 241 GAACCTGGGGCTCGGGCAGTGGCCCTGGGCTTCGAAGATACCGAAGTGACAACGACCG 300
Qy 101 AlaGlyProLeu 104
Db 301 GCGGAGCCGCTG 312

RESULT 2
US-09-750-240-5
; Sequence 5, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; FILE REFERENCE: FAILURE
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3549
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-240-1
Alignment Scores:
Pred. No.: 4.03e-40 Length: 3549
Score: 545.00 Matches: 99
Percent Similarity: 97.06% Conservative: 0
Best Local Similarity: 97.06% Mismatches: 3
Query Match: 95.61% Indels: 0
DB: 10 Gaps: 0

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Db 61 GAACGCAATGGCGACAAGCGTTCCGGCGCCGTCGCACTCGGGCAGGTGGCTTCTGCACG 120
Qy 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
Db 121 CCCCCTATATAGTGGCTCGGGATGCAGAGCCACCCAGCCCGCCCGGGCCCC 180
Qy 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro**LysGlyLys 80
Db 181 CCTCGTGGCCCTGGCAGATGACGCTTCATCCGGAGGGGGCCCAAGGCGCAAG 240
Qy 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
Db 241 GAGCTGGGGCTCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACGCG 300
Qy 101 AlaGly 102
Db 301 GCGGGG 306

RESULT 3
US-09-750-240-10
; Sequence 10, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; FILE REFERENCE: FAILURE
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 3552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-240-10
Alignment Scores:
Pred. No.: 4.03e-40 Length: 3552
Score: 545.00 Matches: 99
```

Percent Similarity:	97.06%	Conservative:	0
Best Local Similarity:	97.06%	Mismatches:	3
Query Match:	95.61%	Indels:	0
DB:	10	Gaps:	0

US-09-750-240-2 (1-104) x US-09-750-240-10 (1-3552)

Qy	1	MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly	20
Db	1	ATGTCATGGTTTATGGCTCTCTGGTCCCTAAAGTGATGAACGGAACAGCGCTGGGT	60
Qy	21	GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr	40
Db	61	GAACGCAATGGGCAGAGAAGCGTTCCGCGCGCGTGGCACTCGGCACGTTGCTCTGCACG	120
Qy	41	ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro	60
Db	121	CCCCGCTATATGACCTGCTCCCGGATGCAGACCACCCAGCCCCACCCTCGCGGCCCC	180
Qy	61	ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro***LysGlyLys	80
Db	181	CCTCGGTGCCCTTGGCAGGATGACGCTTCATCCGAGGGCGCGGCCAGGCAAGCAAG	240
Qy	81	GluLeuGlyLeuArgAlaValAlaLeuGlyPheClnAspThrClnValThrThrPro	100
Db	241	GAGCTGGGGCTCGCGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACGG	300
Qy	101	AlaGly	102
Db	301	GGCGGG	306

## RESULT 4

```

US-09-750-240-12
; Sequence 12, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; FILE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 3582
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified AC-VI
US-09-750-240-12

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US-09-750-240-2 (1-104) x US-09-750-240-12 (1-3582)

Qy	1	MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly	20
Db	22	ATGTCATGGTTAGTGGCTCTCTGGTCCCTTAAGTGGATGAACGGAAACAGCGCTGGGCT	81
Qy	21	GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr	40
Db	82	GAACGCAATGGCAGAAAGCTTCGCGCGCCGTGGCACTCGGCAGGTGGCTTCTGCACG	141
Qy	41	ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro	60
Db	142	CCCGCGCTATATGAGTCGCCCTCCGGGATGCAGAGCCACCCAGCCCCACCCCTCGCGGCGCCC	201
Qy	61	ProArgCysProTrpGlnAspAspAlaPheIleArgArgGlyGlyPro***LysGlyLys	80
Db	202	CCTCGGTGCCCTGGCAGATGACGCCCTTCATCTCGNAGGGCGCGGCCAGGCAGGGCAAG	261
Qy	81	GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrThrPro	100
Db	262	GAGCTGGGGCTGGCGGCAGTGGCCCTCTGAGGATACCGAGGTGCACACGACAGCG	321
Qy	101	AlaGly 102	
Db	322	GGCGGG 327	

## RESULT 5

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US-10-201-000-1
; Sequence 1, Application US/10201000
; Publication No. US20020187540A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; TITLE OF INVENTION: CYCLASE
; FILE REFERENCE: 44481-5028-01-US
; CURRENT APPLICATION NUMBER: US/10/201,000
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US/09/474,076
; PRIOR FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4942
; TYPE: DNA
; ORGANISM: human type VI adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(3648)
US-10-201-000-1

Alignment Scores:
Pred. No.: 5 83e-40 Length: 4942
Score: 545.00 Matches: 99
Percent Similarity: 97.06% Conservative: 0
Best Local Similarity: 97.06% Mismatches: 3
Query Match: 99.61% Indels: 0
DB: 9 Gaps: 0

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US-09-750-240-2 (1-104) X US-10-201-000-1 (1-4942)

Qy 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
 |||||  
 Db 145 ATGTCATGGTTTAGTGGCCCTCGTGCCCTAAAGTGGATGAACGGAAACAGCCTGGGT 204  
 |||||  
 Qy 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
 |||||

```
|||||
Db 205 GAACGCAATGGGCGAAGCGTTTCGGCGCGCGCTTGGCACTCGGCGAGGTGGCTTCTGCACG 264
QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
Db 265 CCCCCGTATGAGCTGCTCCGGGATGAGAGCCACCCAGCCGCCCTCGGGGCCCC 324
QY 61 ProArgCysProTrrpGlnAspAlaPheIleArgArgGlyGlyPro**LysGlyLys 80
Db 325 CCTCGGTGCCCCGGGAGGATGCGCTTCATCCGGAGGGGGCCCGCCAGGCGCAAG 384
QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
Db 385 GAGCTGGGCTCGGGGCGAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACGCG 444
QY 101 AlaGly 102
|||
Db 445 GCGGG 450
|||
RESULT 6
US-09-933-797-165
; Sequence 165, Application US/09933797
; Patent No. US20020155119A1
; GENERAL INFORMATION:
; APPLICANT: Robert A. Sikes et al.
; TITLE OF INVENTION: Isolation and Use of Fetal Urogenital
; FILE REFERENCE: 9901-007-999
; CURRENT APPLICATION NUMBER: US/09/933,797
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US/09/482,933
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: PCT/US99/10746
; PRIOR FILING DATE: 1999-05/14
; PRIOR APPLICATION NUMBER: 60/085,383
; PRIOR FILING DATE: 1998-05-14
; NUMBER OF SEQ ID NOS: 811
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 165
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Murine
US-09-933-797-165
Alignment Scores:
Pred. No.: 9,81e-23 Length: 358
Score: 338.50 Matches: 62
Percent Similarity: 83.54% Conservative: 4
Best Local Similarity: 78.48% Mismatches: 12
Query Match: 59.39% Indels: 1
Gaps: 1
US-09-750-240-2 (1-104) x US-09-933-797-165 (1-358)
QY 1 MetSerTrpPheSerGlyLeuValProLysValAspGluArgLysThrAlaTrpGly 20
Db 123 ATGTCATGTTAGTGGCTCTGCTGCCAAAGTGGATGAACGGAACACAGCTTGGGG 182
QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
Db 183 GAACGCAATGGGCGAAGCGCCCA---CGCCACGCAATCGAGCCAGTGGCTTCTGCVCA 239
QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
Db 240 CCTCGCTACATGAGTGGCTCAAGATGGGAGCCACCCAGCCGCCCTCTGCAGCTAC 299
QY 61 ProArgCysProTrrpGlnAspAlaPheIleArgArgGlyGlyPro**LysGly 79
Db 300 ACTCGGTGCCCTSGCAGGATGAAGCCTTCATCAGGAGGGCGGGCCCGGCGAGGGGT 356
RESULT 7
US-09-728-445-487
; Sequence 487, Application US/09728445
```

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; Patent No. US20020102543A1
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020102543A1el Mutated Mammalian Cells and
; TITLE OF INVENTION: Animals
; FILE REFERENCE: LEX-0102-USA
; CURRENT APPLICATION NUMBER: US/09/728,445
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/168,358
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 891
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 487
; LENGTH: 220
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-728-445-487
Alignment Scores:
Pred. No.: 1.1e-11 Length: 220
Score: 212.50 Matches: 40
Percent Similarity: 85.11% Conservative: 0
Best Local Similarity: 85.11% Mismatches: 6
Query Match: 37.28% Indels: 1
Gaps: 1
Db: 10
US-09-750-240-2 (1-104) x US-09-728-445-487 (1-220)
QY 1 MetSerTrpPheSerGlyLeuValProLysValAspGluArgLysThrAlaTrpGly 20
Db 67 ATGTCATGTTAGTGGCTCTGCTGCCAAAGTGGATGAACGGAACACAGCTTGGGG 126
QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
Db 127 GAACGCAATGGGCGAAGCGCCCA---CGCCACGCAATCGAGCCAGTGGCTTCTGC 183
QY 41 ProArgTyrMetSerCysLeu 47
Db 184 CCTCGCTACATGAGTGGCTC 204
RESULT 8
US-09-815-242-7755/c
; Sequence 7755, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA 011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
```



Qy 17 ThrAlaTrpGlyGluArgAsnGlyGlnLysArgSer-----ArgArg-ArgG1 32

Db	5274	CGGTGAAGCCCATGGGGCCGAACCAAGTTCTCGAAGATGAAGCCGCCGCCGGGAGCGCC	5333
Qy	35	AlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProProSer	54
		:::	
Db	5334	AGTGGTGGG-----CCTGCG---CGGAGTCCCGGGAGACCAAGAGCTCTTCATCA	5381
Qy	55	ProThrProAla-----GlyProPro-----	61
Db	5382	CCCCACCGCTCGCCCCCGCAGGGTGCGTGCGCCGCCGCTCGGCTCTCCCGGT	5441
Qy	62	ArgCysPro 64	
Db	5442	AGATGTCCA 5450	

RESULT 12

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US-09-833-381-1050/C
; Sequence 1050, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homo
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1050
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc:feature
; LOCATION: (1)...(618)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1050

```

QY	65	--TrpGlnAspAspAlaPheIleArgGlycylPro***LysGlyLys 80
Db	380	GAGCGCGCTCGGTGGCGGGTGGCGAGCCCGGCCACGAGGGAAA 331

GENERAL INFORMATION:  
APPLICANT: Gaiger, Alexander

APPLICANT: Mannion, Jane  
APPLICANT: Algate, Paul A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND TREATMENT OF HIV INFECTION

: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS, AND TREATMENT OF HIV INFECTION, AND ASSOCIATED COMPLICATIONS, AND FOR THE PREVENTION OF HIV INFECTION AND ASSOCIATED COMPLICATIONS.

```
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6321
; LENGTH: 280
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-6321

Alignment Scores:
Pred. No.:      2.53      Length:      280
Score:          87.00     Matches:      26
Percent Similarity: 40.00% Conservative: 0
Best Local Similarity: 40.00% Mismatches: 23
Query Match:    15.26% Indels: 16
DB:             9 Gaps: 4

US-09-750-240-2 (1-104) x US-09-796-692-6321 (1-280)
QY 19 TtpGlyGluArgAsn-----GlyGlnLysArgSerArgArgGlyThrArgAla 35
Db 236 TGGGGCCCAAGAGCCACAGCTGAGTGGCTTGTGTCTGAGGAGGAGGACCCGCTGT 177
QY 36 Gly---GlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProSer 54
Db 176 TCCTGGGGTTCACGGTTCCTTCTTGAGGTTGTGT-----CCTCCTTCC 132
QY 55 ProThrProAlaGlyProProArgCysProTtpGlnAspAlaPheIleArgArgGly 74
Db 131 CCACACCTCTGCAGGCTGCCAGCTCTTCTGTGCA-----AGC 93
QY 75 GlyPro***LysGly 79
Db 92 GGGCCCCCAGATGGGT 78

RESULT 14
US-09-764-868-1483
; Sequence 1483, Application US/09764868
; Patent No. US2002016871A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT332
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
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; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1483
; LENGTH: 16489
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-868-1483

Alignment Scores:
Pred. No.:      240      Length:      16489
Score:          87.00     Matches:      26
Percent Similarity: 40.00% Conservative: 0
Best Local Similarity: 40.00% Mismatches: 23
Query Match:    15.26% Indels: 16
DB:             9 Gaps: 4

US-09-750-240-2 (1-104) x US-09-764-868-1483 (1-16489)
QY 19 TtpGlyGluArgAsn-----GlyGlnLysArgSerArgArgGlyThrArgAla 35
Db 359 TGGGGCCCAAGAGCCACAGCTGAGTGGCTTGTGTCTGAGGAGGAGGACCCGCTGT 418
QY 36 Gly---GlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProSer 54
Db 419 TCCTGGGGTTCACGGTTCCTTCTTGAGGTTGTGT-----CCTCCTTCC 463
QY 55 ProThrProAlaGlyProProArgCysProTtpGlnAspAlaPheIleArgArgGly 74
Db 464 CCACACCTCTGCAGGCTGCCAGCTCTTCTGTGCA-----AGC 502
QY 75 GlyPro***LysGly 79
Db 503 GGGCCCCCAGATGGGT 517

RESULT 15
US-09-925-299-608/c
; Sequence 608, Application US/09925299
; Patent No. US2002005627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 608
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (132)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (137)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (138)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (139)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (360)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (373)
; OTHER INFORMATION: n equals a,t,g, or c
```

```
; NAME/KEY: misc_feature
; LOCATION: (377)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (386)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (394)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-608

Alignment Scores:
Pred. No.:      4.16      Length:      398
Score:          86.50     Matches:      28
Percent Similarity: 42.22%  Conservative: 10
Best Local Similarity: 31.11% Mismatches: 35
Query Match:      15.18%  Indels:      17
DB:               10      Gaps:       4

US-09-750-240-2 (1-104) x US-09-925-299-608 (1-398)

QY 13 AspGluArgLysThrAlaTrpClyGlu-----ArgAsnGlyClnLysArgSerArg 29
Db 290 GACCGCGGGAGGAGCGCTTCCACCCGCCAACTCGCGCGGTGAT-----CCCGGT 237
QY 30 ArgArgGlyThrArgAlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAsp 49
Db 236 CGGCGTGACAGTCGCTCGGTGGCGGGAACGTCCCGAGGGCCCCAGGAGCAGGAATCG 177
QY 50 AlaGlu-----ProProSerProThrProAlaGlyProProArgCysPro 64
Db 176 GGGGACTGTCCCTCACTCTCTCGCGCGCAACGAGTGNNGCTTNGCCCGGTGCCCC 117
QY 65 TrpGlnAspAspAlaPheIleArgArg-----GlyGlyPro*** 77
Db 116 CTCGAGCGCGTCTCTGTTTCTCGAAGAACGAAACTTCCTCCAGCGCCCGAGTCCCTTC 57
QY 78 LysGlyLysGluLeuGlyLeuArgAlaVal 87
Db 56 CGAGCGCCGCTCTCTCATCCGGAAGATC 27
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Search completed: March 1, 2003, 13:39:42  
Job time : 67 secs

GenCore version 5.1.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 1, 2003, 09:07:49 ; Search time 263 Seconds  
(without alignments)  
673.833 Million cell updates/sec

Title: US-09-750-240-2

Perfect score: 570

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 3936061 seqs, 852009584 residues

Total number of hits satisfying chosen parameters: 7872122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MAIRIX=biosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09750240@cgn2.1.1.86@runat\_25022003\_103943\_25050 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOB=6 -DELEXT=7

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1: /cgn2.6/ptodata/2/pna/PCT\_NEW\_COMB.seq.\*  
2: /cgn2.6/ptodata/2/pna/US06\_NEW\_COMB.seq.\*  
3: /cgn2.6/ptodata/2/pna/US07\_NEW\_COMB.seq.\*  
4: /cgn2.6/ptodata/2/pna/US08\_NEW\_COMB.seq.\*  
5: /cgn2.6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2.6/ptodata/2/pna/US10\_NEW\_COMB.seq.\*  
7: /cgn2.6/ptodata/2/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
1	545	95.6	1386	1 PCT-US02-36759-83
2	432	75.8	5826	6 US-10-144-771-5921
3	92.5	16.2	4955	7 US-60-423-552-78
4	92.5	16.2	4955	7 US-60-423-552-78
5	90.5	15.9	1173	5 US-09-398-858-13
6	90.5	15.9	1173	5 US-10-320-230-13
7	90.5	15.9	1173	6 US-10-348-110-13
8	90.5	15.9	4884	1 PCT-US02-39133-56
9	90.5	15.9	5079	1 PCT-US02-39133-57
c 10	89.5	15.7	1182	6 US-10-288-985-6
c 11	89.5	15.7	1182	6 US-10-289-980-6

12	89.5	15.7	7193	6 US-10-288-985-1
13	89.5	15.7	7193	6 US-10-289-980-1
c 14	89	15.6	34319	1 PCT-US03-01858-47
15	88.5	15.5	2349	5 US-09-724-676-9445
16	88.5	15.5	2349	5 US-09-724-676-9445
17	88.5	15.5	3394	5 US-09-620-312B-314
c 18	87	15.3	1622	6 US-10-276-781-61
c 19	87	15.3	2241	6 US-10-300-757-17
c 20	87	15.3	2295	6 US-10-300-757-19
c 21	87	15.3	2301	6 US-10-300-757-21
c 22	87	15.3	3717	1 PCT-US03-01363-10
23	86.5	15.2	1038	7 US-60-436-643-4032
c 24	86.5	15.2	1196	6 US-10-144-771-13121
c 25	86.5	15.2	8495	6 US-10-144-779-234
c 26	86	15.1	485	5 US-09-585-645A-59
27	86	15.1	18976	6 US-10-329-079-42
28	86	15.1	61944	6 US-10-329-079-34
29	86	15.1	77536	5 US-09-940-316B-1
c 30	85.5	15.0	1806	6 US-10-329-079-38
c 31	85.5	15.0	1806	6 US-10-392-027-29
c 32	85.5	15.0	2605	1 PCT-US02-29264-2809
c 33	85.5	15.0	2605	1 PCT-US02-29264-2818
c 34	85.5	15.0	2605	1 PCT-US02-29264-2819
c 35	85.5	15.0	2605	1 PCT-US02-29264-2820
c 36	85.5	15.0	14055	1 PCT-US02-37547-1
c 37	85.5	15.0	61944	6 US-10-329-079-34
c 38	85.5	15.0	82746	1 PCT-US02-37547-56
39	84.5	14.8	1020	6 US-10-144-771-44214
c 40	84.5	14.8	2605	1 PCT-US02-29264-2811
c 41	84	14.7	1656	1 PCT-US02-14719-17
c 42	84	14.7	2015	6 US-10-144-771-1266
c 43	84	14.7	57984	5 US-09-949-004-512
c 44	84	14.7	57985	5 US-09-949-004-589
45	83.5	14.6	6099	6 US-10-144-771-15901

#### ALIGNMENTS

RESULT 1  
PCT-US02-36759-83  
; Sequence 83, Application PC/TUS0236759  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: DUGGAN, Brendan M.  
; APPLICANT: YANG, Junming  
; APPLICANT: GIEYZEN, Kimberly J.  
; APPLICANT: LEE, Soo Yeun  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: AZIMZAI, Yalda  
; APPLICANT: WALIA, Narinder K.  
; APPLICANT: WARREN, Bridget A.  
; APPLICANT: BARROSO, Ines  
; APPLICANT: BECHA, Shanya D.  
; APPLICANT: YUE, Henry  
; APPLICANT: LEHR-MASON, Patricia M.  
; APPLICANT: THANGAVELU, Kavitha  
; APPLICANT: LEE, Sally  
; APPLICANT: EMERLING, Brooke M.  
; APPLICANT: KABLE, Amy E.  
; APPLICANT: KHARE, Reena  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: GANDHI, Ameena R.  
; APPLICANT: TRAN, Uyen K.  
; APPLICANT: RICHARDSON, Thomas W.  
; APPLICANT: MARQUIS, Joseph P.  
; APPLICANT: LAL, Preeti G.  
; APPLICANT: FORSYTHE, Ian J.  
; APPLICANT: LEE, Ernestine A.  
; APPLICANT: SWARNAKAR, Anita.  
; APPLICANT: KALLICK, Deborah A.  
; APPLICANT: GRIFFIN, Jennifer A.  
; APPLICANT: ELLIOTT, Vicki S.  
; APPLICANT: GORVAD, Ann E.

; APPLICANT: HAFALIA, April J.A.  
; APPLICANT: ISON, Craig H.  
; APPLICANT: JIN, Pei  
; APPLICANT: JIANG, Xin  
; APPLICANT: JACKSON, Alan  
; APPLICANT: BHATIA, Umesh  
; APPLICANT: BURRILL, John D.  
; APPLICANT: BLAKE, Julie J.  
; APPLICANT: HO, Ann  
; APPLICANT: ZHENG, Wenjin  
; APPLICANT: GAO, Jing  
; TITLE OF INVENTION: RECEPTORS AND MEMBRANE-ASSOCIATED PROTEINS  
; FILE REFERENCE: PF-1279 PCT  
; CURRENT APPLICATION NUMBER: PCT/US02/36759  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: US 60/333,097  
; PRIOR FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 60/335,274  
; PRIOR FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: US 60/340,542  
; PRIOR FILING DATE: 2001-12-14  
; PRIOR APPLICATION NUMBER: US 60/342,166  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: US 60/347,580  
; PRIOR FILING DATE: 2002-01-11  
; PRIOR APPLICATION NUMBER: US 60/348,687  
; PRIOR FILING DATE: 2002-01-14  
; NUMBER OF SEQ ID NOS: 94  
; SOFTWARE: PERL Program  
; SEQ ID NO 83  
; LENGTH: 1386  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No: 7506194CB1  
PCT-US02-36759-83

Alignment Scores:  
Pred. No.: 1.5e-34 Length: 1386  
Score: 545.00 Matches: 99  
Percent Similarity: 97.06% Conservative: 0  
Best Local Similarity: 97.06% Mismatches: 3  
Query Match: 95.61% Indels: 0  
DB: 1 Gaps: 0

US-09-750-240-2 (1-104) x PCT-US02-36759-83 (1-1386)

Qy 1 MetSerTrpPheSerGlyLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
Db 25 ATGTCATGGTTAGTGGCTCTGCTCCCTAAAGTGGATGAACGGAAACAGCCCTGGGGT 84  
Qy 21 GluArgAsnGlyGlnLysArgSerArgGlyThrArgAlaGlyGlyPheCysThr 40  
Db 85 GAACCAATGGCAGAACCGTTCGGCGGCCGTGCACTCGGCAGGTGGCTTCTGCACG 144  
Qy 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
Db 145 CCCGCTATATAGCTGCTCCGGGATGCAGAGCCACCCAGCCACCCCTCGGGCCCC 204  
Qy 61 ProArgCysProTrpGlnAspAlaPheLeuArgArgGlyGlyPro\*\*\*LysGlyLys 80  
Db 205 CCTCGTCCCTGGCAGGATGACGCTTCATCCGGAGGGGGCCCGCCAGGAAAGGCAAG 264  
Qy 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
Db 265 GAGCTGGGGCTCGGGCAGTGGCTTGGGCTTCGAGGATACCGAGGTGACACGACAGCG 324  
Qy 101 AlaGly 102  
Db 325 GGCGGG 330  
RESULT 2

US-10-144-771-5921  
; Sequence 5921, Application US/10144771  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig  
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF  
; FILE REFERENCE: CL001321  
; CURRENT APPLICATION NUMBER: US/10/144,771  
; CURRENT FILING DATE: 2002-05-15  
; NUMBER OF SEQ ID NOS: 47235  
; SEQ ID NO 5921  
; LENGTH: 5826  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-10-144-771-5921

Alignment Scores:  
Pred. No.: 8.16e-25 Length: 5826  
Score: 432.00 Matches: 81  
Percent Similarity: 85.29% Conservative: 6  
Best Local Similarity: 79.41% Mismatches: 13  
Query Match: 75.79% Indels: 2  
DB: 6 Gaps: 2

US-09-750-240-2 (1-104) x US-10-144-771-5921 (1-5826)

Qy 1 MetSerTrpPheSerGlyLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
Db 96 ATGTCATGGTTAGTGGCTCTGCTCCCTAAAGTGGATGAACGGAAACAGCTTGGGGG 155  
Qy 21 GluArgAsnGlyGlnLysArgSerArgGlyThrArgAlaGlyGlyPheCysThr 40  
Db 156 GAACCAATGGCAGAACCGTTCGGCGGCCGTGCACTCGGCAGGTGGCTTCTGCACA 212  
Qy 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
Db 213 CTGCTACATGAGCTGCTCAAGAAATCGGAGCCACCCAGCCCTCTGCACTCAC 272  
Qy 61 ProArgCysProTrpGlnAspAlaPheLeuArgArgGlyGlyPro\*\*\*LysGlyLys 80  
Db 273 ACTCGTCCCTGGCAGGATGAAGCTTCATCAGAGGGCGGGCCCGCAGGGGTGTG 332  
Qy 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
Db 333 GAGCTGGGGCTCGGTCAGTGGCTTGGGGTTTGACGACACTGAGGTG---ACCACACG 389  
Qy 101 AlaGly 102  
Db 390 ATGGGC 395

RESULT 3

US-60-423-552-78  
; Sequence 78, Application US/60423552  
; GENERAL INFORMATION:  
; APPLICANT: American Home Product Inc.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING MAJOR DEP  
; FILE REFERENCE: AM101250L  
; CURRENT APPLICATION NUMBER: US/60/423,552  
; CURRENT FILING DATE: 2002-11-05  
; NUMBER OF SEQ ID NOS: 256  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 78  
; LENGTH: 4955  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-423-552-78

Alignment Scores:  
Pred. No.: 986 Length: 4955  
Score: 92.50 Matches: 25  
Percent Similarity: 48.65% Conservative: 11  
Best Local Similarity: 33.78% Mismatches: 34  
Query Match: 16.23% Indels: 4

```
DB: 7 Gaps: 1
US-09-750-240-2 (1-104) x US-60-423-552-78 (1-4955)
QY 2 SerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGlyGlu 21
Db 2972 GCCTGTGGTACTATGCGAGGGTGGCGAGGGTCAGTTCAATGAAGACGGCTCCTTCATCG 3031
QY 22 ArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThrPro 41
Db 3032 GCCAGTACAGGTCAAAGAGCAAGACGAGGAACACAGAGGCAAGAGCTCAGAGGCCA 3091
QY 42 ArgTyrMetSerCysLeuArgAspAlaGluPro-ProSerProThrProAlaGlyProPr 61
Db 3092 CGTCACCTGTCAATGCTATCTACTCTCTGCGCTAAGCGAGCCACCCAGGCACAGCCACC 3151
QY 61 oArgCysProTrpGlnAspAlaPheIleArgArgGly 74
Db 3152 ACTTTCAGTGGGAGGAGGGG-----AGAAGGGGA 3182
RESULT 4
US-60-427-579-78
; Sequence 78, Application US/60427579
; GENERAL INFORMATION:
; APPLICANT: American Home Product Inc.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING MAJOR DEPRES
; FILE REFERENCE: AM101250L
; CURRENT APPLICATION NUMBER: US/60/427,579
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 256
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 4955
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-427-579-78
Alignment Scores:
Pred. No.: 986 Length: 4955
Score: 92.50 Matches: 25
Percent Similarity: 48.65% Conservative: 11
Best Local Similarity: 33.78% Mismatches: 34
Query Match: 16.23% Indels: 4
DB: 7 Gaps: 1
US-09-750-240-2 (1-104) x US-60-427-579-78 (1-4955)
QY 2 SerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGlyGlu 21
Db 2972 GCCTGTGGTACTATGCGAGGGTGGCGAGGGTCAGTTCAATGAAGACGGCTCCTTCATCG 3031
QY 22 ArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThrPro 41
Db 3032 GCCAGTACAGGTCAAAGAGCAAGAGGGAACACAGAGGCAAGAGCTCAGAGGCCA 3091
QY 42 ArgTyrMetSerCysLeuArgAspAlaGluPro-ProSerProThrProAlaGlyProPr 61
Db 3092 CGTCACCTGTCAATGCTATCTACTCTCTGCGCTAAGCGAGCCACCCAGGCACAGCCACC 3151
QY 61 oArgCysProTrpGlnAspAlaPheIleArgArgGly 74
Db 3152 ACTTTCAGTGGGAGGAGGGG-----AGAAGGGGA 3182
RESULT 5
US-09-398-858-13
; Sequence 13, Application US/09398858
; GENERAL INFORMATION:
; APPLICANT: Lowe, Keith S.
; APPLICANT: Tao, Yumin
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Gregory, Carolyn A.
; APPLICANT: McElver, John A.
```

```
; APPLICANT: Hoerster, George J.
; TITLE OF INVENTION: Cyclin D Polynucleotides, Polypeptides
; FILE REFERENCE: 0926
; CURRENT APPLICATION NUMBER: US/09/398,858
; CURRENT FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 60/101,551
; PRIOR FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1173)
US-09-398-858-13
Alignment Scores:
Pred. No.: 285 Length: 1173
Score: 90.50 Matches: 21
Percent Similarity: 57.78% Conservative: 5
Best Local Similarity: 46.67% Mismatches: 12
Query Match: 15.88% Indels: 7
DB: 5 Gaps: 3
US-09-750-240-2 (1-104) x US-09-398-858-13 (1-1173)
QY 28 SerArgArgGlyThrArgAlaGlyGlyPheCysThrProArgTyrMetSerCysLeu 47
Db 635 GCACGCGCGGAGGA-----GCTGCTGGCTCTTGCAGTCCGCGGAGCTTATCTTGGTG 688
QY 48 ArgAspAlaGluProPro-----SerProThrProAlaGlyProProArgCys--- 63
Db 689 CGGCCAGAGGACCGGCTGCTGCTGCTTCCAGGCTCCGAGATCGCGCGGTTGCAG 748
QY 64 ---ProTrpGlnAsp 67
Db 749 CCGCCCGTGGCCGGAG 763
RESULT 6
US-10-320-230-13
; Sequence 13, Application US/10320230
; GENERAL INFORMATION:
; APPLICANT: Lowe, Keith S.
; APPLICANT: Tao, Yumin
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Gregory, Carolyn A.
; APPLICANT: McElver, John A.
; APPLICANT: Hoerster, George J.
; TITLE OF INVENTION: Cyclin D Polynucleotides, Polypeptides
; FILE REFERENCE: 0926D
; CURRENT APPLICATION NUMBER: US/10/320,230
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/101,551
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 09/398,858
; PRIOR FILING DATE: 1999-09-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1173)
US-10-320-230-13
Alignment Scores:
Pred. No.: 285 Length: 1173
```

Score: 90.50 Matches: 21  
Percent Similarity: 57.78% Conservative: 5  
Best Local Similarity: 46.67% Mismatches: 12  
Query Match: 15.88% Indels: 7  
DB: 6 Gaps: 3

US-09-750-240-2 (1-104) x US-10-320-230-13 (1-1173)

Qy 28 SerArgArgGlyThrArgAlaGlyPheCysThrProArgTyrMetSerCysLeu 47

Db 635 GCACGGCCGAGGA-----GCTGCTGGCTTTCAGCTCCGCGAGCTTATCTTGCCTG 688

Qy 48 ArgAspAlaGluProPro-----SerProThrProAlaGlyProProArgCys--- 63

Db 689 CGGCCAGAGAACCGGCTCGCGGTTTCAGGCCGTCGAGATCGCCGCCGCGGTTCGAG 748

Qy 64 ---ProTrpGlnAsp 67

Db 749 CGCCCGTGGCCGGAG 763

RESULT 7

; Sequence 13, Application US/10348110

; GENERAL INFORMATION:

; APPLICANT: Lowe, Keith S.

; APPLICANT: Tao, Yumin

; APPLICANT: Gordon-Kamm, William J.

; APPLICANT: Gregory, Carolyn A.

; APPLICANT: McElver, John A.

; APPLICANT: Hoerster, George J.

; APPLICANT: Maddock, Sheila E.

; TITLE OF INVENTION: Cyclin D Polynucleotides, Polypeptides

; FILE REFERENCE: 0926D2

; CURRENT APPLICATION NUMBER: US/10/348,110

; PRIOR FILING DATE: 2003-01-21

; PRIOR APPLICATION NUMBER: 60/101,551

; PRIOR FILING DATE: 1998-09-23

; PRIOR APPLICATION NUMBER: 09/398,858

; PRIOR FILING DATE: 1999-09-20

; PRIOR APPLICATION NUMBER: 10/320,230

; PRIOR FILING DATE: 2002-12-16

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 13

; LENGTH: 1173

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(1173)

US-10-348-110-13

Alignment Scores: 285 Length: 1173

Pred. No.: 90.50 Matches: 21

Score: 57.78% Conservative: 5

Percent Similarity: 46.67% Mismatches: 12

Best Local Similarity: 15.88% Indels: 7

Query Match: 6 Gaps: 3

US-09-750-240-2 (1-104) x US-10-348-110-13 (1-1173)

Qy 28 SerArgArgGlyThrArgAlaGlyPheCysThrProArgTyrMetSerCysLeu 47

Db 635 GCACGGCCGAGGA-----GCTGCTGGCTTTCAGCTCCGCGAGCTTATCTTGCCTG 688

Qy 48 ArgAspAlaGluProPro-----SerProThrProAlaGlyProProArgCys--- 63

Db 689 CGGCCAGAGAACCGGCTCGCGGTTTCAGGCCGTCGAGATCGCCGCCGCGGTTCGAG 748

Qy 64 ---ProTrpGlnAsp 67

Db 749 CGCCCGTGGCCGGAG 763

Db 749 CGCCCGTGGCCGGAG 763

RESULT 8

PCT-US02-39133-56

; Sequence 56, Application PC/TUS0239133

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: GRIFFIN, Jennifer A.

; APPLICANT: RAMKUMAR, Jayalaxmi

; APPLICANT: EMERLING, Brooke M.

; APPLICANT: KABLE, Amy E.

; APPLICANT: ELLIOTT, Vicki S.

; APPLICANT: MARQUIS, Joseph P.

; APPLICANT: BAUGHN, Mariah R.

; APPLICANT: GORVAD, Ann E.

; APPLICANT: YUE, Henry

; APPLICANT: LEE, Ernestine A.

; APPLICANT: BECHA, Shanya D.

; APPLICANT: TANG, Y. Tom

; APPLICANT: TRAN, Uyen K.

; APPLICANT: SWARNAKAR, Anita

; APPLICANT: LEE, Sally

; APPLICANT: ISON, Craig H.

; APPLICANT: HAFALIA, April J.A.

; APPLICANT: TRAN, Bao

; APPLICANT: SPRAGUE, William W.

; APPLICANT: KHARE, Reena

; APPLICANT: GANDHI, Ameena R.

; APPLICANT: GIETZEN, Kimberly J.

; APPLICANT: BHATIA, Umesh G.

; APPLICANT: BURRILL, John D.

; APPLICANT: BLAKE, Julie J.

; APPLICANT: HO, Anne

; APPLICANT: Zheng, Wenjin

; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DE

; FILE REFERENCE: PF-1319 PCT

; CURRENT APPLICATION NUMBER: PCT/US02/39133

; CURRENT FILING DATE: 2002-12-04

; PRIOR APPLICATION NUMBER: US 60/340,747

; PRIOR FILING DATE: 2001-12-07

; PRIOR APPLICATION NUMBER: US 60/342,761

; PRIOR FILING DATE: 2001-12-20

; PRIOR APPLICATION NUMBER: US 60/349,705

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: US 60/354,764

; PRIOR FILING DATE: 2002-02-06

; PRIOR APPLICATION NUMBER: US 60/356,216

; PRIOR FILING DATE: 2002-02-12

; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: PERL Program

; SEQ ID NO 56

; LENGTH: 4884

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc-feature

; OTHER INFORMATION: Incyte ID No: 7506414CB1

PCT-US02-39133-56

Alignment Scores: 1.4e+03 Length: 4884

Pred. No.: 90.50 Matches: 39

Score: 32.58% Conservative: 4

Best Local Similarity: 29.55% Mismatches: 42

Query Match: 15.88% Indels: 47

DB: 1 Gaps: 8

US-09-750-240-2 (1-104) x PCT-US02-39133-56 (1-4884)

Qy 10 ProLysValAspGluArgLysThrAlaTrpGlyGluArgAsnGlyGlnLysArgSerArg 29

Db 2877 CTTGGCCGCTCGACGCGCTCGCGGTTGGGCGATCTCTGGCAGTGAACGGCAAGA 2936



```

; SOFTWARE: PERL Program
; SEQ ID NO 57
; LENGTH: 5079
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7506415CB1
PCT-US02-39133-57

Alignment Scores:
Pred. No.: 1.47e+03 Length: 5079
Score: 90.50 Matches: 39
Percent Similarity: 32.58% Conservative: 4
Best local Similarity: 29.53% Mismatches: 42
Query Match: 15.88% Indels: 47
DB: 1 Gaps: 8

US-09-750-240-2 (1-104) x PCT-US02-39133-57 (1-5079)

QY 10 ProLysValAspGluArgLysThrAlaTrpGlyGluArgAsnGlyGlnLysArgSerArg 29
    ||| ::||| ||||| ||| ::|||::|||
Db 3072 CCGTGGCGCTCGCAGCGGCTCGGGGTTGGGACCGCATCTCGGCAGTGAACGGGCAAGA 3131
    ||| ||| ||| ||||| ||||| |||||
QY 30 ArgArgGlyThrArgAlaGlyPheCysThrProArgTyrMetSerCysLeuArgAsp 49
    ||| ||| ||| ||||| ||||| |||||
Db 3132 CGTGGCGGATGCCACGCA-----CCACAGCAGCTACTGCGCTGCTCCG 3176
    ||| ||| ||| ||||| ||||| |||||
QY 50 AlaGluPro-----ProSerProThr--- 56
    ||| ||| ||| ||||| ||||| |||||
Db 3177 GCCCTGCTCGAGCTGCTGCTGCTGGGAGGACCCGGCACCGCGGCTACGGGA 3236
    ||| ||| ||| ||||| ||||| |||||
QY 57 -----ProAlaGly-----ProProArgCysPro 64
    ||| ||| ||| ||||| ||||| |||||
Db 3237 ACTGTGCATCCAGAGGCACCTGGGAGAGGCTGGGCATCAGCATCCCGGGGTGCCAG 3296
    ||| ||| ||| ||||| ||||| |||||
QY 65 -----TrpGlnAspAspAlaPheIleArgArgGly-----GlyPro 76
    ||| ||| ||| ||||| ||||| |||||
Db 3297 GGGCCAGCTGGCAACCCCGCGACCCACACAGCAGGGGCATCTTCATCTCCAAAGGTGAG 3356
    ||| ||| ||| ||||| ||||| |||||
QY 77 **LysGlyLysGluLeuGlyLeuArgAlaValAlaLeuGlyPhe----- 91
    ||| ||| ||| ||||| ||||| |||||
Db 3357 CCCCAGGGGGGACCGCGGCGCAGCGTGGCTGGCTGTGGGTTTGGCGGTGTTGGAGGT 3416
    ||| ||| ||| ||||| ||||| |||||
QY 92 GluAspThrGluValThrThrThrProAlaGlyPro 103
    ||| ||| ||| ||||| ||||| |||||
Db 3417 GAACCACGACAG-----CCTGCTGGGCT 3440
    ||| ||| ||| ||||| ||||| |||||

RESULT 10
US-10-288-985-6/c
; Sequence 6, Application US/10288985
; GENERAL INFORMATION:
; APPLICANT: Barton, Barry
; APPLICANT: Anders, Cecilia
; APPLICANT: Griffin, John Patrick
; APPLICANT: Jensen, Susan
; APPLICANT: Mosher, Roy Henry
; APPLICANT: Paradkar, Ashish Sudhakar
; TITLE OF INVENTION: Novel Process
; FILE REFERENCE: P31733C3
; CURRENT APPLICATION NUMBER: US/10/288,985
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 09/632,540
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 09/137,737
; PRIOR FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: 08/985,666
; PRIOR FILING DATE: 1997-12-05
; PRIOR APPLICATION NUMBER: GB 9702216.4
; PRIOR FILING DATE: 1997-02-04
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6

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Db      946  CGGTGAAGCCCATGGGCGCGAACCAGTTCCTCGAAGATGAAGCCGCCGCCGGGACGCGCC 887
Qy      35  AlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProProSer 54
Db      886  AGTGGTGGG-----CCTGCG---CGGAGTCCCGGGAGACCAGGACGTCTCTTCATCA 839
Qy      55  ProThrProAla-----GlyProPro----- 61
Db      838  CCGCGACCGGCTCGCCCGCGCAGCGGTGCGTGGCGCGCGCTTCGGCCTCTCCCGGT 779
Qy      62  ArgCysPro 64
Db      778  AGATGTCCA 770

RESULT 12
US-10-288-985-1
; Sequence 1, Application US/10288985
; GENERAL INFORMATION:
; APPLICANT: Barton, Barry
; APPLICANT: Anders, Cecilia
; APPLICANT: Griffin, John Patrick
; APPLICANT: Jensen, Susan
; APPLICANT: Mosher, Roy Henry
; APPLICANT: Paradkar, Ashish Sudhakar
; TITLE OF INVENTION: Novel Process
; FILE REFERENCE: P31733C3
; CURRENT APPLICATION NUMBER: US/10/288,985
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 09/632,540
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 09/137,737
; PRIOR FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: 08/985,666
; PRIOR FILING DATE: 1997-12-05
; PRIOR APPLICATION NUMBER: GB 9702216.4
; PRIOR FILING DATE: 1997-02-04
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 7193
; TYPE: DNA
; ORGANISM: S. Clavuligerus
US-10-288-985-1

Alignment Scores:
Pred. No.:      2.6e+03      Length:      7193
Score:          89.50      Matches:      26
Percent Similarity: 49.21%      Conservative: 5
Best Local Similarity: 41.27%      Mismatches: 15
Query Match:      15.70%      Indels:      17
DB:              6          Gaps:      4

US-09-750-240-2 (1-104) x US-10-288-985-1 (1-7193)
Qy      15  ArgLysThrAlaTrpGlyGluArgAsnGlyGlnLysArgSerArgArgGlyThrArg 34
Db      5274  CGGTGAAGCCCATGGGCGCGAACCAGTTCCTCGAAGATGAAGCCGCCGCCGGGACGCGCC 5333
Qy      35  AlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProProSer 54
Db      5334  AGTGGTGGG-----CCTGCG---CGGAGTCCCGGGAGACCAGGACGTCTCTTCATCA 5381
Qy      55  ProThrProAla-----GlyProPro----- 61
Db      5382  CCGCGACCGGCTCGCCCGCGCAGCGGTGCGTGGCGCGCGCTTCGGCCTCTCCCGGT 5441
Qy      62  ArgCysPro 64
Db      5442  AGATGTCCA 5450

RESULT 13
US-10-289-980-1
; Sequence 1, Application US/10289980

```

```

; GENERAL INFORMATION:
; APPLICANT: Anders, Cecilia
; APPLICANT: Barton, Barry
; APPLICANT: Griffin, John Patrick
; APPLICANT: Jensen, Susan
; APPLICANT: Mosher, Roy Henry
; APPLICANT: Paraskar, Ashish Sudhakar
; TITLE OF INVENTION: Novel Compounds
; FILE REFERENCE: P31731D2C2
; CURRENT APPLICATION NUMBER: US/10/289,980
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 10/214,519
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 09/350,976
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/018,806
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: GB 9702218.0
; PRIOR FILING DATE: 1997-02-04
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 7193
; TYPE: DNA
; ORGANISM: Streptomyces clavuligerus
US-10-289-980-1

Alignment Scores:
Pred. No.: 2,6e+03 Length: 7193
Score: 89.50 Matches: 26
Percent Similarity: 49.21% Conservative: 5
Best Local Similarity: 41.27% Mismatches: 15
Query Match: 15.70% Indels: 17
DB: 4 Gaps: 4

US-09-750-240-2 (1-104) x US-10-289-980-1 (1-7193)
QY 15 ArgLysThrAlaTrpGlyGluArgAsnGlyGlnLysArgSerArgArgGlyThrArg 34
||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 5274 CGGTGAAGCCCATGGGGCGAACCAGTCTCGAAGATGAAGCGCGCGCGGACGCC 5333

QY 35 AlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProSer 54
::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 5334 AGTGGTGGG-----CCTGCG---CGGAGTCCCGGAGACGAGCGTCTTCATCA 5381

QY 55 ProThrProAla-----GlyProPro----- 61
||| |||||
Db 5382 CCGCGACCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCTCCCGGT 5441

QY 62 ArgCysPro 64
||| |||||
Db 5442 AGATGTCCA 5450

RESULT 14
PCT-US03-01858-47/c
; Sequence 47, Application PC/TUS0301858
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: RRP SEQUENCES AND KNOCKOUT MICE AND USES THEREOF
; FILE REFERENCE: EX02-004C-PC
; CURRENT APPLICATION NUMBER: PCT/US03/01858
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 10/056,790
; PRIOR FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: US 09/908,419
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/219,289
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 60/277,487
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/304,863
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/277,471

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; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US60/305,017
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/328,491
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 34319
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (34274)..(34275)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (34285)..(34285)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (34297)..(34298)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (34301)..(34301)
; OTHER INFORMATION: n is a, c, g, or t
PCT-US03-01858-47

Alignment Scores:
Pred. No.: 1.63e+04 Length: 34319
Score: 89.00 Matches: 35
Percent Similarity: 42.73% Conservative: 12
Best Local Similarity: 31.82% Mismatches: 38
Query Match: 15.61% Indels: 25
DB: 1 Gaps: 5

US-09-750-240-2 (1-104) x PCT-US03-01858-47 (1-34319)
QY 11 LysValAspGluArgLys-ThrAlaTrpGlyGluArgAsnGlyGlnLysArgSerArgAr 30
||| ||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 5343 AAACCGATGAAGCCAGACCTTCTTGGGTGCGGAGTCTCAGACCAAGGTCGTCAG 5284

QY 30 gArgGlyThrArgAlaGlyPheCysThrProArgTyrMetSerCysLeuArgAsp-- 49
| ||| ||||| ||||| |||||
Db 5283 GGAGGGGGTGTGGAGCGGCG---TGC-----CTGGGCTTCTGCGGACATG 5239

QY 50 AlaGluProProSerProThrProAlaGly-----ProProArgCys----- 63
||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db 5238 GTCCCTCCCCCGAACCCTCAGCGGTGGAAGGCGCCAGGCGAGTCCAGTCCACCC 5179

QY 64 -----ProTrpGlnAspAlaPheIleArgArgGlyGlyPro 76
||| ||||| ::| ::| ::| ::| ::| ::| ::| ::|
Db 5178 ACCACGACCTGCTCTCTGATGATGAGTCGACGACGAGTCTCTCCATAGACCGGCGC 5119

QY 77 ***LysGlyLysLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluVal 96
||| ||||| ::| ::| ::| ::| ::| ::| ::| ::|
Db 5118 AGGGCGGGTGGCGCGGAGGCGGGGAGGCTGCTCTGCGGA-----CCGCTC 5071

QY 97 ThrThrThrProAlaGlyProLeu 104
::| ||||| ||||| |||||
Db 5070 CGTCCGCGCGCGCGCGCGCGCTC 5047

RESULT 15
US-09-724-676-9445
; Sequence 9445, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing

```



GenCore version 5.1.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 1, 2003, 07:59:04 ; Search time 1708 seconds  
(without alignments)  
986.142 Million cell updates/sec

Title: US-09-750-240-2

Perfect score: 570

Sequence: 1 MSWFGSLLPVKVDKRTAWG.....RAVALGFEDTEVTTPAGPL 104

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+p2n.model -DEV=xlh  
-Q/cgn2\_1/USPIO.spool/US09750240/runat\_25022003\_103941\_24976/app\_query.fasta\_1.263  
-DB-EST -Qfmt=fastap -SUFFIX=rest -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS-bits -START=1 -END=1 -MATRIX=blosom62 -TRANS-human4.0.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09750240@cgn2\_1.1.899.@runat\_25022003\_103941\_24976 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*  
1: em\_estha:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_estc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_nam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	432	75.8	618	10	B8866520	B8866520 B8866520
2	354	62.1	631	10	B8866451	B8866451 B8866451
3	200.5	35.2	1011	17	CNS02STX	AL212334 Tetraodon
4	127.5	22.4	941	13	BG916212	BG916212 602814927
5	112	19.6	430	10	AW045174	UI-M-BH1-
6	107.5	18.9	697	14	BQ803437	BQ803437 WHE2837_F
7	101.5	17.8	1259	17	AG065197	AG065197 Pan trogl
8	100	17.5	897	12	BG756761	BG756761 602710232
9	99.5	17.5	278	12	BG558370	BG558370 RHI22_66
10	99.5	17.5	842	12	BF696034	BF696034 601852020
11	99.5	17.5	1048	14	BQ716276	BQ716276 AGENCOURT
12	97.5	17.1	255	14	BM942641	BM942641 UI-M-CG0P
13	97.5	17.1	272	12	BE981360	BE981360 UI-M-CG0P
14	97.5	17.1	645	12	BE900861	BE900861 601673832
15	96	16.8	366	17	BH625429	BH625429 1007107C0
16	96	16.8	611	10	AV691613	AV691613 AV691613
17	95.5	16.8	466	13	BJ255561	BJ255561 RJ255561
18	95	16.7	884	17	CNS02830	AL185471 Tetraodon
19	94.5	16.6	1044	12	BF585283	BF585283 602101946
20	94.5	16.6	1067	17	AG071547	AG071547 Pan trogl
21	94	16.5	421	17	BH750109	BH750109 SALK_0347
22	93.5	16.4	410	9	AI861296	AI861296 603018F11
23	93.5	16.4	544	13	BI676675	BI676675 1c52b05_x
24	93.5	16.4	559	11	AV107600	AV107600 2ea mays
25	93	16.3	385	10	BE400834	BE400834 AHB008.C0
26	93	16.3	514	13	BT431052	BT431052 949064G10
27	93	16.3	514	14	BM706190	BM706190 UI-E-DW0-
28	92.5	16.2	301	12	BF924657	BF924657 IL5-NT022
29	92.5	16.2	310	12	BG014040	BG014040 IL5-GN024
30	92.5	16.2	408	12	BG103906	BG103906 RHI22_38
31	92.5	16.2	411	12	BG463088	BG463088 EM1_47_D0
32	92.5	16.2	599	12	BF483618	BF483618 WHE2335_H
33	92.5	16.2	615	14	BQ838166	BQ838166 WHE2907_C
34	92.5	16.2	707	9	AL820291	AL820291 AL820291
35	92.5	16.2	891	17	CNS03511	AL228142 Tetraodon
36	92.5	16.2	1033	13	BI152351	BI152351 602917520
37	92.5	16.2	1074	14	BM801345	BM801345 AGENCOURT
38	92.5	16.2	371	17	BH746357	BH746357 SALK_0400
39	92	16.1	517	14	BQ620765	BQ620765 TaLr1110D
40	92	16.1	574	12	BG649549	BG649549 EM1_80_G0
41	92	16.1	1070	14	BQ226091	BQ226091 AGENCOURT
42	92	16.1	1265	14	BQ922300	BQ922300 AGENCOURT
43	92	16.1	368	9	AU173954	AU173954 AU173954
44	91.5	16.1	521	10	BE287548	BE287548 601093167
45	91.5	16.1				

# ALIGNMENTS

RESULT 1  
BB866520  
LOCUS BB866520 618 bp mRNA linear EST 27-NOV-2001  
DEFINITION BB866520 RIKEN full-length enriched, colon RCB-0549 Cle-H3 CDNA Mus  
musculus cdna clone G431005N18 5', mRNA sequence.  
ACCESSION BB866520  
VERSION BB866520.1 GI:17112730  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 618)  
AUTHORS Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Ishii Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii

Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al. 2001)

# TITLE JOURNAL COMMENT

Unpublished (2001)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.  
e mouse tissues.  
Location/Qualifiers  
1. .618  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="G431005N18"  
/clone\_lib="RIKEN full-length enriched, colon RCB-0549 Cle-H3 cDNA"  
/tissue\_type="colon"  
/cell\_line="RCB-0549 Cle-H3"  
/note="Pooled cell lines ; (cell\_line=RCB-1751 WEHI 164), (cell\_line=RCB-2116 JC), (cell\_line=RCB-0035 WEHI-3), (cell\_line=RCB-0464 Meth-A), (cell\_line=RCB-0545 OHTA), (cell\_line=RCB-0559 K-1 . Fl), (cell\_line=RCB-1283 B16 melanoma), (cell\_type=B cells, cell\_line=RCB-1702 WEHI 231), (cell\_type=Leydig cells, cell\_line=RCB-2065 MLTC-1), (cell\_type=Nullipotent stem cell, cell\_line=RCB-2070 NE), (tissue\_type=bladder, cell\_line=RCB-0544 MB1-2), (tissue\_type=bone marrow, cell\_type=stroma cell, cell\_line=RCB-0549 SR-4987), (tissue\_type=colon, cell\_line=RCB-0549 Cle-H3), (tissue\_type=kidney, cell\_line=CCL-142 RAG), (tissue\_type=mandibular gland, cell\_line=RCB-1734 SCA-9 clone 15), (strain=BALB/C, cell\_type=B cells, cell\_line=RCB-1669 BCL1 Clone 13.20-383), (strain=C3H, tissue\_type=brain, cell\_line=RCB-1443 BC3H1)"

# FEATURES source

BASE COUNT 105 a 189 c 196 g 127 t 1 others  
ORIGIN  
Alignment Scores:  
Pred. No.: 3.82e-28 Length: 618  
Score: 432.00 Matches: 81  
Percent Similarity: 85.29% Conservative: 6  
Best Local Similarity: 79.41% Mismatches: 13  
Query Match: 75.79% Indels: 2  
DB: 10 Gaps: 2

US-09-750-240-2 (1-104) x BB866520 (1-618)

QY 1 MetSerTrpPheSerGlyLeuValProLysValAspGluArgLysThrAlaTrpGly 20  
|||||  
Db 37 ATGTGTCATGTTAGTGGGCTCTCTGTTCCAAAGTGGATGAACGGAAACACGCTTGGGGG 96  
|||||

QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40  
|||||  
Db 97 GAACCGAATGGCAGCAAGCGCCA---CGCCACGCGAATCGAGCCAGTGGCTCTGCGCA 153  
|||||

QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60  
|||||  
Db 154 CCTCGCTACATGAGCTGCTCAAGAATCGGAGCCACCGCCACTCTCTCGAGCTCAC 213  
|||||

QY 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro\*\*\*LysGlyLys 80  
|||||  
Db 214 ACTCGTGGCTCGCAGATGATGATTCATCAGAGGGCGGGCGGAGGGGTGG 273  
|||||

QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100  
|||||  
Db 274 GAGCTGGGGCTCGGCTCAGTGGCTTGGGTTTGACGACACTGAGGTG---ACCACCG 330  
|||||

QY 101 AlaGly 102  
|||

Db 331 ATGGGC 336  
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# RESULT 2

BB866451

LOCUS

DEFINITION

BB866451

ACCESSION

BB866451

VERSION

BB866451.1

KEYWORDS

EST.

SOURCE

house mouse.

Mus musculus

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 631)

AKIMURA, T., ARAKAWA, T., CARNINCI, P., FURUNO, M., HANAGAKI, T.,

HAYATSU, N., HIRAMOTO, K., HIRAO, T., HIROZANE, T., IMOTANI, K., ISHII

Y., ITO, M., KAWAI, J., KOJIMA, Y., KONNO, H., KODA, M., MATSUYAMA, T.,

NUMASAKI, R., OKAZAKI, Y., OKIDO, T., NAKAMURA, M., NISHI, K.,

NUMASAKI, R., OKAZAKI, Y., OKIDO, T., NAKAMURA, M., NISHI, K.,

SAITO, R., SAKAI, C., SAKAI, K., SAKAZUME, N., SASAKI, D., SATO, K.,

SHIBATA, K., SHINAGAWA, A., SHIRAKI, T., SOGABE, Y., SUZUKI, H., TAGAWA

A., TAKAHASHI, F., TAKAKU-AKAHIRA, S., TANAKA, T., TOMARU, A., TOYA, T.,

WATAHIKI, A., YASUNISHI, A., MURAMATSU, M. and HAYASHIZAKI, Y., et al.

RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al. 2001)

Unpublished (2001)

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Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,

URL: http://genome.gsc.riken.go.jp/

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh

M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,

Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura

S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and

Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara

Y. and Hayashizaki, Y.

Y. and Hayashizaki, Y.  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
further details.  
e mouse tissues.

## FEATURES

## source

```
1. .631
Location/Qualifiers
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="G431005J18"
/clone_lib="RIKEN full-length enriched, colon RCB-0549
Cle-H3 cDNA"
/tissue_type="colon"
/cell_line="RCB-0549 Cle-H3"
/note="pooled cell lines ; (cell_line=RCB-1751 WEHI 164),
(cell_line=RCB-2116 JC), (cell_line=RCB-0035 WEHI-3),
(cell_line=RCB-0464 Meth-A), (cell_line=RCB-0545 OHTA),
(cell_line=RCB-0559 K-1 F1), (cell_line=RCB-1283 B16
melanoma), (cell_type=B cells, cell_line=RCB-1702 WEHI 231
), (cell_type=leydig cells, cell_line=RCB-2065 MLTC-1),
(cell_type=Nullipotent stem cell, cell_line=RCB-2070 NE),
(tissue_type=bladder, cell_line=RCB-0544 MBT-2),
(tissue_type=bone marrow, cell_type=stroma cell,
cell_line=RCB-2028 SR-4987), (tissue_type=colon,
cell_line=RCB-0549 Cle-H3), (tissue_type=kidney,
cell_line=CCL-142 RAG), (tissue_type=submandibular gland,
cell_line=CRU-1734 SCA-9 clone 15), (strain=BALB/C,
cell_type=B cells, cell_line=RCB-1669 BCL1 Clone 13.20-3B3
), (strain=C3H, tissue_type=brain, cell_line=RCB-1443
BC3H1)"
```

BASE COUNT 90 a 217 c 174 g 150 t

## ORIGIN

## Alignment Scores:

```
Pred. No.: 2,26e-21 Length: 631
Score: 354.00 Matches: 69
Percent Similarity: 74.51% Conservatives: 7
Best Local Similarity: 67.65% Mismatches: 24
Query Match: 62.11% Indels: 2
DB: 10 Gaps: 2
```

US-09-750-240-2 (1-104) x BB866451 (1-631)

```
QY 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20
|||||
Db 37 ATGTCATGGTTAGTGGCCCTCTGTCCTCCACAGTGTGAACGGAACAGCTTGGGG 96
|||||
QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
|||||
Db 97 GAACCTTTGGCAGAGCGCCCA--CGCACGCTAATCGACGCTCTCTGGCG 153
|||||
QY 41 ProArgTyrMetSerCysLeuArgAspAlaGluProProSerProThrProAlaGlyPro 60
|||||
Db 154 CCTGTCTACTGAGCTGCTCCGACGTGGAGCCACCCAGCCCTCTGCTGTAC 213
|||||
QY 61 ProArgCysProTrpGlnAspAlaPheIleArgArgGlyGlyPro***LysGlyLys 80
|||||
Db 214 ACTTGGTGCCTTGGCAGGATGAAGCCTTCATCAAGAGGCGCGCGGGGGTGTG 273
|||||
QY 81 GluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThrThrPro 100
|||||
Db 274 GATCTGGGCTGGCGCCAGTGGCCCTCGGGTTGACGACACT---GTGGTGAGCACCT 330
|||||
QY 101 AlaGly 102
|||
Db 331 ATCGGC 336
|||
```

## RESULT 3

## CNS02STX/c

## LOCUS

DEFINITION Tetraodon nigroviridis genome survey sequence PUC-ori end of clone

162F16 of library G from Tetraodon nigroviridis, genomic survey  
sequence.  
AL212334  
AL212334.1 GI:7871153  
GSS: genome survey sequence.  
Tetraodon nigroviridis.  
Tetraodon nigroviridis.  
Tetraodon nigroviridis.  
Actinopterygii; Neopterygii; Chordata; Craniata; Vertebrata; Euteleostomi;  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodon.  
1 (bases 1 to 1011)  
Roest-Crollius H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,  
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,  
Saurin, W. and Weissenbach, J.  
Human gene number estimate provided by genome wide analysis using  
Tetraodon nigroviridis DNA sequence  
Unpublished  
2 (bases 1 to 1011)  
Roest-Crollius H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,  
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and  
Weissenbach, J.  
Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis  
Unpublished  
3 (bases 1 to 1011)  
Genoscope.  
Direct Submission  
Submitted (12-APR-2000)  
This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at  
<http://www.genoscope.cns.fr/Tetraodon>.

## FEATURES

## source

```
1. .1011
Location/Qualifiers
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="162F16"
/clone_lib="G"
/note="Genoscope sequence ID : COAG162DC08SP1-end :
PUC-ori"
```

BASE COUNT 191 a 297 c 324 g 175 t 24 others

## ORIGIN

## Alignment Scores:

```
Pred. No.: 7.14e-08 Length: 1011
Score: 200.50 Matches: 46
Percent Similarity: 61.54% Conservatives: 10
Best Local Similarity: 50.55% Mismatches: 17
Query Match: 35.18% Indels: 19
DB: 17 Gaps: 4
```

US-09-750-240-2 (1-104) x' CNS02STX (1-1011)

```
QY 1 MetSerTrpPheSerGlyLeuLeuValProLysValAspGluArgLysThrAlaTrpGly 20
|||||
Db 283 ATGTCCTGGTTTCACTGGTTTCTAGTGGCCAGATGACGACCAAGAGCGCTGGGG 224
|||||
QY 21 GluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThr 40
|||||
Db 223 GAGCGCAATGCAAGAAGCCCAACCGAAGGAGGCTCG-----TCTCTCTGCAAC 173
|||||
QY 41 ProArgTyrMetSerCysLeuArgAsp-----AlaGluProProSer-----Pro 55
|||||
Db 172 CCCCGTTCACATGAGTGCCTCGGGACCCCGACCCATGAGCCCTCTCGGAGCGCC 113
|||||
QY 56 ThrProAlaGlyProProArgCysProTrpGlnAspAlaPheIleArgArgGly 75
|||||
Db 112 CT-CCATCAGCACCCG-----CGGAGGGGTGGC 84
|||||
QY 76 Pro***LysGlyLysGluLeuGlyLeuArgAla 86
|||||
Db 83 GGGGCGCGTGGGGCGCGCGCAACTTCGGAGT 51
|||||
```

## RESULT 4

BG916212 941 bp mRNA linear EST 05-JUN-2001  
 LOCUS 602814927F1 NCI\_CGAP\_Mam4 Mus musculus cDNA clone IMAGE:4937095 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BG916212  
 VERSION BG916212.1 GI:14296688  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 941)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth  
 Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM10870 row: f column: 08  
 High quality sequence stop: 151.

## FEATURES

Source

Location/Qualifiers

1..941

/organism="Mus musculus"

/strain="NMRI"

/db\_xref="taxon:10090"

/clone="IMAGE:4937095"

/clone\_lib="NCI\_CGAP\_Mam4"

/tissue\_type="tumor, gross tissue"

/dev\_stage="5 months"

/lab\_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site.1: SalI;  
 Site.2: NotI; Cloned unidirectionally. Primer: Oligo dr.  
 Library constructed by Life Technologies. Investigators  
 providing samples: Lothar Hennighausen/Priscilla Furth,  
 NIH Reference for transgenic model: Li et al., Cell Growth  
 and Differentiation 7, 3-11 (1996)."  
 and Differentiation 7, 3-11 (1996)."  
 206 a 234 c 311 g 189 t 1 others

## BASE COUNT

ORIGIN

## Alignment Scores:

Pred. No.: 0.143 Length: 941  
 Score: 127.50 Matches: 38  
 Percent Similarity: 57.14% Conservative: 21  
 Best Local Similarity: 49.35% Mismatches: 26  
 Query Match: 22.37% Indels: 13  
 DB: 13 Gaps: 4

US-09-750-240-2 (1-104) x BG916212 (1-941)

QY 1 MetSerTrpPheSerGlyLeuLeu-ValProLys-ValAspGluArgLysThrAlaTrpG 20  
 Db 12 ATGTCATGTTGAGAGGGCTCTGGATCCCAACGTGGATGGAACGAAACAGCTTGGG 71  
 QY 20 lyGluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGlyGlyPheCys- 39  
 Db 72 GGAAGCGCAATGGCAGAGCGCCCA---CGCCACGCGAATCGAGCCAGTGGTTCAT-G 127  
 QY 40 -----ThrProArgTyrMetSerCys-----LeuArgAspAlaGluProProS 54  
 Db 128 CAGCGACGCTGCTCATCATGAGTGTGCGTCAACAAATGTCGAGACGACACCGAGCA 187  
 QY 54 erProThrProAlaGly-----ProProArgCysProTrpGln 66  
 Db 188 CCACGACGTCNCNCGCAGCGTGCACAAATCGGAGTGGCCCTATAGG 234

## RESULT 5

AW045174/c 430 bp mRNA linear EST 18-SEP-1999  
 LOCUS UI-M-BHL-ahh-a-03-0-UI.s1 NIH\_BMAP\_M\_S2 Mus musculus cDNA clone  
 DEFINITION UI-M-BHL-ahh-a-03-0-UI 3', mRNA sequence.  
 ACCESSION AW045174  
 VERSION AW045174.1 GI:5905703  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 430)  
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 9704477  
 COMMENT Contact: Chin, H  
 National Institute of Mental Health  
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
 20892-9643, USA  
 Tel: 301 443 1706  
 Fax: 301 443 9890  
 Email: mestr@mail.nih.gov  
 Oligo-dr track not found, Not I site shown in beginning of sequence  
 is likely internal to the message. cDNA Library Preparation: M.B.  
 Soares Lab Clone distribution: NIH BMAP cDNA clones will be made  
 available by the means that is soon to be determined. When NIH  
 determines the means for distribution of the BMAP cDNA clones, this  
 record will be updated accordingly when that means is determined.  
 The following repetitive elements were found in this cDNA sequence:  
 94-126, >GC-rich#Low-complexity  
 Seg primer: M13 Forward  
 POLYA-No.

## FEATURES

source

Location/Qualifiers

1..430

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UI-M-BHL-ahh-a-03-0-UI"

/clone\_lib="NIH\_BMAP\_M\_S2"

/dev\_stage="27-32 days"

/lab\_host="DH10B (Life Technologies)"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
 polylinker; Site.1: Not I; Site.2: Eco RI; The  
 NIH\_BMAP\_M\_S2 library is a subtracted library derived from  
 NIH\_BMAP\_M\_S1, which in turn is a subtracted library  
 derived from a mixture of normalized libraries from ten  
 regions of the mouse brain (cerebellum, brain stems,  
 olfactory bulbs, hypothalamus, cortex, amygdala, basal  
 ganglia, pineal gland, striatum, hippocampus). The driver  
 used for subtraction consisted of a pool of 5,000 clones  
 obtained from non-normalized and a pool of 2,000 clones  
 obtained from non-normalized and normalized mouse brain  
 spinal cord libraries.  
 TAG\_SEQ=None found"

76 a 130 c 152 g 72 t  
 BASE COUNT  
 ORIGIN

## Alignment Scores:

Pred. No.: 1.52 Length: 430  
 Score: 112.00 Matches: 34  
 Percent Similarity: 42.27% Conservative: 7  
 Best Local Similarity: 35.05% Mismatches: 38  
 Query Match: 19.65% Indels: 18  
 DB: 10 Gaps: 4

US-09-750-240-2 (1-104) x AW045174 (1-430)

QY 1 MetSerTrpPheSerGlyLeu-----LeuValProLysValAspGluArg 15  
 ::::::::::: |||||  
 ::::::::::: |||||



```

Db 411 GTTCTTGGCCTGATGCCTGCTGGCAGCATGCGCAGCGACCCGTTGGAAGCGA 352
Qy 16 LysThrAlaTrpGlyGluArgAsnGlyGlnLysArg-----SerArgArgArgGlyThr 33
Db 351 CTGGAGCCTGGAGCGCTCCCTGTCACGATAGACACCAAGGAGCGGTAGATATCG 292
Qy 34 ArgAlaGlyGlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProPro 53
Db 291 ACTCTGGGGCCCACTGCTCGCAGACAAGGTACAGTCAGGGCACACATGCCCCCTAGG 232
Qy 54 Ser-----ProThrProAlaGlyProProArgCysProTrpGlnAspAsp 68
Db 231 TCCCGCGCCTCGGAGAACCAACGCGAGTGGCGCCAGGTCTCCTCGGGTCCCTCCC 172
Qy 69 AlaPhe-----IleArgArgGlyGlyPro***LysGly 79
Db 171 GGCTTTCCCAAGCTTGCAGCATCACAGCTCTCGGCCCGTGGCGGC 121

RESULT 6
BQ803437/c 697 bp mRNA linear EST 30-JUL-2002
LOCUS WHE2837_F07_K132S Triticum monococcum vernalized apex cDNA library
DEFINITION Triticum monococcum cDNA clone WHE2837_F07_K13, mRNA sequence.
ACCESSION BQ803437
VERSION BQ803437.1 GI:22018406
KEYWORDS EST.
SOURCE Triticum monococcum.
ORGANISM Triticum monococcum

REFERENCE
AUTHORS Anderson,O.D., Chao,S., Crossman,C., Dubcovsky,J., Echenique,V.,
Lazo,G.R., Pham,J., Rausch,C.J., Stamova,B., Wilson,C. and Wood,J.
TITLE The structure and function of the expressed portion of the wheat
genomes - Vernalized apex cDNA library from Triticum monococcum
JOURNAL Unpublished (2002)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105959773
Fax: 5105959818
Email: oanderson@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: SK primer.

FEATURES
source
1..697
location/Qualifiers
/organism="Triticum monococcum"
/cultivar="G3116"
/db_xref="taxon:4568"
/clone="WHE2837_F07_K13"
/clone_lib="Triticum monococcum vernalized apex cDNA
library"
/tissue_type="Vernalized apex"
/dev_stage="One month old plants"
/lab_host="E. coli XL0LR"
/notes="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; One-month old plants were
subjected to vernalization treatment by placing them in
the cold room at 6 C, under 15hr light/9hr dark condition.
Total RNA was prepared from apex tissue extracted from
plants with no cold treatment; and from plants with 2-week
, 4-week and 6-week cold treatment separately. Equal
amount of total RNA was pooled from all four samples, a
cDNA library was made using pooled polyA RNA and cDNA
clones were in vivo excised at the University of
California, Davis (V. Echenique, B. Stamova, J. Dubcovsky
). Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."
109 a 258 c 217 g 113 t

```

```

Alignment Scores:
Pred. No.: 5 84 Length: 697
Score: 107.50 Matches: 40
Percent Similarity: 33.86% Conservative: 3
Best Local Similarity: 31.50% Mismatches: 43
Query Match: 18.86% Indels: 41
DB: 14 Gaps: 5

US-09-750-240-2 (1-104) x BQ803437 (1-697)
Qy 15 ArgLysThrAlaTrp-GlyGluArg-----AsnGlyGlnLysArgSerArgArgG1 32
Db 696 AGGGCGCGCTCTGGGGCGGTAGCGGGTGGTGAAGGCCACGCCGCGCGGG 637
Qy 32 YThrArgAlaGlyGlyPheCysThrProArgTyrMetSerCys----- 46
Db 636 CACTGCGTCTCCGGGT---TGCCGACCCAGATGTGGGTCTGTCGCGGAGCTGGCGTCGGAG 580
Qy 47 -----LeuArgAspAlaGluProProSerProThrProAlaG1 59
Db 579 CCGTGCAGACTGCACCGGCCATGCCGAGCCCTCCACCGCAGCTCTGTGCGGTGAAG 520
Qy 59 YProProArg----- 62
Db 519 ACCACCGCGAGCGCGCTTTCTTGGGGTAGCGCGCGCGGCGGTGATCTGCTCG 460
Qy 63 -----CysProTrpGlnAspAspAlaPheIleArgArgGlyPro***Ly 78
Db 459 AGGTGTAGAGACTTGGCCATGGAGCACTCGCCGT-----CGGAGAGCTGTCGTCGCGAGC 406
Qy 78 sGly-LysGluLeuGlyLeuArgAlaValAlaLeuGlyPheGluAspThrGluValThr 98
Db 405 AGGACACGGTCTTCGCACCGCGCGCTTGAGCTTGGCGTGGCGGGGAGAGGTACTGC 346
Qy 98 hrThrProAlaGlyPro 103
Db 345 TGGTCGATGTGCTCCA 329

RESULT 7
AG065197 1259 bp DNA linear GSS 03-NOV-2001
LOCUS Pan troglodytes DNA, clone: PTB-054I03.F, genomic survey sequence.
DEFINITION AG065197
ACCESSION AG065197
VERSION AG065197.1 GI:16616999
KEYWORDS GSS.
SOURCE Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-054I03.F.
ORGANISM Pan troglodytes
REFERENCE
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE BAC end sequences of Library PTB
JOURNAL Unpublished
REFERENCE
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpses@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY Vector : pKS145
R.Site 1 : SacI

```



High quality sequence stop: 218  
POLYA=No.

# FEATURES

source Location/Qualifiers

1. .278  
/organism="Sorghum propinquum"  
/db\_xref="taxon:132711"  
/clone\_lib="Rhizome2 (RHIZ2)"  
/note="Organ: Rhizomes; Vector: pBluescript II from Lambda  
zap II; Site\_1: XhoI; Site\_2: EcoRI; the library was made  
from poly-A RNA in the cloning vector lambda ZAP II.  
Clones to be sequenced were prepared by mass excision."

BASE COUNT 41 a 126 c 66 g 45 t

## ORIGIN

Alignment Scores:  
Pred. No.: 12.2 Length: 278  
Score: 99.50 Matches: 29  
Percent Similarity: 49.32% Conservative: 7  
Best Local Similarity: 39.73% Mismatches: 24  
Query Match: 17.46% Indels: 13  
DB: 12 Gaps: 5

US-09-750-240-2 (1-104) x BG558370 (1-278)

QY 18 AlaTrpGlyGluArgAsnGlyGlnLysArgSerArgArgGlyThrArgAlaGly--- 36  
Db 273 GCCTGG-----AGAGCAGGTGGAAGGGGAGGGAAGGGTGCAGGCCCTGGCTG 223  
QY 37 GlyPheCysThrProArg-----TyrMetSerCysLeuArgAspAla 50  
Db 222 GGATTCTGCACGCGCGAGGAGGCGCTGTAGTGTGTGTC---GGGCCCGCG 166  
QY 51 GluProSerProThrProAlaGlyProProArgCysProThrGlnAspAlaPhe 70  
Db 165 CCGCCCGCTGCGCGCGCGTGTCTCCATCTGCCCTTACGACCCCTGATTC 106  
QY 71 IleArgGlyGlyPro\*\*\*LysGlyLysGluLeuGly 83  
Db 105 TTGCTCCGGAAGGC-----AAGGGGAGGAGGAGG 73

## RESULT 10

BF696034 842 bp mRNA linear EST 22-DEC-2000  
LOCUS 601852020F1 NIH\_MGC\_56 Homo sapiens cDNA clone IMAGE:4075829 5',  
mRNA sequence.

ACCESSION BF696034  
VERSION BF696034.1 GI:11981442

## KEYWORDS

EST.

## SOURCE

human.

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 842)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: CLONETECH Laboratories, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM928 row: h column: 06  
High quality sequence stop: 188.

## FEATURES

source

Location/Qualifiers  
1. .842  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:4075829"  
/clone\_lib="NIH\_MGC\_56"

/tissue\_type="primitive neuroectoderm"  
/lab\_host="PH10B (T1 phage-resistant)"  
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site\_1:  
SfiI (ggccgctggcc); Site\_2: SfiI (ggccattatggcc);  
double-stranded cDNA was prepared from cell line RNA.  
and 3' adaptors were used in cloning as follows: 5'  
adaptor sequence: 5'-CAGGCGCATATGGCC-3' and 3' adaptor  
sequence: 5'-ATTCTAGAGCGGAGCGCGGCGGACATG-dt(30)AN-3'  
(where B = A, C, or G and N = A, C, G, or T). Average  
insert size 1.85 kb (range 0.9-4.0 kb). 15/15 colonies  
contained inserts by PCR. This library was enriched for  
full-length clones and was constructed by Clontech  
Laboratories (Palo Alto, CA)."

BASE COUNT 158 a 250 c 340 g 94 t  
ORIGIN

Alignment Scores:  
Pred. No.: 34.4 Length: 842  
Score: 99.50 Matches: 26  
Percent Similarity: 45.59% Conservative: 5  
Best Local Similarity: 38.24% Mismatches: 36  
Query Match: 17.46% Indels: 1  
DB: 12 Gaps: 1

US-09-750-240-2 (1-104) x BF696034 (1-842)

QY 17 ThrAlaTrpGlyGluArgAsnGlyGlnLysArgSerArgArgArg---GlyThrArgAla 35  
Db 258 TCACGTGTGCGAAGCTCCGGGGAGGACCCAAAGGAAGAGCGGCTAGGACGAGGCC 317  
QY 36 GlyGlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProSerPro 55  
Db 318 GGGGGCTCCCAATTCCTATGAGAGCTGGGGCTCTAAAGAGCCCGGAGGCCT 377  
QY 56 ThrProAlaGlyProProArgCysProTrpGlnAspAlaPheIleArgGlyGly 75  
Db 378 CGGCGCGCGGCGCGTGAAGTCTCCAGGGCGGATGACCAAGAACTTGCAGGTCGGC 437  
QY 76 Pro\*\*\*LysGlyLysGluLeuGly 83  
Db 438 CAGAGTGTGAGCTGAGGGGGGT 461

## RESULT 11

BQ716276 1048 bp mRNA linear EST 16-JUL-2002  
LOCUS BQ716276  
DEFINITION AGENCOURT\_8296836 Lupski\_sympathetic\_trunk Homo sapiens cDNA clone  
IMAGE:6194275 5', mRNA sequence.

ACCESSION BQ716276

VERSION BQ716276

KEYWORDS EST.

SOURCE human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 1048)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Dr. James R. Lupski  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM13599 row: d column: 20  
High quality sequence stop: 454.

## FEATURES

source

Location/Qualifiers  
1. .1048  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

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/clone="IMAGE:6194275"
/clone_lib="Lupski_sympathetic_trunk"
/sex="male"
/tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
```

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/note="vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCAGCGTCCG-3' and
5'-CAGTAGTCTAGATCGGAGCGGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, not amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine); available through Life
Technologies."
```

```
BASE COUNT 191 a 370 c 374 g 109 t 4 others
ORIGIN
```

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Alignment Scores:
Pred. No.: 42-2 Length: 1048
Score: 99.50 Matches: 24
Percent Similarity: 55.56% Conservative: 11
Best Local Similarity: 38.10% Mismatches: 26
Query Match: 17.46% Indels: 2
DB: 14 Gaps: 1
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US-09-750-240-2 (1-104) x B0716276 (1-1048)
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Qy 26 LysArgSerArgArgGlyThrArgAlaGlyGlyPheCysThrProArgTyrMetSer 45
Db 719 CGGAAGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 778
Qy 46 CysLeuArg-AspAlaGluProSerProThrProAlaGlyProProArgCysProThr 65
Db 779 GCCCAGAGGTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 838
Qy 65 pGlnAspAla----PheIleArgArgGlyGlyPro**LysGlyLysGluLeuGlyLe 84
Db 839 ACGGGAGGAGCGCGTGCCTGGAACGCGGGGACCGCGCGCGCGCGCGCGCGCGCGCG 898
Qy 84 uArgAla 86
Db 899 CCGCGCC 905
```

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RESULT 12 BM942641 255 bp mRNA linear EST 29-APR-2002
LOCUS UI-M-CG0p-bdb-c-10-0-UI.r1 NIH_BMAP_Ret4_S2 Mus musculus cDNA clone
DEFINITION UI-M-CG0p-bdb-c-10-0-UI 5', mRNA sequence.
```

```
ACCESSION BM942641
VERSION BM942641.1 GI:19402504
KEYWORDS EST.
```

```
SOURCE house mouse.
```

```
ORGANISM
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 255)
```

```
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
```

```
Genome Res. 6 (9), 791-806 (1996)
```

```
97044477
```

```
COMMENT
```

```
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
```

```
Tel: 301 443 1706
```

```
Fax: 301 443 9890
```

```
Email: mEst@mail.nih.gov
```

```
Tissue Procurement: Dr. Xin-Yuan Fu, Yale University School of
Medicine
```

```
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
```

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com).

The following repetitive elements were found in this cDNA

sequence: 201-248, >GC-rich#Low\_complexity

Seq primer: M13 REVERSE.

#### FEATURES

source

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Location/Qualifiers
1..255
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-CG0p-bdb-c-10-0-UI"
/clone_lib="NIH_BMAP_Ret4_S2"
/lab_host="DH10B (Life Technologies)"
/note="vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_Ret4_S2 library is a subtracted library,
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.uiowa.edu. The tissue
for this library was contributed by Dr. Xin-Yuan Fu, Yale
University School of Medicine"
```

```
BASE COUNT 44 a 75 c 91 g 45 t
ORIGIN
```

```
Alignment Scores:
Pred. No.: 16-8 Length: 255
Score: 97.50 Matches: 24
Percent Similarity: 38.24% Conservative: 2
Best Local Similarity: 35.29% Mismatches: 19
Query Match: 17.11% Indels: 23
DB: 14 Gaps: 1
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US-09-750-240-2 (1-104) x BM942641 (1-255)
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```
Qy 20 GlydLuarAsnGlyGlnLysArgSerArgArgGlyThr----- 33
Db 216 GGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 157
```

```
Qy 34 -----ArgAlaGly 36
Db 156 TGGCCTCTCTCATTCGCCGTGACCTTGAAGAAGCGCTTGACTCGTGATGAAGAGCGTCC 97
```

```
Qy 37 GlyPheCysThrProArgTyrMetSerCysLeuArgAspAlaGluProSerProThr 56
Db 96 CACTGGGACACTCCACGACAAACTTCTGTACCACCTCTGCAACTCCGCCACATCCATCT 37
```

```
Qy 57 ProAlaGlyProProArgCysPro 64
Db 36 CCCCGCGCGCGCTCCGCCCTCTTCCC 13
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#### RESULT 13

```
BE981360
```

```
LOCUS
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```
DEFINITION BE981360 272 bp mRNA linear EST 29-APR-2002
UI-M-CG0p-bdb-c-10-0-UI.s1 NIH_BMAP_Ret4_S2 Mus musculus cDNA clone
```

```
ACCESSION BE981360
VERSION BE981360.1 GI:10650389
```

```
KEYWORDS EST.
```

```
SOURCE house mouse.
```

```
ORGANISM
```

```
Mus musculus
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
1 (bases 1 to 272)
```

```
Bonaldo,M.F., Lennon,G. and Soares,M.B.
```

```
Normalization and subtraction: two approaches to facilitate gene
```

```
discovery
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```
Genome Res. 6 (9), 791-806 (1996)
```

```
97044477
```

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COMMENT
```

```
Contact: Chin, H
```

```
National Institute of Mental Health
```







XX	(RBCG ) UNIV CALIFORNIA.
XX	PA Hammond HK, Gao M;
XX	PI WPI: 2001-418260/44.
DR	P-FSDB: AAE04309.
XX	
XX	Novel polynucleotide encoding a modified adenyllylcyclase polypeptide
PT	useful for enhancing cardiac function in mammalian hearts, and for
PT	treating heart disease, especially congestive heart failure .
XX	
FS	Example 5; Page 115-119; 153pp; English.
XX	
CC	The present invention relates to methods and compositions for enhancing
CC	cardiac function in mammalian hearts by inserting transgenes encoding
CC	beta-adrenergic signalling proteins (beta-ASP) which increase
CC	beta-adrenergic responsiveness within the myocardium using in vivo
CC	gene therapy. The beta-ASPs of the invention include beta-adrenergic
CC	receptors (beta-AR), adenyllylcyclases (also referred as adenylcyclase,
CC	adenylate cyclase and cAMP synthetase) and G-protein receptor kinase
CC	(GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
CC	in mammalian hearts and for treating heart disease, especially
CC	congestive heart failure. The present cDNA sequence encodes human
CC	partial cardiac adenylcyclase VI (ACVI) isoform which is used for
CC	generating a third beta-ASP transgene, used in the exemplification
CC	of the invention.
XX	
SQ	Sequence 1812 BP; 361 A; 539 C; 507 G; 405 T; 0 other;
	Query Match 100.0%; Score 1812; DB 22; Length 1812;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 1812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 GTTAAGTGTGCTGGGCATCCTCGCGCAGTCGACGTGCGGGCGCTTTCCACGACAG 60
Db	1 GTTAACGTGTGCTGGGATCCTCGCGCAGTCGACGTGCGGGCGCTTTCCACGACAG 60
Qy	61 CGCGCACCCCTCTGCGGGCTCTGCGGCCGTGTTCTTGATACATCGCATACAG 120
Db	61 CGCGCACCCCTCTGCGGGCTCTGCGGCCGTGTTCTTGATACATCGCATACAG 120
Qy	121 CTCTTCCCATTCCGCATCGGGCTGCCCTCTCAGCGGCTGGGCTCTCCACCTTGGAT 180
Db	121 CTCCTCCCCATCCGCATCGGGCTGCCCTCTCAGCGGCTGGGCTCTCCACCTTGCAT 180
Qy	181 TTGATCTTGGCTGGCAACTTAACCGTGGTGATGCTTCTCTGGAAGCAGCTCGGTGCC 240
Db	181 TTGATCTTGGCTGGCAACTTAACCGTGGTGATGCTTCTCTGGAAGCAGCTCGGTGCC 240
Qy	241 AATGTGCTGTCTTCTCTGCACAACCTCATTAGCATCTGCACACATATCCACAGAG 300
Db	241 AATGTGCTGTCTTCTCTGCACCACCTCATTTAGCATCTGCACACATATCCACAGAG 300
Qy	301 GTGTCTCAGCGCCAGGCTTTTCAGGAGACCCGCGAGTTACATCCAGGCCGGCTCCACCTG 360
Db	301 GTGTCTCAGCGCCAGGCTTTTCAGGAGACCCGCGAGTTACATCCAGGCCGGCTCCACCTG 360
Qy	361 CAGCATGAGAATCGGCACGAGCGGTGCTGTGTCGGTATGTCGCCACGACGTTGCC 420
Db	361 CAGCATGAGAATCGGCACGAGCGGTGCTGTGTCGGTATGTCGCCACGACGTTGCC 420
-Qy	421 ATGAGATGAAGAAGACATCAACACAAAAAAGAGACATGTTCCACAAGATCTACATA 480
Db	421 ATGAGATGAAGAAGACATCAACACAAAAAAGAGACATGTTCCACAAGATCTACATA 480
Qy	481 CAGAAGCATGACAATGTTCAGCATCCTGTTTGCAGACATTTAGGGCTTCACGACCTGGCA 540
Db	481 CAGAAGCATGACAATGTTCAGCATCCTGTTTGCAGACATTTAGGGCTTCACGACCTGGCA 540
Qy	541 TCCAGTGCACTCGCAGGAGCTGGTCATGACCTGAATGAGCTTCTTGCCTGGTTTGCAC 600
Db	541 TCCAGTGCACTCGCAGGAGCTGGTCATGACCTGAATGAGCTTCTTGCCTGGTTTGCAC 600





Db 1216 CGCATCCACATCACTCGGGCAACACACTGCAGTACTGAACGGGACTACGAAGTGGAGCCA 1275  
QY 961 GGCGGTGGTGGCAAGCGCAACGCGTACCTCAAGGAGCAGACACATTTGAGACTTTTCCTCATC 1020  
Db 1276 GGCGGTGGTGGCAAGCGCAACGCGTACCTCAAGGAGCAGACACATTTGAGACTTTTCCTCATC 1335  
QY 1021 CTGGGCGCCAGCCAGAAACGGAAGAGGAGAGGATGCTGGCCAAAGCTGCAGCGGACT 1080  
Db 1336 CTGGGCGCCAGCCAGAAACGGAAGAGGAGAGGATGCTGGCCAAAGCTGCAGCGGACT 1395  
QY 1081 CGGGCCAACTCCATGGAAGGGCTGATGCCGATGGTTCCTGATCGTGCCTTCTCCCGG 1140  
Db 1396 CGGGCCAACTCCATGGAAGGGCTGATGCCGATGGTTCCTGATCGTGCCTTCTCCCGG 1455  
QY 1141 ACCAAGACTCCCAAGSCCTTCGCCAGATGGGCATTTGATTCACGACCAAGACACCGG 1200  
Db 1456 ACCAAGACTCCCAAGSCCTTCGCCAGATGGGCATTTGATTCACGACCAAGACACCGG 1515  
QY 1201 GGCACCCAAAGATCCCTGAACCCCTGAGGATGAGTTCCTGAGCCGCTGGCATC 1260  
Db 1516 GGCACCCAAAGATCCCTGAACCCCTGAGGATGAGTTCCTGAGCCGCTGGCATC 1575  
QY 1261 GATGCCCGCAGCATTTGATCAGCTGCGAAGGACCATGTGGCCGGTTTTGTCTACCTTC 1320  
Db 1576 GATGCCCGCAGCATTTGATCAGCTGCGAAGGACCATGTGGCCGGTTTTGTCTACCTTC 1635  
QY 1321 CAGAGAGAGGATTTTGAAGAAGTACTCCCGGAAGTGGATCCCGCTTCGGAGCCTAC 1380  
Db 1636 CAGAGAGAGGATTTTGAAGAAGTACTCCCGGAAGTGGATCCCGCTTCGGAGCCTAC 1695  
QY 1381 GTTGCCTGTGCCCTGTGTCTTCTCTCTCATCTGCTTCATCCAGCTTCTAATTTTCCCA 1440  
Db 1696 GTTGCCTGTGCCCTGTGTCTTCTCTCTCATCTGCTTCATCCAGCTTCTAATTTTCCCA 1755  
QY 1441 CACTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCCTGCTGCTAATCACCGTG 1500  
Db 1756 CACTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCCTGCTGCTAATCACCGTG 1815  
QY 1501 CTGATCTGTGCTGTACTCTCTGTGTTCTCTTCCCTAAGGCCCTGCAACGCTCTGTCC 1560  
Db 1816 CTGATCTGTGCTGTACTCTCTGTGTTCTCTTCCCTAAGGCCCTGCAACGCTCTGTCC 1875  
QY 1561 CGCAGATTGTCCGCTCAGGGGCACATAGCAGCGAGTTGGCATCTTTTCCGTCCTGCTT 1620  
Db 1876 CGCAGATTGTCCGCTCAGGGGCACATAGCAGCGAGTTGGCATCTTTTCCGTCCTGCTT 1935  
QY 1621 GTGTTTACTTCTGCCATTTGCCACATGTTCACTGTAAACACACACCCCATACGGAGCTGT 1680  
Db 1936 GTGTTTACTTCTGCCATTTGCCACATGTTCACTGTAAACACACACCCCATACGGAGCTGT 1995  
QY 1681 GCAGCCCGGATGCTGAATTTAACCCTGTGATCACTCACTGCTGCCCTGCCACCTGCAGCAGCTC 1740  
Db 1996 GCAGCCCGGATGCTGAATTTAACCCTGTGATCACTCACTGCTGCCCTGCCACCTGCAGCAGCTC 2055  
QY 1741 AATTACTCTCTGGGCTTGATGCTCCCTGTGTGAGGGACCATGCCACCTGCAGCTTTT 1800  
Db 2056 AATTACTCTCTGGGCTTGATGCTCCCTGTGTGAGGGACCATGCCACCTGCAGCTTTT 2115  
QY 1801 CTTGAGGTGTTTC 1812  
Db 2116 CTTGAGGTGTTTC 2127

RESULT 3  
AAD08563  
ID AAD08563 standard; DNA; 3549 BP.

XX AAD08563;

XX 04-SEP-2001 (first entry)

DE Human cardiac adenylcyclase VI (ACVI) isoform #1 DNA.

XX

KW Human; cardiant; beta-adrenergic signalling protein; beta-ASP;  
KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
KW adenylcyclase; adenylyate cyclase; cAMP synthetase;  
KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
KW cardiac adenylcyclase VI; ACVI isoform; beta-ASP transgene; ds.  
XX  
OS Homo sapiens.  
XX  
XX Location/Qualifiers  
FH 1..3504  
FT /tag= a  
FT /product= "Human cardiac adenylcyclase VI isoform #1"  
FT /EC\_number= "4.6.1.1"  
XX  
XX WO200148164-A2.  
PN 05-JUL-2001.  
XX 26-DEC-2000; 2000WO-US35411.  
XX 27-DEC-1999; 99US-0472667.  
XX (REGC ) UNIV CALIFORNIA.  
XX Hammond HK, Gao M;  
XX WPI: 2001-418260/44.  
XX P-PSDB; AAE04310.  
XX Novel polynucleotide encoding a modified adenylcyclase polypeptide  
XX useful for enhancing cardiac function in mammalian hearts, and for  
XX treating heart disease, especially congestive heart failure -  
XX  
XX Example 5; Page 122-129; 153pp; English.  
XX The present invention relates to methods and compositions for enhancing  
XX cardiac function in mammalian hearts by inserting transgenes encoding  
XX beta-adrenergic signalling proteins (beta-ASP) which increase  
XX beta-adrenergic responsiveness within the myocardium using in vivo  
XX gene therapy. The beta-ASPs of the invention include beta-adrenergic  
XX receptors (beta-AR), adenylcyclases (also referred to as adenylylase,  
XX adenylyate cyclase and cAMP synthetase) and G-protein receptor kinase  
XX (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
XX in mammalian hearts and for treating heart disease, especially  
XX congestive heart failure. The present DNA sequence encodes human  
XX cardiac adenylcyclase VI (ACVI) isoform which is used for generating  
XX a third beta-ASP transgene, used in the exemplification  
XX of the invention.

SQ Sequence 3549 BP; 699 A; 1025 C; 1061 G; 764 T; 0 other;

Query Match 99.8%; Score 1808.4; DB 22; Length 3549;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TAACGTGTGTCTGGGCATCTGCGGCAGTGCAGGTGCGGGCGCTTTCGCAGCAGACCC 62

Db 636 TAACGTGTGTCTGGGCATCTGCGGCAGTGCAGGTGCGGGCGCTTTCGCAGCAGACCC 695

QY 63 GGCAGACCCCTCTGCGGGCCTCTGGTGCCTGTGTCTTTGTATACATCGCATACAGCT 122

Db 696 GGCAGACCCCTCTGCGGGCCTCTGGTGCCTGTGTCTTTGTATACATCGCATACAGCT 755

QY 123 CCTCCCATCCGATCGCGGCTGCCCTCCTCAGCGCCCTCCACCTTCGATTT 182

Db 756 CCTCCCATCCGATCGCGGCTGCCCTCCTCAGCGCCCTCCACCTTCGATTT 815

QY 183 GATCTTGGCTGGCAACTTAACCGTGGTGGTATGCTTCTCTCTGGAAGCAGCTCGGTGCCAA 242

Db 816 GATCTTGGCTGGCAACTTAACCGTGGTGGTATGCTTCTCTCTGGAAGCAGCTCGGTGCCAA 875

QY 243 TGTGCTGTCTTCTCTGCAACCAAGTCAATAGCATCTGCACACATATCCAGCAGAGT 302

|||||

Db 876 TGTGCTGCTGTTCTCTGACCAACGTCATTAGCATCTGCACACACTATATCCAGCAGGT 935  
QY 303 GTCTACGCGCAGGCCCTTTTCAGAGAGACCCGCAAGTTACATCCAGCGCGGCTCCACCTGCA 362  
Db 936 GTCTACGCGCAGGCCCTTTTCAGAGAGACCCGCAAGTTACATCCAGCGCGGCTCCACCTGCA 995  
QY 363 GCATGAGAAATCGGACGAGCGGCTGCTGCTGTCGGTATTGCCCCAGACAGCTTGCCAT 422  
Db 996 GCATGAGAAATCGGACGAGCGGCTGCTGCTGTCGGTATTGCCCCAGCAGCTTGCCAT 1055  
QY 423 GGAGATGAAGAGACATCAACACAAAAGAGACATGTTCCACAAGATCTACATACA 482  
Db 1056 GGAGATGAAGAGACATCAACACAAAAGAGACATGTTCCACAAGATCTACATACA 1115  
QY 483 GAAGCATGACAATGTCAGCATCTCTGTTTGACAGACATTGAGGGCTTACCAGCCTGGCATC 542  
Db 1116 GAAGCATGACAATGTCAGCATCTCTGTTTGACAGACATTGAGGGCTTACCAGCCTGGCATC 1175  
QY 543 CCAGTGCACTGGCAGAGCTGGTTCATGACCCTGAATGAGCTCTTTGCCCGGGTTTGACAA 602  
Db 1176 CCAGTGCACTGGCAGAGCTGGTTCATGACCCTGAATGAGCTCTTTGCCCGGGTTTGACAA 1235  
QY 603 GCTGGCTGGGAGAAATCACTGCTGAGGATCAAGATCTTGGGGACTGTTACTACTGT 662  
Db 1236 GCTGGCTGGGAGAAATCACTGCTGAGGATCAAGATCTTGGGGACTGTTACTACTGT 1295  
QY 663 GTCAGGGCTGCCGAGCGCGGCGGACCATGCCACTGCTGTGTGAGATGGGGTAGA 722  
Db 1296 GTCAGGGCTGCCGAGCGCGGCGGACCATGCCACTGCTGTGTGAGATGGGGTAGA 1355  
QY 723 CATGATTGAGGCCATCTCGCTGGTGTGCTGAGGTGACAGGTGTGAATGTGAACATGCGCGT 782  
Db 1356 CATGATTGAGGCCATCTCGCTGGTGTGCTGAGGTGACAGGTGTGAATGTGAACATGCGCGT 1415  
QY 783 GGGCATCCACAGCGGGCGCTGCACTGCGGGCTCTTGGCTTGGGAAATGGCAGTTCGA 842  
Db 1416 GGGCATCCACAGCGGGCGCTGCACTGCGGGCTCTTGGCTTGGGAAATGGCAGTTCGA 1475  
QY 843 TGTGTGTCTCAATGATGTGACCTTGGCCAAACCATGGAAGCAGAGAGCGGGCTGGCG 902  
Db 1476 TGTGTGTCTCAATGATGTGACCTTGGCCAAACCATGGAAGCAGAGAGCGGGCTGGCG 1535  
QY 903 CATCCACATCACTGGGCAACACTGCACTGCTGAAACGGGGACTTACGAAGTGGAGCCAGG 962  
Db 1536 CATCCACATCACTGGGCAACACTGCACTGCTGAAACGGGGACTTACGAAGTGGAGCCAGG 1595  
QY 963 CCGTGGTGGCAAGCGCAACGGTACCTCAAGGAGCAGCACAATTGAGACTTTCCTCATCCT 1022  
Db 1596 CCGTGGTGGCAAGCGCAACGGTACCTCAAGGAGCAGCACAATTGAGACTTTCCTCATCCT 1655  
QY 1023 GGGCGCCAGCCAGAAACGGAAAGAGAGAAAGGCATGCTGCCCAAGCTGCAGCGGACTCG 1082  
Db 1656 GGGCGCCAGCCAGAAACGGAAAGAGAGAAAGGCATGCTGCCCAAGCTGCAGCGGACTCG 1715  
QY 1083 GGCCAACTCCATGGAAGGGCTGATGCGCGGATGGGTTTCCTGATCGTGCCTTCTCCCGGAC 1142  
Db 1716 GGCCAACTCCATGGAAGGGCTGATGCGCGGATGGGTTTCCTGATCGTGCCTTCTCCCGGAC 1775  
QY 1143 CAGGACTCCAGGCCCTTCGCCAGATGGGCATTGATGATTCACGAAGAACACACCGGG 1202  
Db 1776 CAGGACTCCAGGCCCTTCGCCAGATGGGCATTGATGATTCACGAAGAACACACCGGG 1835  
QY 1203 CACCCAGATGCCCTGAACCTTGAGGATGAGGTGGATGAGTTCTTGAGCGGTGCCATCGA 1262  
Db 1836 CACCCAGATGCCCTGAACCTTGAGGATGAGGTGGATGAGTTCTTGAGCGGTGCCATCGA 1895  
QY 1263 TGCCCGCAGCATTTGATCAGCTGCGGAAGACCATTGTGCGCGGTTTTTGTCTCAGCTTCCA 1322  
Db 1896 TGCCCGCAGCATTTGATCAGCTGCGGAAGACCATTGTGCGCGGTTTTTGTCTCAGCTTCCA 1955  
QY 1323 GAGAGAGATTTTGAGAGAAGTACTCCCGAAGGTGGATCCCGGCTTCGAGCGCTACGT 1382  
Db 1956 GAGAGAGATTTTGAGAGAAGTACTCCCGAAGGTGGATCCCGGCTTCGAGCGCTACGT 2015

QY 1383 TGCTGTGCCCTGTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCACA 1442  
Db 2016 TGCTGTGCCCTGTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCACA 2075  
QY 1443 CTCACCCCTGATGCTGGGATTTATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCT 1502  
Db 2076 CTCACCCCTGATGCTGGGATTTATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCT 2135  
QY 1503 GATCTGTGCTGTACTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1562  
Db 2136 GATCTGTGCTGTACTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2195  
QY 1563 CAGCATTTGCTCCGCTCAGCGGCACATAGCACCGCAGTTGGCATCTTTTCCGCTGCTGCTGCT 1622  
Db 2196 CAGCATTTGCTCCGCTCAGCGGCACATAGCACCGCAGTTGGCATCTTTTCCGCTGCTGCTGCT 2255  
QY 1623 GTTTACTTCTGCCATTTGCCAACATGTTACCTGTGTAACACACCCCCATAGCGAGCTGTC 1682  
Db 2256 GTTTACTTCTGCCATTTGCCAACATGTTACCTGTGTAACACACCCCCATAGCGAGCTGTC 2315  
QY 1683 AGCCCGGATGCTGAATTTAACACCTGCTGACATCAGTGCCTGCACCTGCACCTGCAGAGCTCAA 1742  
Db 2316 AGCCCGGATGCTGAATTTAACACCTGCTGACATCAGTGCCTGCACCTGCAGAGCTCAA 2375  
QY 1743 TTACTTCTTGGGCTGGATGCTCCCTGCTGTGAGGGCACCATGCCACCTGCAGCTTTCC 1802  
Db 2376 TTACTTCTTGGGCTGGATGCTCCCTGCTGTGAGGGCACCATGCCACCTGCAGCTTTCC 2435  
QY 1803 TGAGGTGTTT 1812  
Db 2436 TGAGGTGTTT 2445  
RESULT 4  
AAD08567  
ID AAD08567 standard; DNA; 3552 BP.  
XX  
AC AAD08567;  
XX  
DT 04-SEP-2001 (first entry)  
XX  
DE Human cardiac adenylycyclase VI (ACVI) isoform #2 DNA.  
XX  
KW Human; cardiant; beta-adrenergic signalling protein; beta-ASP;  
KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
KW adenylycyclase; adenylate cyclase; cAMP synthetase;  
KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
KW cardiac adenylycyclase VI; ACVI isoform; beta-ASP transgene; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..3507  
FT /\*tag= a  
FT /product= "Human cardiac adenylycyclase VI isoform #2"  
FT /EC\_number= "4.6.1.1"  
XX  
PN W0200148164-A2.  
XX  
PD 05-JUL-2001.  
XX  
PF 26-DEC-2000; 2000WO-US35411.  
XX  
PR 27-DEC-1999; 99US-0472667.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Hammond HK, Gao M;  
XX  
DR WPI; 2001-418260/44.  
XX  
P-PSDB; AAE04311.

PT Novel polynucleotide encoding a modified adenylyl cyclase polypeptide  
PT useful for enhancing cardiac function in mammalian hearts, and for  
PT treating heart disease, especially congestive heart failure -  
XX

PS Claim 6; Page 134-140; 153pp; English.

XX The present invention relates to methods and compositions for enhancing  
CC cardiac function in mammalian hearts by inserting transgenes encoding  
CC beta-adrenergic signalling proteins (beta-ASP) which increase  
CC beta-adrenergic responsiveness within the myocardium using in vivo  
CC gene therapy. The beta-ASPs of the invention include beta-adrenergic  
CC receptors (beta-AR), adenylyl cyclases (also referred as adenylyl cyclase,  
CC adenylylate cyclase and cAMP synthetase) and G-protein receptor kinase  
CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
CC in mammalian hearts and for treating heart disease, especially  
CC congestive heart failure. The present DNA sequence encodes human  
CC cardiac adenylyl cyclase VI (ACVI) isoform which is used for generating  
CC a fourth beta-ASP transgene, used in the exemplification  
XX of the invention.

SQ Sequence 3552 BP; 686 A; 1037 C; 1068 G; 761 T; 0 other;

Query Match 97.3%; Score 1763.4; DB 22; Length 3552;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 1789; Conservative 0; Mismatches 21; Indels 3; Gaps 1;

QY 3 TAACTGTGTGGGCATCTGGCGCAGTCAGGTGGGGCGCTTTCGCAGCAGACCC 62  
DB TTTACGTGTGTGGGCATCTGGCGCAGTCAGGTGGGGCGCTTTCGCAGCAGACCC 695  
QY 63 GGGAGCCCCCTCTGGGGCCTCTGGTGGCCCTGTGTCTTTTATACATCGCATACACGCT 122  
DB GGGAGCCCCCTCTGGGGCCTCTGGTGGCCCTGTGTCTTTGTCTACATCGCTACACGCT 755  
QY 123 CTCTCCCATCCGATCGCGGCTGCGTCTCAGCGGCTGGCCCTCCACCTTCGATTT 182  
DB CTCTCCCATCCGATCGCGGCTGCGTCTCAGCGGCTGGGGCTCTCCACCTTCGATTT 815  
QY 183 GATCTTGGCCTGGCACTTAAACCGTGGTGATGCCCTTCTCGAAGCAGCTCGGTGCCAA 242  
DB GATCTTGGCCTGGCACTTAAACCGTGGTGATGCCCTTCTCGAAGCAGCTCGGTGCCAA 875  
QY 243 TGTGCTGCTGTCTTGACCAACGTCATATAGCATCTGCACACATATCCAGCAGAGT 302  
DB TGTGCTGCTGTCTTGACCAACGTCATATGGCATCTGCACACATATCCAGCAGAGT 935  
QY 303 GTCTCAGCCCGAGGCTTTTCAGAGACCGCAGTTACATCCAGGCGCGCTCCACCTGCA 362  
DB GTCTCAGCCCGAGGCTTTTCAGAGACCGCGGTACATCCAGGCGCGCTCCACCTGCA 995  
QY 363 GCATGAGATCGGCAGCAGGCGTGTGCTGTGGTATTTGCCCGCAGCAGTTGCCAT 422  
DB GCATGAGATCGGCAGCAGGCGTGTGCTGTGGTATTTGCCCGCAGCAGTTGCCAT 1055  
QY 423 GGAGATGAAGAGACATCAACAAAAAAGAAC----ATGTTCCACAAGATCTACAT 479  
DB GGAGATGAAGAGACATCAACAAAAAAGAACATGATGTTCCACAAGATCTACAT 1115  
QY 480 ACAGAAGCATGACAATGTGAGCATCTGTGTTGCAGACATTTAGGGCTTCACAGCCTGGC 539  
DB ACAGAAGCATGACAATGTGAGCATCTGTGTTGCAGACATTTAGGGCTTCACAGCCTGGC 1175  
QY 540 ATCCCAGTGCATGGCAGGAGCTGGTATGACCTGATGAGCTTTTGGCCGGTTTGA 599  
DB ATCCCAGTGCATGGCAGGAGCTGGTATGACCTGATGAGCTTTTGGCCGGTTTGA 1235  
QY 600 CAAGTGGCTGGGAGATCACTGCTGAGGATCAAGATCTTTGGGGAGCTGTACTAG 659  
DB CAAGTGGCTGGGAGATCACTGCTGAGGATCAAGATCTTTGGGGAGCTGTACTAG 1295  
QY 660 TGTGTGAGGCTGCGGAGGCCCGGCGACCATGCCACTCTGCTGTGGAGATGGGGT 719  
DB TGTGTGAGGCTGCGGAGGCCCGGCGACCATGCCACTCTGCTGTGTGGAGATGGGGT 1355

QY 720 AGACATGATTGAGGCCATCTCCTGCTAGTGTGAGGTGACAGGTGTGAATGTGAACATGCG 779  
DB AGACATGATTGAGGCCATCTCCTGCTAGTGTGAGGTGACAGGTGTGAATGTGAACATGCG 1415  
QY 780 COTGGGCATCCACAGCGGGCGGTGACATGCGGCGCTCTTGGCTTTCGCGAAATGGCAGTT 839  
DB COTGGGCATCCACAGCGGGCGGTGACATGCGGCGCTCTTGGCTTTCGCGAAATGGCAGTT 1475  
QY 840 CGATGTGTGGTCCCAATGATGTGACCTGGCCAAACACATGGAAGCAGGAGCGGGCTGG 899  
DB CGATGTGTGGTCCCAATGATGTGACCTGGCCAAACACATGGAAGCAGGAGCGGGCTGG 1535  
QY 900 CGCATCCACATCACTCCGGCAACACTGCAGTACCTGAACGGGAGTACGAAGTGGAGCC 959  
DB CGCATCCACATCACTCCGGCAACACTGCAGTACCTGAACGGGAGTACGAAGTGGAGCC 1595  
QY 960 AGGCGGTGTGGCAAGCGCAACGCTACCTCAAGGAGCAGCACATTTGAGACTTTCTCAT 1019  
DB AGGCGGTGTGGCAAGCGCAACGCTACCTCAAGGAGCAGCACATTTGAGACTTTCTCAT 1655  
QY 1020 CCTGGGCGCCAGCCAGAAACGGAAGAGAGAAAGGCATGCTGGCCAGCTCGCGGAC 1079  
DB CCTGGGCGCCAGCCAGAAACGGAAGAGAGAAAGGCATGCTGGCCAGCTCGCGGAC 1715  
QY 1080 TCGGGCCAACTCCATGGAAGGGCTGATGCGCGATGGGTTCCTGATCGTGCCTTCTCCG 1139  
DB TCGGGCCAACTCCATGGAAGGGCTGATGCGCGATGGGTTCCTGATCGTGCCTTCTCCG 1775  
QY 1140 GACCAAGGACTCCAAAGGCTTCCGCCAGATGGGCATTTGATGATTCAGCAAGAACACCG 1199  
DB GACCAAGGACTCCAAAGGCTTCCGCCAGATGGGCATTTGATGATTCAGCAAGAACACCG 1835  
QY 1200 GGGCCACCAAGATGCCCTGAACCTCAGGATGAGTGGATGATTCCTGAGCCGTGCCAT 1259  
DB GGGCCACCAAGATGCCCTGAACCTCAGGATGAGTGGATGATTCCTGAGCCGTGCCAT 1895  
QY 1260 CGATCCCGCAGCATTTGATCAGCTCGGAAGGACCATGTGCGCCGGTTTTCTCTCACCTT 1319  
DB CGATCCCGCAGCATTTGATCAGCTCGGAAGGACCATGTGCGCCGGTTTTCTCTCACCTT 1955  
QY 1320 CCAGAGAGAGGATTTGAGAAGAACTACTCCCGGAAGTGGATCCCGGTCGGAGCCTA 1379  
DB CCAGAGAGAGGATTTGAGAAGAACTACTCCCGGAAGTGGATCCCGGTCGGAGCCTA 2015  
QY 1380 CTTTCCTGTCGCTGTTGGTCTTCTGCTTCATCTGCTTATCCAGCTTCTAATTTTCC 1439  
DB CTTTCCTGTCGCTGTTGGTCTTCTGCTTCATCTGCTTATCCAGCTTCTAATTTTCC 2075  
QY 1440 ACACCTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTAATCACCGT 1499  
DB ACACCTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTAATCACCGT 2135  
QY 1500 GCTGATCTGCTGCTGATCTCTGTTGGTCTCTGTTCCCTAAGGCGCTGCAACGCTGTC 1559  
DB GCTGATCTGCTGCTGATCTCTGTTGGTCTCTGTTCCCTAAGGCGCTGCAACGCTGTC 2195  
QY 1560 CCGCAGCATTTGCTCCCTCACGGGCACATAGCACCCAGTTGGCATCTTTTCCGCTCTGCT 1619  
DB CCGCAGCATTTGCTCCCTCACGGGCACATAGCACCCAGTTGGCATCTTTTCCGCTCTGCT 2255  
QY 1620 TGTGTTTACTTCTGCCATTGCCAATGTTTACCTGTAAACACACCCCCATACGAGCTG 1679  
DB TGTGTTTACTTCTGCCATTGCCAATGTTTACCTGTAAACACACCCCCATACGAGCTG 2315  
QY 1680 TGCACCCCGGATGCTGAATTTAAACCTGCTGACATCACTGCTGCCACCTGCACGAGT 1739  
DB TGCACCCCGGATGCTGAATTTAAACCTGCTGACATCACTGCTGCCACCTGCACGAGT 2375  
QY 1740 CAATTTACTCTCTGGGCTGGATGCTCCCTGTGTGAGGGCACCATGCCACCTGAGCTT 1799  
DB CAATTTACTCTCTGGGCTGGATGCTCCCTGTGTGAGGGCACCATGCCACCTGAGCTT 2435





Db 1077 GGAGATGAAAGAGACATCAACACAAAAAAGAGACATGATGTTCCACAAGATCTACAT 1136  
QY 480 ACAGAGCATGACAATGTACGATCCTGTTTGCAGACATTTGAGGGCTTCACGAGCCTGGC 539  
Db 1137 ACAGAGCATGACAATGTACGATCCTGTTTGCAGACATTTGAGGGCTTCACGAGCCTGGC 1196  
QY 540 ATCCAGTGCACATGCGCAGAGCTGGTCAATGACCTGAATGAGTCTTTCCCGGTTGA 599  
Db 1197 ATCCAGTGCACATGCGCAGAGCTGGTCAATGACCTGAATGAGTCTTTCCCGGTTGA 1256  
QY 600 CAAGCTGGCTGCGGAGAAATCACTGCTGAGGATCAAGATCTTGGGGAGCTTTACTACTG 659  
Db 1257 CAAGCTGGCTGCGGAGAAATCACTGCTGAGGATCAAGATCTTAGGAGAGCTTTACTACTG 1316  
QY 560 TGTGTAGGGCTGCGGAGAGCCCGGCGGACCATGCCACTGCTGTGTGAGATGGGGT 719  
Db 1317 CGTGTAGGGCTGCGGAGAGCCCGGCGGACCATGCCACTGCTGTGTGAGATGGGGT 1376  
QY 720 AGACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATGCG 779  
Db 1377 AGACATGATCGAGCCATCTCGCTGGTGGTGGTGAAGTGAACAGTGTGAACGTGAACATGCG 1436  
QY 780 CGTGGGATCCACAGCGGGCGGTGACCTGCGCGCTCTTGGCTTGGGAAATGGCAGTT 839  
Db 1437 TGTGGGATCCACAGCGGAGCTGTGATTCGGCGCTCTTGGCTTACGGAATGGCAGTT 1496  
QY 840 CGATGTGTGTTCAATGATGTACCTGACCTGACCTGAACGGGACTACGAAGTGGAGCC 959  
Db 1497 TGATGTCTGTCAAAAGATGTACCTGACCTGACCTGAACGGGACTATGAGTGGAGCC 1613  
QY 960 AGCCGCTGGTGGCAAGCGCAACGCTACCTCAAGGAGCAGCATTTGAGACTTTCTCAT 1019  
Db 1614 AGCCGCTGGTGGTGAACCAATGCTACCTCAAGGAGCAGTGTGAGACTTTCTCAT 1673  
QY 1020 CTTGGGCGCCAGCAAGAAAGAGAGAGAAAGGATGCTGCGCAAGCTTCAGCGGAC 1079  
Db 1674 ACTTGGCGCCAGCAAGAAAGAGAGAGAAAGGATGCTGCGCAAGCTTCAGCGGAC 1733  
QY 1080 TCGGGCAACTCCATGGAAGGGTGTATGCGCGATGGTTCCTGATGCTGCTTCTCCCG 1139  
Db 1734 ACGGGCAACTCCATGGAAGGGTGTATGCGCGATGGTTCCTGATGCTGCTTCTCCCG 1793  
QY 1140 GACCAAGGACTCAAGGCTTCGCGCAGATGGGATTTGATGATTCAGCAAGAACACCG 1199  
Db 1794 GACCAAGGACTCAAGGCTTCGCGCAGATGGGATTTGATGATTCAGCAAGAACACCG 1853  
QY 1200 GGGCACCAGATGCCCTGAACCTGAGGATGAGGTGGATGCTGAGCGGTGCCAT 1259  
Db 1854 GGTGCGCAAGATGCTGGAACCTGGAATGAGGTGGATGCTGAGCGGTGCCAT 1913  
QY 1260 CGATGCCCGCAGCATTTGATGAGTGGGAGGACCATGTGCGCGGTTTTTGTCTACCTT 1319  
Db 1914 CGATGCCCGCAGCATTTGATGAGTGGGAGGACCATGTGCGCGGTTTTTGTCTACCTT 1973  
QY 1320 CCAGAGAGAGATTTTGAAGAGTACTCCCGAAGGTGGATCCCGCTTCGAGGCTA 1379  
Db 1974 CCAGAGAGAGATTTTGAAGAGTACTCCCGAAGGTGGATCCCGCTTCGAGGCTA 2033  
QY 1380 CGTTGCTGTGCCCTGTGCTTCTGCTTCATGCTGCTCATCCAGCTTCTAATTTTCCC 1439  
Db 2034 CGTTGCTGTGCCCTGTGCTTCTGCTTCATGCTGCTTCATCCAGCTTCTCACTTCCC 2093  
QY 1440 AACTCCACCTGATGCTTGGGATTTATGCGAGCATCTTCTGCTGCTGCTAATCAACCGT 1499  
Db 2094 AACTCCACCTGATGCTTGGGATTTATGCGAGCATCTTCTGCTGCTGCTAATCAACCGT 2153  
QY 1500 GCTGATCTGTGCTGTACTCTGCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 1559  
Db 2154 GCTGATCTGTGCTGTACTCTGCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 2213

QY 1560 CCAGCAGATTGTCGGCTACGGGCACATAGCACGAGTTGGCATCTTTTCCGTCCTGCT 1619  
Db 2214 CCAGCAGATTGTCGGCTACGGGCACATAGCACGAGTTGGCATCTTTTCCGTCCTGCT 2273  
QY 1620 TGTGTTTACTTCTGCCATTGCCAACATGTTACCTGTAAACACACACCCCATAGGAGCTG 1679  
Db 2274 TGTGTTTACTTCTGCCATTGCCAACATGTTACCTGTAAACACACACCCCATAGGAGCTG 2333  
QY 1680 TGAGCCCGGATGCTGAATTTAACACCTGCTGACATCAGCTGCGCCACCTGCAGAGCT 1739  
Db 2334 TGAGCCCGGATGCTGAATTTAACACCTGCTGACATCAGCTGCGCCACCTGCAGAGCT 2393  
QY 1740 CAATTAATCTCTGGCCTGATGCTCCCTGTGTGAGGCGACCATGCCACCTGCAGCTT 1799  
Db 2394 CAATTAATCTCTGGCCTGATGCTCCCTGTGTGAGGCGACCATGCCACCTGCAGCTT 2453  
QY 1800 TCCTGAGGTGTTT 1812  
Db 2454 TCCTGAGTACTTC 2466

RESULT 7  
AAQ42525  
ID AAQ42525 standard; DNA; 4046 BP.  
XX  
AC AAQ42525;  
XX  
DT 14-SEP-1993 (first entry)  
XX  
DE Cardiac adenylyl cyclase gene.  
XX  
KW Regulation; cardiac function; heart; heart failure; ss.  
XX  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
FT CDS 131..3627  
FT /\*tag= a  
XX  
PN EP543137-A.  
XX  
PD 26-MAY-1993.  
XX  
PF 12-OCT-1992; 92BP-0117374.  
XX  
PR 18-NOV-1991; 910S-0793961.  
XX  
PA (AMCY ) AMERICAN CYANAMID CO.  
XX  
PI Ishikawa Y;  
XX  
WPI; 1993-168873/21.  
DR P-PSDB; AAR37309.  
XX  
PT Purified DNA encoding cardiac adenylyl cyclase - useful to screen  
for cpds. which stimulate activity of the cyclase  
XX  
PS Claim 1; Fig 2; 34pp; English.  
XX  
CC A canine heart cDNA library was constructed in lambda gt10 and was  
screened with a 970 bp AatI-HincII fragment from type I adenylyl  
cyclase cDNA probe (encodes the first cytoplasmic domain of adenylyl  
cyclase, which has significant homology to other previously known  
types of adenylyl cyclase). One positive clone, of 5.4 kb was obd.  
CC  
CC Positive colonies were subcloned into pUC18 and further subcloned  
and sequenced bidirectionally. The 5.4 kb clone was used to  
CC  
CC rescreen the library and on overlapping clone contg. the 5' end of  
the gene was isolated. Together the two clones cover the complete  
canine cardiac adenylyl cyclase gene. The gene is suspected of  
CC  
CC being involved in the regulation of cardiac function and it is thought  
that decreased activity of adenylyl cyclase in the heart may be a  
CC  
CC major factor in the development of heart failure. Thus the adenylyl



AM CYCLIC AMP; adenosine monophosphate; screening; stimulation;

KW	ADP
KW	CVC

KW	ADP
KW	CVC





Db 2067 TCGCCTGTGCCCTCTCGTGTCTTCTGCTTCATCTGTTTCATCCAGTTCTCTCGTATTCAC 2126  
Qy 1442 ACTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTTAATCACCCTGC 1501  
Db 2127 ACTCCGCTGATCTCGGGATTTATGCCGGGATCTTCTTTGCTGCTGGTCAACCGTGC 2186  
Qy 1502 TGATCTGTCTGTACTCTGCTGTGCTTCTGCTTCCCTAAGGCCCTGCAACCTCTGTCTCC 1561  
Db 2187 TCATCTGTCTGTGCTCTCTGCTGCTTCTTCTTCCCAACGCCCTGCAAGCCCTGTCC 2246  
Qy 1562 GGAGCATTCGCTGACATGCGGACATAGACCCGACGTGAGTGGCATCTTTCCGCTCTGCTG 1621  
Db 2247 GCAGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2306  
Qy 1622 TGTCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1681  
Db 2307 TGTCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2366  
Qy 1682 CAGCCCGGATGCTGAATTTAACAACCTGCTGACATCACTGCTGCTGCTGCTGCTGCTGCTG 1741  
Db 2367 CGGCCGGATGCTGAATTTAACAACCTGCTGACATCACTGCTGCTGCTGCTGCTGCTGCTG 2426  
Qy 1742 ATTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1801  
Db 2427 ATTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2486  
Qy 1802 CTGAGGTGTT 1811  
Db 2487 CTGAGTACTT 2496

RESULT 9  
ID ABI99680 standard; cDNA; 5841 BP.  
XX  
AC ABI99680;  
XX  
DT 07-MAR-2002 (first entry)  
XX  
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:716.  
XX  
KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;  
KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.  
XX  
OS Mus musculus.  
XX  
PN WO200188188-A2.  
XX  
PD 22-NOV-2001.  
XX  
PF 18-MAY-2001; 2001WO-JP04192.  
XX  
PR 18-MAY-2000; 2000JP-0145977.  
XX  
PA (UYUNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
XX  
PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;  
XX  
DR WPI; 2002-034733/04.  
DR P-FSDB; ABB57257.  
XX  
PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring  
PT expression levels of particular genes defined in the specification or  
PT by determining the expression profile of a gene group comprising these  
PT genes -  
XX  
PS Claim 2; Page 1771-1780; 2690pp; English.  
XX  
CC The present invention describes a method for examining ischaemic  
CC conditions, comprising measuring the expression levels of particular  
CC genes (I) in a test sample or determining the expression profile of a  
CC gene group in the sample comprising genes selected from (I). The method

CC is useful for examining the ischaemic condition (e.g. compressive  
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring  
CC expression levels of particular genes (ABI99202 to ABI99912, encoding  
CC the protein sequences in ABB57020 to ABB57374) or by determining the  
CC expression profile of a gene group comprising these genes. The  
CC expression levels or expression profiles produced by these genes are  
CC used as an indicator when screening for ischaemic condition-improving  
CC drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914  
CC represent PCR primers for a mouse ischaemic condition related sequence,  
CC which are used in the exemplification of the present invention.  
XX  
SQ Sequence 5841 BP; 1214 A; 1558 C; 1673 G; 1396 T; 0 other;  
Query Match 79.0%; Score 1431.8; DB 24; Length 5841;  
Best Local Similarity 87.7%; Pred No. 0;  
Matches 1588; Conservative 0; Mismatches 217; Indels 6; Gaps 2;  
Qy 5 AGCTGTGCTGGGCATCTCTGCGGCGAGTGCAGGTGCGGGCGCTTTTCGCGAGACCCCGC 64  
Db 727 ATGTGCTCTGGGCATCTCTAGCAGCGGTGCAAGTGGGGGTGCCCTGGCGCAATCCAC 786  
Qy 65 GCAGCCCTCTCGGGCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 124  
Db 787 ACAGCCCTCTCGGGCCTCTTGGTGGCCGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 846  
Qy 125 TCCCATCGCATGCGGCTGCGCTCCTCAGCGGCTGCGGCTCCTCCACCTTGCATTTGA 184  
Db 847 TTCCCATTCGCGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 906  
Qy 185 TCTTGCCCTGCGCACTTAACCGTGTGATGCTTCTCTGGAAGCAGCTGCGGTGCCAATG 244  
Db 907 TTTTGCCCTGCGAGCTCAACAGCAGCGGCCCTCTCTTTGGAAGCAGCTGCGGTGCTAAGC 966  
Qy 245 TGCTGCTGCTCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 304  
Db 967 TGGTCTCTCTCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1026  
Qy 305 CTCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 364  
Db 1027 CTCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1086  
Qy 365 ATGAGAAATCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 424  
Db 1087 ATGAGAAATCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1146  
Qy 425 AGATGAAGAGACATCAACACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 481  
Db 1147 AGATGAAGAGAGACATCAACACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1206  
Qy 482 AGAAGCATGACAATGTCAGCATCTCTGTTTGCAGACATGAGGGGCTTCACGACGCTGGCAT 541  
Db 1207 AGAAGCATGACAATGTCAGCATCTCTGTTTGCAGACATGAGGGGCTTCACGACGCTGGCAT 1266  
Qy 542 CCCAGTGCAGTCCGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601  
Db 1267 CCCAGTGCAGTCCGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1326  
Qy 602 AGCTGGCTGCGGAGAGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 661  
Db 1327 AGCTGGCTGCGGAGAGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1386  
Qy 662 TGTGAGGCTGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 721  
Db 1387 TGTGAGGCTGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1446  
Qy 722 ACATGATTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 781  
Db 1447 ACATGATTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1506  
Qy 782 TGGGCGATCCACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 841  
Db 1507 TGGGCGATCCACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1566

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QY 842 ATGTGTGGTCCAATGATGTGACCCCTGGCCCAACACATGSAAGCAGGAGAGCGGCGCTGGCC 901
Db 1567 ATGTCTGGTCAAAAGATGTGACCCCTGGCTTAACACATGGAGGCGGGGGC---GGCCGGC 1623
QY 902 GCATCCACATCACTCGGGGCAACACTGCAGTACCTGAACGCGGGACTAGGAAGTGGAGCCAG 961
Db 1624 GCATCCACATCACTCGGGGCTACACTGCAGTACTTGAACGCGGGACTATGAGTGGAGCCAG 1683
QY 962 GCCGTGTGGCAAGCGGCAACCGGTACCTCAAGGAGCAGCACATTCAGACTTTCCTCATCC 1021
Db 1684 GCCGTGTGTGACGCAATGCGTACCTCAAGGAGCAGTGCATTCAGACCTTCTCTATAC 1743
QY 1022 TGGCGCCAGCCAGAAACGAAAGAGAGAGAGAGCATGCTGGCCAACTGCAGCGGACTC 1081
Db 1744 TTGGCGCAGCCAAACGAAAGAGAGAGAGAGCATGCTGGCCAACTGCAGCGGAGAC 1803
QY 1082 GGGCAACTCCATGGAAGGCGCTGATGCCGATGGGTTCCTGATCGCTTCTCCCGGA 1141
Db 1804 GGGCAACTCCATGGAAGGAGTATGCCCCGCTGGGTTCCTGACCGTCCCTTCTCCCGGA 1863
QY 1142 CCAGGACTCCAGGCGCTTCCGCCAGATGGGCATTCGATGATTCAGCAAAAGACAACCGGG 1201
Db 1864 CCAGGACTCTAAGGCATTCGCCAGATGGGCATTCGATGATTCAGCAAAAGACAACCGGG 1923
QY 1202 GCACCCAAAGATGCCCTGAACCCCTGAGGATGAGGTGGATGATTCCTGAGCGGTGCCATCG 1261
Db 1924 GTGCCAAAGATGCTCTGAACCCCTGAAGATGAGGTGGATGATTCCTGGCGGAGCCATCG 1983
QY 1262 ATGCCCCAGCATGATGACCTGCGGAGGAGACCATGTCGCCCGTTCCTGCTACCTTCC 1321
Db 1984 ATGCCCCAGCATGAGCAACTGCGTAAAGACCATGTCGCCCGTTCCTGCTACCTTCC 2043
QY 1322 AGAGAGAGGATTTTGAGAAGAAGTACTCCCGAAGTGGATCCCGCTTCGGAGCCCTACG 1381
Db 2044 AGAGAGAGATCTTGAGAAGAAGTATTCAGGAAAGTAGATCTCGTTCGGAGCCCTACG 2103
QY 1382 TTGCCTGTGCCCTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTCCAC 1441
Db 2104 TCGCCTGTGCCCTCTCGTCTTCTGCTTCATCTGCTTCATCCAGCTCCTTGTGTCCAT 2163
QY 1442 ACTCCACCCGTATGCTTGGGATTTATCCAGCATCTTCTGCTGCTGCTGCTAATCACCGTGC 1501
Db 2164 ACTCCACCCGTATGCTGCGGATTTATCCGCTATCTTCTGCTGCTGCTGCTGCTGCTGCTG 2223
QY 1502 TGATCTGTGCTGTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1561
Db 2224 TGATCTGTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2283
QY 1562 GCAGCATTTGCGGCTACGGGCAACATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCTTG 1621
Db 2284 GCAATATTGTCGGCTACGGGTGCACAGCACCGCGGTGGAAATCTTCTCGGTTCTGCTTG 2343
QY 1622 TGTTTACTTCTGCCATTTGCCAATGTTTCACTGTATACCCACACCCCATACGGAGCTGTG 1681
Db 2344 TGTTCATCTGTGCATCGCAACATGTTTACCTGTATATCATACCCCAATAAGGACCTGCG 2403
QY 1682 CAGCCCGGATGCTGAATTTAACAACCTGCTGCATCACTGCTGCTGCTGCTGCTGCTGCTGCTG 1741
Db 2404 CGGCCCGGATGCTGAATTTAACAACCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2463
QY 1742 ATTACTCTGTGGGCTGGATGCTCCCTGTGTGAGGAGCACCATTGCCACCTGCAGCTTTC 1801
Db 2464 ATTACTCTGTGGACTGGATGCTCCCTGTGTGAGGAGCACCACCCACCTGCAGCTTTC 2523
QY 1802 CTGAGGTGTTTC 1812
Db 2524 CTGAGTACTTC 2534
```

RESULT 10  
AA00462  
ID AAX00462 standard; DNA; 4523 BP.  
XX

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AC AAX00462; AC
XX 25-MAY-1999 (first entry) DT
XX Human type V adenylyl cyclase coding sequence. DE
XX Type V adenylyl cyclase; human; hac5; heart disease; brain; therapy; diagnosis; ds. KW
XX Homo sapiens. OS
XX WO9901546-A1. PN
XX 14-JAN-1999. PD
XX 01-JUL-1998; 98WO-US13540. PF
XX 01-JUL-1997; 97US-0886362. PR
XX 01-JUL-1997; 97US-0070901. PR
XX (CORT-) COR THERAPEUTICS INC. PA
XX Tomlinson JA; PI
XX WPI; 1999-106048/09. DR
XX P-PSDB; AAW30600. DR
XX Newly isolated and purified human type V adenylyl cyclase (hac5) polypeptide - useful for identifying potential therapeutic agents that modulate hac5 activity, and for the diagnosis of hac5-associated diseases and disorders XX
XX Claim 3; Fig 1a-h; 40pp; English. PS
XX This sequence encodes the human type V adenylyl cyclase (hac5) of the invention. hac5 has a similar putative structure to other adenylyl cyclase isoforms but, like type VI, is distinguishable in that it has a larger N-terminus and a relatively shorter C-terminus as it lacks the C2b region. The hac5 polypeptides are useful in assays that screen for potential therapeutic agents, which modulate hac5 activity. These polypeptides are also useful in assays for the diagnosis of diseases and disorders. Agonists of hac5 are useful control agents in such assays, and they may have useful effects in vivo for treating disease. Antibodies acting as (ant)agonists have diagnostic and therapeutic effects, and are useful in immunoassays for hac5. (Ant)agonists are particularly useful in treating diseases caused by abnormal hac5 activity (e.g. in the heart and brain), and in diseases, which are alleviated by modulating hac5 activity. The oligonucleotides are useful in methods that inhibit or regulate hac5 expression in vivo and in vitro. The cloning of the human isoform of AC5 enables the development of tissue-specific and selective pharmacological agents for use in treating particular human diseases CC associated with hac5. CC
XX SQ Sequence 4523 BP; 840 A; 1419 C; 1428 G; 836 T; 0 other;
Query Match 49.4%; Score 895; DB 20; Length 4523;
Best Local Similarity 69.8%; Pred. No. 5.7e-229;
Matches 1277; Conservative 0; Mismatches 525; Indels 27; Gaps 4;
QY 5 ACGTGTGTCTGGGCGATCCTTGGCGGCGAGTGCAGGTTCGGGGGCGCTTTCGACGACAGACCGCG 64
Db 1046 ATGGCGTCATCGCGTGGTGTGCTGGCGCTCCAGGTGTGGGCGCTGCTGCGCGAGCCAC 1105
QY 65 GCAGCCCTCTGGGGCTCTGGTGGCCCTGTGTTCTTTGTATACATGCATGACGAGTCC 124
Db 1106 GCAGCGCTCTGAGGCGATCTGTTGGACCGTGTCTTCTATCTATACCATCTACACGCTGC 1165
QY 125 TCCCATCCGATCGGGCTGCGTCTCAGCGGCTGGGCGCTCTCCACCTTGATTTGA 184
Db 1166 TGCCCGTGGCATCGCGGCGCGAGTGTCTCAGCGGGGTGCTCTGTCGCCCTCCACCTGG 1225
QY 185 TCTTGGCTGGCAACTTAACCGTGGTGTGATGCCTTCTCTGGAAGCAGCTCGGTGCCAATG 244
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Db 1226 CCATGCCCTTCCACCAACAGCCAGACCAAGTTCCTGCTGAAGAGCTTGTGTCACATG 1285  
QY 245 TGTGCTGTTCCTCTCTCACCACACGCTCATAGCATCTGCACACACTATCCAGCAGAGGTGT 304  
Db 1286 TTCTCATTTCTCTCGACCAACATCGTGGGTCTCTGCACCCACTATCCGGCTGAGGTCT 1345  
QY 305 CTCAGCGCCAGGCTTTTCAGGAGACCCGAGTTACATCCAGGCCCGGCTCCACCTCGAC 364  
Db 1346 CCAGAGACAGGCTTTCCAGGAGACCCGAGAGTGATCCAGGCGGGCTCCACTCGCAGC 1405  
QY 365 ATGAGAAATCGGACGAGGAGCGGCTGCTGCTGCTGGTATTTGCCAGCAGGTTGCCATGG 424  
Db 1406 GGGAGAACAGCAGCAGGAGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1465  
QY 425 AGATGAAGAAGACATCAACACAAAAAAGA ---CATGTTCCACAAGATCTACATAC 481  
Db 1466 AGATGAAGCAGACATCAACGCCAAGCAGGAGGATGATGTTCCATAAGATTTACATCC 1525  
QY 482 AGAAGCATGACAAATGTACGATCCTGTTTGCAGACATTCAGGGCTTTCACCGCTGGCAT 541  
Db 1526 AGAAACATGACAACTGAGCATCCTGTTTGTGCTGACATCGAGGCTTCACGAGCCTGGCGT 1585  
QY 542 CCAGTGTCACTGGCAGGAGCTGCTCATGACCTGATGAGCTCTTTGCCCGGTTTGACA 601  
Db 1586 CCAGTGTCACTGGCAGGAGCTGCTCATGACCTCAACGAGCTCTTCGCCCGCTTTGACA 1645  
QY 602 AGTGTGCTGCGGAGATCACTGCTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTG 661  
Db 1646 AGTGTGCGGCAGAGATCACTGTTTACGTATTAAAGATCTTGGGGATGTTATTACTGG 1705  
QY 662 TGTGAGGCTGCGGAGGAGCGGCGGACCATGCCACTGCTGCTGTGTGGAGATGGGGGTAG 721  
Db 1706 TCTCGGGGTGCTGAAAGCAAGGGGTGACCAAGCCCACTGCTGTGTGGAGATGGGCATGG 1765  
QY 722 ACATGATTCAGGCACTCTCGCTGAGTGAGTGAGTGACAGGTGTAATGTGAACATCGCG 781  
Db 1766 ACATGATCAGGCCATCTCGTTGGTCCGGAGGTGACAGGGTGAACGTGAACATCGCGT 1825  
QY 782 TGGGATCCACAGCGGCGGCTGCACTGCGGCTGCTTGGCTTGGGAAATGCGAGTTGCG 841  
Db 1826 TGGGAATTCACAGCGGCGGCTGCACTGCGGCTGCTTGGCTGCTGAGAGTGGCAGTTGCG 1885  
QY 842 ATGTGTGTTCATGATGTGACCTTGGCCCAACACACATGGAAGCAAGCCGGCTGGCC 901  
Db 1886 AGTCTGGTCTAACGATGTACGCTAGCCAGCCACACATGAGGCTGGCGCAAGGCGAGAC 1945  
QY 902 GCATCCACATCACTCGGCAACACTGCACTGTAACGCGGACTACGAGGTGAGGCCAG 961  
Db 1946 GCATCCACATCACCAGGCTACACTCACTGTAATGGGACTACGAGGTGGAGCCAG 2005  
QY 962 GCGGTGGTGGCAAGCGCAACGCTACCTCAAGGAGCAGACATTCAGACTTTCTCTCATCC 1021  
Db 2006 GCTGTGGGGCGAGCGCAACGCTACCTCAAGGAGCAGATATCGAGACTTTCTCTCATCC 2065  
QY 1022 TGGGCGCCAGCAGAAACGGAAGGAGAAAGGATGCTGCCAAGCTGCGAGCGGACTC 1081  
Db 2066 TGGCTGTGACCCAGAAAGCGGAAGAGAGGCGCATGATCGCCAAAGATGAACCCGCGA 2125  
QY 1082 GGGCCAACTCCATGAAAGGCTGATGCGCGGATGGTTCTCGATCGCTGCTTCTCC --- 1137  
Db 2126 GAACCAACTCCATCGGCAACACCCACACACTGCGGGGCTGAGCGCCCTCTCTACACC 2185  
QY 1138 -----CGGACCAAGGACTCCAAGGCTTCCGCCAGATGGGCATTCATGATTCACGA 1189  
Db 2186 ACCTGGTGGCAACACAGGTGTCCAAGGATGAAGCGGATGGCTTTGAAGACCCCA --- 2242  
QY 1190 AAGACAACCGGGCACCACCAAGATGCCCTGAACCTTCAGGATGAGTGGATGTTCTTGA 1249  
Db 2243 ---AGACAAGAACGCCAGGAGATGCGCAACCCCTGAGGATGAAGTGGATGATGTTCTGG 2299  
QY 1250 GCGGTGCCATGATCGCCGACAGATTGATGATGATGATGATGATGATGATGATGATGATG 1309  
Db 2300 GCGGTGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2359

QY 1310 TGTCACTTCCAGAGAGGATTTTGAAGAAGTACTCCCGAAGGTGGATGCCCGCT 1369  
Db 2360 TCTGACCTTCAGGAGCCTGACTTAGAAGAAGAGTACTCCAGCAGGTAGAGACCGAT 2419  
QY 1370 TCGGAGCCTACGTTGCTGCCCCCTGTTGGTCTTCTGCTCAATCTCTCATCCAGCTTC 1429  
Db 2420 TTGGTGCCTATGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2479  
QY 1430 TAATTTTCCACATCCACCCCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGC 1489  
Db 2480 CCATGCTGCCACCTCCATATTATCATGCTCAGCTTTCACCTGACCTTCCCTGCTGCTGA 2539  
QY 1490 TAATCACTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1549  
Db 2540 CCTTGGTGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2599  
QY 1550 AACGCTGTCCCGCAGCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1609  
Db 2600 AGACCTCTCCAGGAAGATCGTGGGTCCAAAGATGAACAGACCCCTGCTGCTGCTGCTGCTG 2659  
QY 1610 CCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1669  
Db 2660 CCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2719  
QY 1670 TACGAGCTGTGCAGCCCGGATGCTGAATTTAAACACTGCTGACATCACTGCTGCTGCTGCTG 1729  
Db 2720 TGTGGCTGCTTGGCAGAGGACACACATCAGCGCAGCCAGGTCACAGCGTGTACG 2779  
QY 1730 TGCAGAG-----CTCAATTAATCTCTGCGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 1783  
Db 2780 TGGCGAGTTCGCGGCTCAACTACAGCTGGCGATGAGCAGGGCTTCTGCTGCGAGCCCT 2839  
QY 1784 TGCCACCTGCACTTCTGCTGAGGTGCT 1812  
Db 2840 GGCCCACTGCACTTCCCGAGTACTTC 2868

## RESULT 11

AAQ95540

ID AAQ95540 standard; DNA; 4356 BP.

XX AAQ95540;

XX AC

XX 31-JAN-1996 (first entry)

XX DT

XX Cardiac adenyllyl cyclase gene.

XX DE

XX Cardiac adenyllyl cyclase; effector enzyme; ss.

XX KW

XX Homo sapiens.

XX OS

XX Key Location/Qualifiers

XX FH

XX CDS 148..3702

XX FT

XX /\*tag= a

XX XX

XX TW243453-A.

XX XX

XX 21-MAR-1995.

XX XX

XX 02-JUL-1992; 92TW-0105242.

XX PF

XX 12-JUN-1992; 92US-0899068.

XX PR

XX (AMCY ) AMERICAN CYANAMID CO.

XX PA

XX WPI; 1995-214006/28.

XX DR

XX P-PSDB; NAR78519.

XX XX

XX Cardiac adenyllyl cyclase and corresp. DNA - having specified

XX PT

XX sequences

XX PS

PS Claim 1; Fig 2; 45pp; Chinese.

xx AAQ9540 encodes AAR78519, the novel effector enzyme cardiac adenylyl  
CC cyclase.  
xx  
SQ Sequence 4356 BP; 836 A; 1372 C; 1373 G; 775 T; 0 other;  
  
Query Match 48.88; Score 884.6; DB 16; Length 4356;  
Best Local Similarity 69.1%; Pred. No. 3.4e-226;  
Matches 1259; Conservative 0; Mismatches 549; Indels 15; Gaps 3;  
  
QY 5 ACGTGGTCTGGGCATCCTGGCGCAGTCGAGTCGGGGGGCTTTTCGACGACACCCGC 64  
DB 821 ACGGCTCATCGCGTGGTCTGGCGCTGAGGTGGGGCTGCTCTCCCCAGCGC 880  
  
QY 65 GCAGCCCTCTGGGGCTCTGGTGCCTGTGTTCTTATACATCGCATACGCTCC 124  
DB 881 GCAGCGCTCGAGGGCATCTGGTGACCGTGTCTTCATCTACACCATCTACAGGTGC 940  
  
QY 125 TCCCATCCGATCGCGGCTGCGGTCTCTCAGCGCCCTGGGCCCTTCCACCTTGCATTGA 184  
DB 941 TGCCTGTGCGATCGGGCGCGGTCTCTCAGCGAGTGTCTCTGCGGCCCTGCACCTGG 1000  
  
QY 185 TCTGGCTGGCACTTAACGGTGGTATGCTTCTCTGAGGACGCTCGGTGCCAATG 244  
DB 1001 CCATGCGCTCTGGCGCCCAAGCCGAGACCGGTTCCTGCTCAAGCAGCTGCTCTCCAATG 1060  
  
QY 245 TGCTGTCTTCTCTGCACCAACGTCAATTAGCATCTGCACACACTATCCAGCAGAGTGT 304  
DB 1061 TCCTCATTTTCTCTGCACCAACATGCTGGGTGCTGTACCCACTACCCGGCTGACGTCT 1120  
  
QY 305 CTCAGCCCGAGGCTTTTCAGGACCGCGAGTTACATCCAGGCGCGCTCCACCTGCAGC 364  
DB 1121 CCCAGACACAGGCTTCCAAGAGACCGGGAGTGCATCCAGGACGSGCTCCACTCGCAAC 1180  
  
QY 365 ATGAGAAATCGCAGCAGGCGGTGCTGTCTGCGGTATTTGCCACGACGTTGCCATGG 424  
DB 1181 GGGAGAACCAACAGACAGAGCGGCTCTGCTGTCTGCTCTGCCCGCAGGTTGCCATGG 1240  
  
QY 425 AGATGAAGAGACATCAACACAAAAAAGAAGA--CATGTTCCACAAGATCTACATAC 481  
DB 1241 AGATGAAGCAGACATCAATGCCAAGCAGGAGGATATGATTTCCATAAGATTTACATCC 1300  
  
QY 482 AGAAGATGACAATGTACAGATCCTGTTTCAGACACATGAGGGCTTCACCAAGCTTGGCAT 541  
DB 1301 AGAAACATGACAAGTGAAGATCCTGTTTCTGACATCGAGGGCTTCACCAAGCTTGGCAT 1360  
  
QY 542 CCAGTGCATCTGGCAGGAGCTGGTCAATGACCTGATGAGCTCTTTGCCCGGTTTGACA 601  
DB 1361 CCCAGTGCATGCCAGGAGCTGGTCAATGACGCTCAATGAGCTCTTGCGCCGCTTCGACA 1420  
  
QY 602 AGCTGGCTGGGAGAAATCACTGCTGAGGATCAAGATCTTTGGGGAGCTGTACTACTGTG 661  
DB 1421 AGCTGGCTGGGAGAAATCACTGTTAGGTATTAAGATCTTGGGGAGTGTATTACTGTG 1480  
  
QY 662 TGTACGGCTGCCGGAGGCGCGGACCATGCCACTGCTGTGTGGAGATGGGGTAG 721  
DB 1481 TCTCTGGGCTGCCGTAAGCAGGCGCGACCAACGCCACTGCTGCTGGTGGAGATGGGCATGG 1540  
  
QY 722 ACATGATTGAGGCCATCTCCCTGGTAGCTGAGTGCAGGTGCAATGTGAATGGCGG 781  
DB 1541 ACATGATTGAGGCCATCTCCCTGGTAGGAGTGCAGGGGTGAACGTTGAACATGGCGG 1600  
  
QY 782 TGGGCATCCACAGCGGGCGGTGCATCTGCGCGCTCTTGGCTTGGGAAATGGCAGTTCG 841  
DB 1601 TGGGAATTCACAGCGGGCAGTACATGCGGTGTCTTGTCTCAGGAAGTGGCAGTTCG 1660  
  
QY 842 ATGTGTGTTCCATGATGTGACCTTGCCCAACCACTGGAAGCAGGAAGCGGGCTGGCC 901  
DB 1661 ACCTCTGGTCTAATGACGTCACTGCGCCCAACCATATGGAAGCTGGAGGCAAGGCTGGGC 1720  
  
QY 902 GCATCCACATCACTCGGGCAACACTGCAGTACCTGACGGGGACTACGAAGTGGAGCCAG 961  
DB 1721 GCATCCACATCAACAAAGGCCACACTCAGCTACCTGAACGGTGTACTAGAGTGGAGCCAG 1780

QY 962 GCGTGTGGCAAGCGCAAGCGGTACCTCAAGGAGCAGACATTCAGACTTTCTCATCC 1021  
DB 1781 GCTCGGGGGAGCGCAAGCGCTACCTCAAGGAGCAGATGTCGACACCTTCTCATCC 1840  
  
QY 1022 TGGCGCCAGCCAGAAACGAGAGAGAGGATGCTGGCCAAAGCTGACGAGGACTC 1081  
DB 1841 TGGCTCACCCAGAGCGGAAAGAAAGAGGCGCATGTCGCCAAGATGAATGCCAGA 1900  
  
QY 1082 GGCCCAACTCCATGGAAGGGCTGATGCGCGATGGGTTCCTGATCGTTCCTTCCCGGA 1141  
DB 1901 GAACCAACTCCATTTGGGCACAACGCCCTGCGGGGGCGGAAAGCTCCCTTCTTACAAC 1960  
  
QY 1142 CCAAGGACTCCAAAGCGCTTCGCCAGATGGCATTTGATATCCAGCAAAAGCAACCGG 1201  
DB 1961 ACCTAGAGGCAACCCAGGTGTCCAAGGAGATGAAGCCATGGGCTTCGAGAGCCCCAAG 2020  
  
QY 1202 GCA-----CCCAAGATGCCCTGAACCTGAGGATGAGGTGGATTCCTGAGCCGTG 1255  
DB 2021 ACAAGAACGCCAGAAAGTGCAGAACCTGAGGATGAAGTGGATGAATTTCTGGCGCG 2080  
  
QY 1256 CCATCGATGCGCCGACGATTCATCAGCTGCGGAAGGACCATGTCGCGGGTTTTTGTCTCA 1315  
DB 2081 CCATTTGACGCCAGGAGCATCGACAGCTGCGGTGCGGACGCTCCGCAAGTTCTCTCTGA 2140  
  
QY 1316 CTTTCCAGAGAGAGGATTTTGAAGAAAGTACTCCCGAAAGGTGGATCCCGCTTCGGAG 1375  
DB 2141 CTTTCAGGAGCGCTGACTTAGAAAAGAGTACTCCAAGCAGGTGGATACCGATTCGGTG 2200  
  
QY 1376 CTTACGTTGGCTGCGCTGTTGCTTCTCTCTCATCTGCTTCATCCAGGCTTCTAATTT 1435  
DB 2201 CTTACGTTGGCATGTCGCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2260  
  
QY 1436 TCCACACATCCACCTGATGTTGGGATTTATGCCAGCATCTTCTCTGCTGCTGCTAATCA 1495  
DB 2261 TACCCCACTCCGTTTCTCATGTTGAGTTTCTACTTGACCTGTTTCTCTGCTGCTGCTG 2320  
  
QY 1496 CCGTGTGATCTGTGCTGTGTACTCTCTGTTCTCTGTTCCCTTAAGGCCCTGCAACGTC 1555  
DB 2321 TGGTATTTGTGCTGCTGATCTATTCCTCGGTGAAGCTCTTCCCGGGCGCGTCCAGAGCC 2380  
  
QY 1556 TGTCCCGCAGCATTTGCTCCGCTCAGGGCAGACATAGCAGCCGAGTTTGGCATCTTTTCCGTCC 1615  
DB 2381 TCTCGAGGAAGCTGCTGCGCTCCAAAGACCAACAGCAGCCCTGGTGGGGTGTTCACCATCA 2440  
  
QY 1616 TGCTTGTGTTTACTTCTGCCATTTGCCAACAATGTTTCACTGTAAACCACACCCCATACGA 1675  
DB 2441 CCCTGTTGTTTCTGCTGCGCTTTCGTCACCATGTTTCAATGTTGTAACCTCCGAGGACCTGTTGG 2500  
  
QY 1676 GCTGTGACGCCCGGATGCTGAATTTTAACACCTGCTGACATCACTGCTGCAACCT----- 1730  
DB 2501 GCTGCTGGCGGAGGACACACATCAGCAGCCCGGGTCAACGCGTGCACGTTGGCGG 2560  
  
QY 1731 -GCAGCAGCTCAATTAATCTCTCTGGGCTGGATGCTCCCTGTGTGTGAGGGACCATGCCCCA 1789  
DB 2561 CGTGGCGGCAACCTCAGCCTGGGCGACGAGCAGGSGCTTCTGCGGCACGCCCTGGGCCA 2620  
  
QY 1790 CTTGACGCTTTCTCTGAGGTGTTT 1812  
DB 2621 CTTGCAACTTCCCGAGTACTTC 2643

RESULT 12  
AAQ37543  
ID AAQ37543 standard; cDNA; 4356 BP.  
XX  
AC AAQ37543;  
XX  
DT 17-JUN-1993 (first entry)  
XX  
DE Cardiac adenylyl cyclase type V gene.  
XX  
KW CACV; therapy; diagnostic; cardiac function; cyclic AMP; cAMP; heart;

failure; ss.  
Canis familiaris.  
Key Location/Qualifiers  
CDS 148..3702  
/\*tag= a  
EP529622-A.  
03-MAR-1993.  
27-AUG-1992; 92EP-0114637.  
29-AUG-1991; 91US-0751460.  
(AMCY ) AMERICAN CYANAMID CO.  
Ishikawa Y, Konaki AF;  
WPI; 1993-068688/09.  
P-PSDB; AAR32882.  
Isolated nucleic acid mol. encoding Cardiac adenylyl cyclase type  
v - useful for determining and modifying cardiac function  
Claim 1; Page 15-27; 38pp; English.  
Left ventricular tissue of canine heart was used as a source of mRNA.  
A cDNA library was prepd. in lambda gt10 phage. A 970 bp Aat-HincII  
fragment from type I adenylyl cyclase cDNA was used as probe. The  
clones isolated were used to obtain cDNA encoding CACV. This probe  
may also be used to screen a human cardiac cDNA library to obtain  
the cDNA encoding human CACV. CACV, its analogues and antibodies  
are useful in therapy or diagnostic assays, e.g. in modifying and  
determining cardiac function. A decrease in CACV content of the  
heart contributes to impaired cAMP prodn. and in heart failure. The  
CACV can also be used to screen for cpds. which stimulate or inhibit  
the activity of the cyclase.  
Sequence 4356 BP; 837 A; 1367 C; 1377 G; 775 T; 0 other;  
Query Match 48.8%; Score 883.4; DB 14; Length 4356;  
Best Local Similarity 68.9%; Pred. No. 7.2e-226;  
Matches 1243; Conservative 0; Mismatches 551; Indels 9; Gaps 2;  
QY 5 ACGTGTGCTGGGCATCCTGGCGGAGTCAGGTGCGGGGCGCTTCGCGACGACCCCG 64  
DB 821 ACGCGCTATCGCGGTGGTGGCGGTGCAGGTGGTGGGCTGTGCTGCCCGCCAGCCGC 880  
QY 65 GCAGCCCTCTGCGGGCTCTGCTGCGCTGTGCTTTGTATACATCGCATACACGCTCC 124  
DB 881 GCAGCGCTCCGAGGCGATCTGGTGACCGTGTCTTCATCTACACCATCTACAGCTGC 940  
QY 125 TCCCAATCCGATGCGGGTGGCGCTCTCAGCGGCTGGCGCTCTCCACTTGCATTGGA 184  
DB 941 TGCCTGTGCGCATGCGGGCGCGCTCTCAGCGGAGTGTCTCTGCGGCCCTGCACCTGG 1000  
QY 185 TCTTGCGCTGGCAACTTACCGTGGTGTATGCTCTCTCTGGAAGCAGCTCGGTGCCAATG 244  
DB 1001 CCATCGCCTGGCGGCAACGCCCGGCTTCTGTCTCAAGCAGCTCGCTCTCCAAATG 1060  
QY 245 TGTGCTGTCTCTGCACCAACGCTATTAGCATCTGCACACATATCCAGCAGAGGTCT 304  
DB 1061 TCCATATTTCTCTGCACCAACATCTGGGTGTCTGTATCCCACTACCCGGCTGAGGTCT 1120  
QY 305 CTCAGCGCGGCTTTTACAGGACCCCGAGTTACATCCAGGCGCGGCTTCCACCTGCGAC 364  
DB 1121 CCAGAGACAGCGCTTCCAAAGACCCGGAGTGCATCCAGGCGCGCTCCACTCGCAAC 1180  
QY 365 ATGAGNAATCGGACGAGGCGGCTGCTGCTGCTGGTATTTGCCCGACGACGTTGCCATGG 424  
DB 1181 GGGAGAACCAACGAGGAGCGGCTCTGCTGTCTGCTCTGCTGCTGCTGCTGCTGCTGCTG 1240

QY 425 AGATGAAGAAGACATCAACACAAAAAAGAGAC---ATGTTCCCAAGATCTACATAC 481  
DB 1241 AGATGAAGACACATCAATGCAAGCAGGAGATATGATGTTCCATAAGATTTTATTC 1300  
QY 482 AGAAGCATGACAATGTTCAGCATCTCTGTTTGCAGACATTTAGGGGCTTCCACGAGCTGGCAT 541  
DB 1301 AGAAACATGACAACGTGAGCATCTCTGTTGCTGACATCGAGGCTTCCACGAGCTGGCAT 1360  
QY 542 CCCAGTGCCTGCGCAGGAGCTGGTCATGACCTGNAATGAGCTCTTTGGCCCGGTTTGACA 601  
DB 1361 CCCAGTGCCTGCGCAGGAGCTGGTCATGACCTCAATGAGCTCTTCGCGCCCTTCGACA 1420  
QY 602 AGCTGGCTGCGGAGAACTACTGCTGAGGATCAAGATCTTTGGGGACTCTTACTACTGTG 661  
DB 1421 AGCTGGCTGCGGAGAACTACTGTTTACGTATTAAGATCTCTGGGGATGTTTATTACTGTG 1480  
QY 662 TGTGAGGGCTGCGGAGGCCGCGGACCATGCCCACTGCTGTGTGGAGATGGGGGTAG 721  
DB 1481 TCTCTGGGCTGCTGAAGCGAGGCGGACACGCCCACTGCTGCGTGGAGATGGGCATGG 1540  
QY 722 ACATGATTGAGGCCATCTGCTGCTGAGGTGACAGGTGACAGGTGATGATGAAACATCGCG 781  
DB 1541 ACATGATTGAGGCCATCTGCTGGTCCGGGAGGTGACAGGGGTGAACGTGAACATCGCGG 1600  
QY 782 TGGGCATCCACAGCGGCGCTGCACTGCGGCGCTCTTGGCTTGGGAAATGCGAGTTCCG 841  
DB 1601 TGGGAATTCACAGCGGCGAGTACACTGCGGTGCTCTCAGGAAGTGGCAGTTCCG 1660  
QY 842 ATGTGTGTCCTCAATGATGTGACCTGGCCCAACACATGAAGCAGGAAAGCCGGGTGGCC 901  
DB 1661 AGCTGTGCTTCAATGACGTGAGCTGGCCCAACATATGAAGCTGGAGCAAGGCTGGGC 1720  
QY 902 GCATCCACATCACTCGGCAACACTGCACTGCTGACGCGGACTACGAAGTGGAGCCAG 961  
DB 1721 GCATCCCAATCAAGGCCACACTGACCTGCTGAACTGACAGGTGGAGGCGAG 1780  
QY 962 GCGGTGTTGGCAAGCGCAACGCGTACTCAAGGAGCAGCACATTTGAGACTTTCCTCATCC 1021  
DB 1781 GCTGCGGGGCGAGCGCAACGCTACTCTCAAGGAGCAGATATCGAGACCTTCTCATCC 1840  
QY 1022 TGGGCGCCAGCAGAAACGGAAGAGGAGGAGGATGCTGGCCAAAGTCAGCGGAGCTC 1081  
DB 1841 TCGCGTGCACCCAGAGCGGAAGAAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1900  
QY 1082 GGGCAACTCCATGGAAGGCTGATGCGCGGATGGTTCCTGATGCTGCTGCTTCTCCCGA 1141  
DB 1901 GAACCAACTCCATTTGGGCAACACCGCCCACTGGGGGGCGGAGACGCTTCTCTCAACC 1960  
QY 1142 CCAAGGACTTCCAAAGGCTTCCCGCCAGATGGGCAATTTGATTTCCAGCAAGACACCGG 1201  
DB 1961 ACCTAGGAGGCAACCAAGGTGTCCAAGGAGATGAAGGCAATGGGCTTCGAAGACCCCAAG 2020  
QY 1202 GCA-----CCCAAGATGCCCTGAACCCCTGAGGATGAGGTGATGATGATGATGATGATG 1255  
DB 2021 ACAAGAACCCCGGAGGAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2080  
QY 1256 CCATGATGCGCGCAGCATTGATGAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1315  
DB 2081 CCATTGACGCCAGGAGCATCGAGGCTGCGGTGCGGAGCAGCTGCGGCAAGTTCTCTCTGA 2140  
QY 1316 CTTTCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1375  
DB 2141 CTTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2200  
QY 1376 CTTACGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1435  
DB 2201 CTTACGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2260  
QY 1436 TCCACACATCCACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1495  
DB 2261 TACCACCTCCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2320





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QY 842 ATGTGTGGTCCAAATGATGTGACCCCTGGCCAAACACACATGGAAGACAGACCCGGGTGGCC 901
Db 1261 AGTGTGGTCTAACGATGTACACTGGCCAAACACACATGGAAGCTGGCGGAAGGCGCC 1320
QY 902 GCATCCACATCACTCGGCAACACTGCGAGTACCTGAACGGGACACTACGAAGTGGAGCCAG 961
Db 1321 GCATCCACATCACTCAAGGCCACACTCAACTACTGAACGGGACACTATGAGTGGAGCCAG 1380
QY 962 GCGGTGGTGGCAAGGCAACGCGTACCTCAAGGAGCAGCACATTCAGACATTCCTTCATCC 1021
Db 1381 GCTGTGGTGGTGGCGCATGCTACCTCAAGGAGCAGACATCGAGACCTTCCTCATCC 1440
QY 1022 TGGGGCCCAAGCAGAAACGGAAGAGGAAAGGAGATGCTGCGCCAGCTGCGAGCGAGCTC 1081
Db 1441 TCGCGTGTACCCAGAGCGGAAGAAGAGAGAGGCGCATGATCGCCCAAGATGAACCGCCAGA 1500
QY 1082 GGGCAACTCCATGGAAGGCTGATGCGCGGATGGTTCCTGATCGCTTCTCC---- 1137
Db 1501 GAACCAACTCCATGGACACAATCGCCCTCACTGGGGAGCTGAGCGCCCTTCTTACAACC 1560
QY 1138 -----CGGACCAAGGACTCCAAGGCCCTCCGCCAGATGGGCATTTGATGATTCAGCA 1189
Db 1561 ACTTGGTGGCAACACAGGTGTCCAGGAATGAAGAGATGGCTTGAGGACCCCA--- 1617
QY 1190 AAGACAACCGGGGACCCCAAGATGCCCTGAACCCCTGAGGATGAGTGGATGCTCTGA 1249
Db 1618 ---AGCAAGAATGCCAGGAAGTGCACACCTGAGGATGAAGTGGACGAGTTCTTGG 1674
QY 1250 GCGTGCCATCGATGCCCGCAGCATGATCAGCTGCGGAGAGCAACATGTGCGCCGGTTT 1309
Db 1675 GTCGAGCCATCGATGCCAGGATATTGACAGACTCGCATCCGAACACGCTCCGAAAGTTCC 1734
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QY 1370 TCGGAGCCPACGTTGCGCTGCGCTGTTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTC 1429
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QY 1550 AAGCTGTGTCGCGACATGTCGCTACGGCTACGGGCAATAGCACCGCAGTTGCGATCTTTT 1609
Db 1975 AGACACTCTCCAGGAAGATGTCGCTATCCCAAGAAGAACACACCCCTGTCGGGTGTTCA 2034
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QY 1730 TGCAGCAG-----CTCAATTAATCTCTGGGCTTGATGCTCCCTGTGTGAGGCAACCA 1783
Db 2155 TGATGAGTTCGGCTTCAACTACAGCCTGGGCGAGCAGGCGCTCTGTGCGAGCGCC 2214
QY 1784 TGGCCACCTGCGAGCTTCTCTGAGGTTC 1812
Db 2215 AGTCCAATGCAACTTCCAGAGTACTTC 2243
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RESULT 14  
AAD28058  
ID AAD28058 standard; cDNA; 3137 BP.  
XX

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AC AAD28058;  
XX  
DT 22-APR-2002 (first entry)  
XX  
DE Human adenylyl and guanylyl cyclase (ADGUC)-2 cDNA.  
XX  
KW Human; adenylyl and guanylyl cyclase; ADGUC-2; cardiovascular disorder;  
KW angina pectoris; myocardial infarction; vision disorder; keratitis;  
KW Iritis; cataract; neurological disorder; epilepsy; Alzheimer's disease;  
KW Pick's disease; stroke; mental disorder; mood and anxiety disorder;  
KW reproductive disorder; infertility; endometriosis; impotence; asthma;  
KW smooth muscle disorder; migraine; bacterial infection; gene therapy;  
KW transgenic animal; vaccine; enzyme; ss.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..2514  
FT /*tag= a  
FT /product= "Human ADGUC-2 protein"  
FT  
XX WO200202757-A2.  
XX  
XX 10-JAN-2002.  
XX  
XX 26-JUN-2001; 2001WO-US20491.  
XX  
XX 29-JUN-2000; 2000US-215476P.  
XX 04-AUG-2000; 2000US-223545P.  
XX 31-AUG-2000; 2000US-229876P.  
XX 22-SEP-2000; 2000US-234838P.  
XX 29-SEP-2000; 2000US-236483P.  
XX  
XX (INCY-) INCYTE GENOMICS INC.  
XX  
XX Gandhi AR, Tribouley C, Ding L, Lu DAM, Lee EA, Yue H, Yang J;  
XX Baughn MR, Thornton M, Yao MG, Walia NK, Tang YT, Elliott VS;  
XX Lu Y;  
XX  
XX WPI; 2002-154740/20.  
XX P-PSDB; AAE17130.  
XX  
XX Novel human adenylyl and guanylyl cyclases and polynucleotides encoding  
XX the cyclases, useful for treating, diagnosing or preventing  
XX cardiovascular, neurological, vision, reproduction and smooth muscle  
XX disorders  
XX  
XX Claim 5; Page 112-113; 116pp; English.  
XX  
XX The invention relates to human adenylyl and guanylyl cyclases (ADGUC)  
XX preferably ADGUC1-ADGUC5 and nucleic acid molecules encoding such  
XX polypeptides. ADGUC sequences are useful in the diagnosis, prevention  
XX and treatment of cardiovascular disorders (e.g. angina pectoris,  
XX myocardial infarction, ischaemic heart disease, hypertension and  
XX atherosclerosis), vision disorders (e.g. keratoconjunctivitis sicca,  
XX keratitis, Iritis, cataract), neurological disorders (e.g. epilepsy,  
XX Alzheimer's disease, Pick's disease, Huntington's disease, dementia,  
XX Parkinson's disease, Creutzfeldt-Jakob disease, stroke, schizophrenia,  
XX mental disorders including mood and anxiety and prion diseases including  
XX kuru), reproductive disorders (e.g. infertility, endometriosis,  
XX impotence, uterine fibroid and gynaecomastia), smooth muscle disorders  
XX (e.g. arrhythmias, asthma and migraine) and bacterial infections.  
XX ADGUC polynucleotides are useful for creating knock-in humanised animals  
XX or transgenic animals to model human diseases. They are useful in  
XX somatic or germline gene therapy. ADGUC polynucleotides are also useful  
XX for detecting differences in the chromosomal location due to  
XX translocation, inversion, etc. among normal, carrier or affected  
XX individuals. ADGUC polypeptides are useful in a number of drug screening  
XX techniques and in vaccines. The present sequence is human ADGUC-2 cDNA.  
XX  
XX Sequence 3137 BP; 553 A; 973 C; 1044 G; 567 T; 0 other;  
XX
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Query Match

44.1%; Score 799; DB 24; Length 3137;



Best Local Similarity 73.5%; Pred. No. 2.4e-203; Matches 1069; Conservative 0; Mismatches 365; Indels 21; Gaps 3;		
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Db	1184	TGCGGTGCGCATCGGGCGCAGTGTCTCAGCGGGTGTCTCTCGCGCCCTCCACCTGG 1243
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Db	1244	CCATCGCCCTCGGCACCAAGCCAGGACCAAGTTCCTGCTGAAGCAGCTGTCTCCAATG 1303
QY	245	TGCTGTCTTCTCTGCAACCACTCATATAGCATCTGCACACACTATCCAGCAGAGTGT 304
Db	1304	TTCTCATTTTCTCTGCAACCACTCATCTGGTGTCTGCACCCACTATCCGCTGAGTCT 1363
QY	305	CTAGCCCGAGGCTTTCAGAGACCCGCGAGTTTACATCCAGGCCCGGCTCCACCTGCAGC 364
Db	1364	CCCAGACAGAGTTCAGAGAGACCCGAGAGTGCATCCAGCGCGGCTCCACTCGCAGC 1423
QY	365	ATGAAATCGCAGCAGGCGGTCTGCTGCTGCTGATTCGCCCGCAGCTTGCCTATGG 424
Db	1424	GGGAGACCAAGCAGCAGGAGCGCTCTGCTGCTGCTGCTTCCCGCTCATGTTGCCATGG 1483
QY	425	AGATGAAGAGACATCAACACAAAAAAGA ---CATGTTCCACAAGATCTTACATAC 481
Db	1484	AGATGAAGCAGACATCAACGCCCAAGCAGGAGATATGATGTTCCATAAGATTTACATCC 1543
QY	482	AGAGCATGACATGTGAGCATCTCTGTTTCAGACATTTGAGGGCTTCACAGCCTGCAT 541
Db	1544	AGAAACATGACAGTGAAGATCTCTGTTGCTGACATCGAGGGCTTCACCAGCCTGGCGT 1603
QY	542	CCAGTCACTTGCAGAGAGTGTGTCATGACCTGATGAGTCTTTGCCCGTTCGACA 601
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QY	562	TGTCAGGGCTTGGCGGGCCCGGCGGACCATGCCCACTGCTGTGTGGAGATGGGGTAG 721
Db	1724	TCTCGGGGCTGCGCTGAAGCAAGGGCTGACCAACGCCCACTGCTGTGTGGAGATGGCATGG 1783
QY	722	ACATGATTGAGGCATCTCGCTGCTAGCTGAGGTGACAGGTGCAATGTGAACATGCGCG 781
Db	1784	ACATGATCAGAGGCATCTCTGTTGGTCGGGAGGTGACAGGGGTGAACGTGAACATGCGTG 1843
QY	782	TGGGCATCCACAGCGGGCGGTGCATCTGCGCGCTTCCTTGGCTTTCGCGAAATGGCAGTGC 841
Db	1844	TGGGAATTCACAGCGGGCGAGTACATCTGCGGTGTCTCTGCTTCAGGAAGTGGCAGTTCG 1903
QY	842	ATGTGTGTCATATGATGTGACCTTGCCCAACCATGGAAGCAGGAAGCGGGCTGGCC 901
Db	1904	ACGTCTGGTCTAACGATGTACGCTAGCCCAACCATGGAAGTGGCGGCAAGCAGGAC 1963
QY	902	GCATCCACATCACTTCGGGCAACACTGCAGTACCTTGAACGGGACTACGAAGTGGAGCCAG 961
Db	1964	GCATCCACATCAAGAGGCTTACTCACTTACCTTGAATGGGACTACGAGGTGGAGCCAG 2023
QY	962	GCCGTGTGGCAAGCGCAACCGTACTCAAGGAGCAGCAGCATTTGACTTTCCTCATCC 1021
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QY	1310	TGCTCACCTTCCAGAGAGAGGATTTTGAAGAAGTACTCCCGGAAGGTGATCCCGCT 1369
Db	2378	TCCTGACCTTCAGGAGCGCTGACTTAGAGAAGAAGTACTCCAAGCAGGTAGACGACGAT 2437
QY	1370	TGGAGCCTAGTTCCTGCTGCGCTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTC 1429
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XX	ABL07501;	
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XX		Drosophila melanogaster expressed polynucleotide SEQ ID NO 16985.
DE		Drosophila; developmental biology; cell signalling; insecticide;
KW		pharmaceutical; gene; ss.
XX		Drosophila melanogaster.
XX		WO200171042-A2.
PN		
XX		27-SEP-2001.
XX		
PF		23-MAR-2001; 2001WO-US09231.
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PR		23-MAR-2000; 2000US-191637P.
PR		11-JUL-2000; 2000US-0614150.
XX		(PEKE ) PE CORP NY.
PA		
XX		Venter JC, Adams M, Li PWD, Myers EW;
PI		
XX		WPI; 2001-656860/75.
DR		P-PSDB; ABB63398.
DR		
XX		New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
PT		
PT		
XX		Claim 1; SEQ ID NO 16985; 2lpp + Sequence Listing; English.
PS		
XX		The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (ABL161176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL161175) and the encoded proteins  
CC (ABB57737-ABB72072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
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Best Local Similarity 57.7%; Pred. No. 1.2e-108;  
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Search completed: February 28, 2003, 23:39:05  
Job time : 301.906 secs

Result No.	Score	Query		Length	DB	ID	Description
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2	1808.4	99.8	3549	10	US-09-750-240-5		Sequence 5, Appli
3	1763.4	97.3	3552	10	US-09-750-240-10		Sequence 10, Appli
4	1763	97.3	4942	9	US-10-201-000-1		Sequence 1, Appli
5	1657.8	91.5	3582	10	US-09-750-240-12		Sequence 12, Appli
6	895	49.4	4523	9	US-10-175-158-1		Sequence 1, Appli
7	319.4	17.6	2601	10	US-09-925-297-352		Sequence 352, App
8	284	15.7	3518	9	US-10-121-911-2		Sequence 2, Appli
9	216.8	12.0	4473	10	US-09-751-100B-1		Sequence 1, Appli
10	209.4	11.6	4985	12	US-10-071-223-1		Sequence 1, Appli
11	207.8	11.5	5515	10	US-09-751-100B-98		Sequence 98, Appli
12	124.4	6.9	330	9	US-09-764-868-182		Sequence 182, App
13	124.4	6.9	330	9	US-09-989-442-71		Sequence 71, Appli
14	124.4	6.9	330	10	US-09-764-869-445		Sequence 445, App
15	79.2	4.4	11881	9	US-09-764-868-1351		Sequence 1351, Ap
16	79.2	4.4	11881	9	US-09-764-868-1353		Sequence 1353, Ap
17	79.2	4.4	11881	10	US-09-764-869-2184		Sequence 2184, Ap
18	64.4	3.6	1259	9	US-10-051-643-123		Sequence 123, App
19	64.4	3.6	1259	9	US-09-880-505-123		Sequence 123, App



; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 5									
; LENGTH: 3549									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-09-750-240-5									
Query Match 99.8%; Score 1808.4; DB 10; Length 3549;									
Best Local Similarity 99.9%; Pred. No. 0;									
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
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QY	63	GCCAGCCCTCTGCGGGCTCTGGTCCCTGTGTTCTTTGTATACATCCATACAGCT	122						
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QY	243	TGTGCTGCTGCTTCTCTGCACCAACGTCATTAGCATCTGCACACATATCCACGAGGT	302						
DB	876	TGTGCTGCTGCTTCTCTGCACCAACGTCATTAGCATCTGCACACATATCCACGAGGT	935						
QY	303	GTCTACGGCCAGGCTTTTCAGAGACCCGCGAGTTACATCCAGCCCGGCTCCACCTGCA	362						
DB	936	GTCTACGGCCAGGCTTTTCAGAGACCCGCGAGTTACATCCAGCCCGGCTCCACCTGCA	995						
QY	363	GCATGAGATTCGCGACGAGCGGTGCTGCTGCTCGGTATTCGCCACGACGCTGCCAT	422						
DB	996	GCATGAGATTCGCGACGAGCGGTGCTGCTGCTCGGTATTCGCCACGACGCTGCCAT	1055						
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QY	843	TGTGTCCTCAATGTATGACCTTGCCCAACCATGGAAGCAGGAGCCGGCTGGCCG	902						
DB	1476	TGTGTCCTCAATGTATGACCTTGCCCAACCATGGAAGCAGGAGCCGGCTGGCCG	1535						
QY	903	CATCCACATCACTGGGGCAACATCTCAGTACCTGAACGGGACTACGAAGTGGAGCCAG	962						

RESULT 3  
US-09-750-240-10  
; Sequence 10, Application US/09750240  
; Patent No. US20020103147A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammon, H. K.  
; APPLICANT: Insel, P. A.  
; APPLICANT: Ping, P.  
; APPLICANT: Post, S. R.  
; APPLICANT: Gao, M.



Qy 1800 TCCTGAGGTGTC 1812  
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Db 2436 TCCTGAGTACTC 2448

RESULT 4

US-10-201-000-1  
; Sequence 1, Application US/10201000  
; Publication No. US20020187540A1  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, James E.  
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL  
; FILE REFERENCE: 44481-5028-01-US  
; CURRENT APPLICATION NUMBER: US/10/201,000  
; CURRENT FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: US/09/474,076  
; PRIOR FILING DATE: 1999-12-12  
; PRIOR APPLICATION NUMBER: PCT/US98/13694  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/070,904  
; PRIOR FILING DATE: 1997-07-01  
; PRIOR APPLICATION NUMBER: 08/886,550  
; PRIOR FILING DATE: 1997-07-01  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4942  
; TYPE: DNA  
; ORGANISM: human type VI adenylyl cyclase  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (145)..(3648)  
US-10-201-000-1

Query Match 97.3%; Score 1763; DB 9; Length 4942;  
Best Local Similarity 98.7%; Pred. No. 0;  
Matches 1788; Conservative 0; Mismatches 20; Indels 3; Gaps 1;

Qy 5 ACGTGGTGTGGGCATCTGGCGCAGTGCAGGTGCGGGGGCGCTTCGCGAGCACCCGC 64  
Db 782 ACGTGGTGTGGGCATCTGGCGCAGTGCAGGTGCGGGGGCGCTTCGCGAGCACCCGC 841  
Qy 65 GCAGCCCTCTGCGGGGCTCTGFGCCCTGTGTTTGTATACATCGCATACAGCTCC 124  
Db 842 GCAGCCCTCTGCGGGGCTCTGFGCCCTGTGTTTGTATACATCGCATACAGCTCC 901  
Qy 125 TCCCATCCGATCGGGGCTGCCCTCTCTAGCGGCTTGGGCTCTCCACCTTGCATTTGA 184  
Db 902 TCCCATCCGATCGGGGCTGCCCTCTCTAGCGGCTTGGGCTCTCCACCTTGCATTTGA 961  
Qy 185 TCTTGGGCTGGCACTTAACGGTGGTGTATGCTTCTCTGGAAGCAGCTGGTGCCAAATG 244  
Db 962 TCTTGGGCTGGCACTTAACGGTGGTGTATGCTTCTCTGGAAGCAGCTGGTGCCAAATG 1021  
Qy 245 TGCTGTGTTCTCTGACCAACCTCATATAGCATCTGCACACACTATCCAGCAGAGTGT 304  
Db 1022 TGCTGTGTTCTCTGACCAACCTCATATGTCATCTGCACACACTATCCAGCAGAGTGT 1081  
Qy 305 CTCAGCGCAGGCGCTTTTCAGGAGACCGCGAGTTATCATCCAGGCGCGCTCCACCTGCAGC 364  
Db 1082 CTCAGCGCAGGCGCTTTTCAGGAGACCGCGGTTACATCCAGGCGCGCTCCACCTGCAGC 1141  
Qy 365 ATGAGATCGGCACGACGAGGGGTGCTGCTGTCGGTATTTGCCCGCAGAGTTGCCATGG 424  
Db 1142 ATGAGATCGGCACGAGGAGGGGTGCTGCTGTCGGTATTTGCCCGCAGAGTTGCCATGG 1201  
Qy 425 AGATGAAGAGAGACATCAACACAAAAAAGAAGAC ---ATGTTCCACAAGATCTACATAC 481  
Db 1202 AGATGAAGAGAGACATCAACACAAAAAAGAAGAGATGTTGCCACAGATCTACATAC 1261

Qy 482 AGAAGCATGACAATGTTCAGCATCTCTGTTTGAGACATTTAGGGCTTACCAGCCTGGCAT 541  
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Db 1262 AGAAGCATGACAATGTTCAGCATCTCTGTTTGAGACATTTAGGGCTTACCAGCCTGGCAT 1321  
Qy 542 CCCAGTGCATGCGCAGAGGCTGTCTATGACCCCTGAATGAGCTCTTTGCCGGTTTGACA 601  
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Db 1322 CCCAGTGCATGCGCAGAGGCTGTCTATGACCCCTGAATGAGCTCTTTGCCGGTTTGACA 1381  
Qy 602 AGCTGGCTGGGAGAACTACCTGCTGAGGATCAAGATCTTTGGGAGACTGTTACTACTGTG 661  
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Db 1382 AGCTGGCTGGGAGAACTACCTGCTGAGGATCAAGATCTTTGGGAGACTGTTACTACTGTG 1441  
Qy 662 TGTGAGGCTGCCGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 721  
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Db 1442 TGTGAGGCTGCCGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1501  
Qy 722 ACATGATTGAGGCCATCTCGCTGTGTAGCTGAGGTGACAGGTGTGAATGTGAACATGGCG 781  
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Db 1502 ACATGATTGAGGCCATCTCGCTGTGTAGCTGAGGTGACAGGTGTGAATGTGAACATGGCG 1561  
Qy 782 TGGGCATCCACAGCGGCGGCTGCACCTGCGGCGTCTTGGCTTGGGAAATGGCAGTTCG 841  
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Db 1562 TGGGCATCCACAGCGGCGGCTGCACCTGCGGCGTCTTGGCTTGGGAAATGGCAGTTCG 1621  
Qy 842 ATGTGTGTTCAATGATGTGACCTTGGCCAAACACATGGAAGCAGGAGGCGGCTGGCC 901  
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Db 1622 ATGTGTGTTCAATGATGTGACCTTGGCCAAACACATGGAAGCAGGAGGCGGCTGGCC 1681  
Qy 902 GCATCCACATCCTCGGGCAACACTGCAGTACCTGAAACGGGAGCTACGAGGTGAGCCAG 961  
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Db 1682 GCATCCACATCCTCGGGCAACACTGCAGTACCTGAAACGGGAGCTACGAGGTGAGCCAG 1741  
Qy 962 GCGTGTGGCAAGCGCAACCGCTACCTCAAGGAGCAGACATTTGAGACTTTCTCATCC 1021  
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Db 1742 GCGTGTGGCAAGCGCAACCGCTACCTCAAGGAGCAGACATTTGAGACTTTCTCATCC 1801  
Qy 1022 TGGCGCGCAGCAGAAACGGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1081  
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Db 1802 TGGCGCGCAGCAGAAACGGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1861  
Qy 1082 GGGCCAACTCATGGAAGGCGTGTATGCGCGCATGGGTTCTGTGATCGTCTCCCGGA 1141  
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Db 1862 GGGCCAACTCATGGAAGGCGTGTATGCGCGCATGGGTTCTGTGATCGTCTCCCGGA 1921  
Qy 1142 CCAAGGACTCCAAGCGCTTCCGCCAGATGGGCAATTGATTTCCAGCAAAACAAACCGGG 1201  
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Db 1922 CCAAGGACTCCAAGCGCTTCCGCCAGATGGGCAATTGATTTCCAGCAAAACAAACCGGG 1981  
Qy 1202 GCACCCAAAGATGCCCTGAAACCCCTGAGGATGAGGTGGATGCTTCTGAGCCGTGCCATCG 1261  
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Db 1982 GCACCCAAAGATGCCCTGAAACCCCTGAGGATGAGGTGGATGAGTTCTGAGCCGTGCCATCG 2041  
Qy 1262 ATGCCCCCAGCATTTGATCAGCTGCGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1321  
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Db 2042 ATGCCCCCAGCATTTGATCAGCTGCGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2101  
Qy 1322 AGAGAGAGGATTTTGAAGAAGTACTCCCGGAAGGTGGATCCCGCTTCCGAGCCCTACG 1381  
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Db 2102 AGAGAGAGGATTTTGAAGAAGTACTCCCGGAAGGTGGATCCCGCTTCCGAGCCCTACG 2161  
Qy 1382 TTGCGCTGTGCGGCTTGGGATTTATGCCAGCATCTTCTGCTCATCGCTGCTGCTGCTGCTG 1441  
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Db 2162 TTGCGCTGTGCGGCTTGGGATTTATGCCAGCATCTTCTGCTCATCGCTGCTGCTGCTGCTG 2221  
Qy 1442 ACTCCACCCCTGATGCTTTGGGATTTATGCCAGCATCTTCTGCTCATCGCTGCTGCTGCTG 1501  
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Db 2222 ACTCCACCCCTGATGCTTTGGGATTTATGCCAGCATCTTCTGCTCATCGCTGCTGCTGCTG 2281  
Qy 1502 TGATCTGTGCTGTACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1561  
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Db 2282 TGATCTGTGCTGTACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2341  
Qy 1562 GCAGCATTTGTCGCTACGCGGCACATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCTTG 1621



Db 2342 GCAGCATGTCGCTCACGGGCACATAGCACCGCAGTTGGCATCTTTTCGCTCCTGTTG 2401  
QY 1622 TGTGTTACTTCTGCAATGTCACATGTTACCTGTTAACACACCCCATACGAGGAGCTGTG 1681  
Db 2402 TGTGTTACTTCTGCAATGTCACATGTTACCTGTTAACACACCCCATACGAGGAGCTGTG 2461  
QY 1682 CAGCCCGGATGCTGAATTTAAACACCTGCTGACATCACTGCTGCCACCTGCAGCAGCTCA 1741  
Db 2462 CAGCCCGGATGCTGAATTTAAACACCTGCTGACATCACTGCTGCCACCTGCAGCAGCTCA 2521  
QY 1742 ATTACTCTCTGGCCCTGGATGCTCCCTGTGTGAGGGGCACATGCCCCACCTGCGAGCTTTC 1801  
Db 2522 ATTACTCTCTGGCCCTGGATGCTCCCTGTGTGAGGGGCACATGCCCCACCTGCGAGCTTTC 2581  
QY 1802 CTGAGGTGTTTC 1812  
Db 2582 CTGAGTACTTTC 2592

RESULT 5  
US-09-750-240-12  
: Sequence 12, Application US/09750240  
: Patent No. US20020103147A1  
: GENERAL INFORMATION:  
: APPLICANT: Hammon, H. K.  
: APPLICANT: Insel, P. A.  
: APPLICANT: Ping, P.  
: APPLICANT: Post, S. R.  
: APPLICANT: Gao, M.  
: TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART  
: FILE REFERENCE: 220002056723  
: CURRENT APPLICATION NUMBER: US/09/750,240  
: CURRENT FILING DATE: 2001-10-12  
: PRIOR APPLICATION NUMBER: US 09/472,667  
: PRIOR FILING DATE: 1999-12-27  
: PRIOR APPLICATION NUMBER: US 09/008,097  
: PRIOR FILING DATE: 1998-01-16  
: PRIOR APPLICATION NUMBER: US 08/924,757  
: PRIOR FILING DATE: 1997-09-05  
: PRIOR APPLICATION NUMBER: US 60/048,933  
: PRIOR FILING DATE: 1997-06-16  
: PRIOR APPLICATION NUMBER: US 08/708,661  
: PRIOR FILING DATE: 1996-09-05  
: NUMBER OF SEQ ID NOS: 13  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 12  
: LENGTH: 3582  
: TYPE: DNA  
: ORGANISM: Artificial Sequence  
: FEATURE:  
: OTHER INFORMATION: Modified AC-VI  
US-09-750-240-12

Query Match 91.5%; Score 1657.8; DB 10; Length 3582;  
Best Local Similarity 95.4%; Pred. No. 0;  
Matches 1730; Conservative 0; Mismatches 77; Indels 6; Gaps 2;

QY 3 TAACTGTGTGCTGGGATCCTGGCGGAGTGCAGGTGCGGGCGCTTTCGCGAGCAGACC 62  
Db 657 TTACGTGTGTGCTGGGATCCTGGCGGAGTGCAGGTGCGGGCGCTTTCGCGAGCAGACC 716  
QY 63 GCGACGCCCTCTGCGGGCTCTGTTGCCCTGTGTTCTTTGTATACATCGCATACACGCT 122  
Db 717 GCGACGCCCTCTGCGGGCTCTGTTGCCCTGTGTTCTTTGTATACATCGCATACACGCT 776  
QY 123 CTTCCCATCCGATCGGGCTGCCCTCTCAGCGGCTTGGGCTCTCCACCTTGCATTT 182  
Db 777 CTTCCCATCCGATCGGGCTGCCCTCTCAGCGGCTTGGGCTCTCCACCTTGCATTT 836  
QY 183 GATCTGGCTGGCACTTAACTGGTGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAA 242

Db 837 GATCTGGCTTGGCACTTAACTGGTGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAA 896  
QY 243 TGTGCTGCTGTTCTCTGCAACCAACGTCTATTAGCATCTGCACACACATATCCAGCAGAGT 302  
Db 897 TGTGCTGCTGTTCTCTGCAACCAACGTCTATTAGCATCTGCACACACATATCCAGCAGAGT 956  
QY 303 GTCTCAGCCCGAGGCTTTTCAGGAGACCCGCGAGTTACATCCAGGCGCGCTCCACCTGCA 362  
Db 957 GTCTCAGCCCGAGGCTTTTCAGGAGACCCGCGGTTACATCCAGGCGCGCTCCACCTGCA 1016  
QY 363 GCATGAGAAATCCGACGAGGCGGCTGCTGCTGTCGGTATTGCCCCACGACGTTGCCAT 422  
Db 1017 GCATGAGAAATCCGACGAGGCGGCTGCTGCTGTCGGTATTGCCCCACGACGTTGCCAT 1076  
QY 423 GGAGATGAAAGAGACATCAACACAAAAAAGAAAGAC ---ATGTTCCACAAGATCTACAT 479  
Db 1077 GGAGATGAAAGAGACATCAACACAAAAAAGAAAGACATGTTTCCACAAGATCTACAT 1136  
QY 480 ACAGAAGCATGACAATGTGACGATCCTGTTTGCAGACATTTGAGGGCTTCCACGAGCTGCG 539  
Db 1137 ACAGAAGCATGACAATGTGACGATCCTGTTTGCAGACATTTGAGGGCTTCCACGAGCTGCG 1196  
QY 540 ATCCAGTGCCTGCGCAGGAGCTGGTCATGACCCCTGAATGAGCTCTTTGCCCGGTTTGA 599  
Db 1197 ATCCAGTGCCTGCGCAGGAGCTGGTCATGACCTTGAATGAGCTCTTTGCCCGGTTTGA 1256  
QY 600 CAAGCTGGCTCGGAGAAATCACTGCTGAGGATCAAGATCTTTGGGGGAGCTGTTACTACTG 659  
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QY 660 TGTGTCAGGGCTGCGGAGGCGCGGCCCACTGCTGAGGATGAGGCTGCTGTTGGAGATGGGGT 719  
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QY 720 AGACATGATGAGGCGCATCTCCGTCGTGAGTGTGAGGTGACAGTGTGAATGTGAACATGCG 779  
Db 1377 AGACATGATGAGGCGCATCTCCGTCGTGAGTGTGAGGTGACAGTGTGAATGTGAACATGCG 1436  
QY 780 CGTGGGCATCCACAGCGGCGCTGACCTGCGCGCTGCTTGGCTTGCAGAAATGCGAGTT 839  
Db 1437 TGTGGGCATCCACAGCGGCGCTGACCTGCGCGCTGCTTGGCTTGCAGAAATGCGAGTT 1496  
QY 840 CGATGTGTGCTCAATGATGTGACCTTGGCCCAACACATGGAAGCAGGAGCGGCGCTG 899  
Db 1497 TGATGTGTGCTCAACGATGTGACCTTGGCCCAACACATGGAAGCAGGCGGCGCTG ---GGCG 1553  
QY 900 CCGATCCACATCACTCGGCGCAACACTGACGTACCTGAAAGCGGAGCTACGAAGTGGAGCC 959  
Db 1554 GCGCATCCACATCACTCGGCGCTACACTGCACTGTTGAACGGGGAGCTATGAGGTGGAGCC 1613  
QY 960 AGGCGTGTGTCGCAAGCGCAACCGGTACCTCAAGGAGCAGACATTTGACACTTTCTCAT 1019  
Db 1614 AGGCGTGTGTCGCAAGCGCAACCGGTACCTCAAGGAGCAGACATTTGACACTTTCTCAT 1673  
QY 1020 CTTGGCGCCAGCCAGAAACGGAAGAGAGAAAGGCAATGCTGGCCAAAGCTGCAGCGGAC 1079  
Db 1674 ACTTGGCGCCAGCCAGAAACGGAAGAGAGAAAGGCAATGCTGGCCAAAGCTGCAGCGGAC 1733  
QY 1080 TCGGGCAACTCCATGGAAGGCTGATCCGCGGATGGGTTCTCTGATGCTGCTTCTCCG 1139  
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QY 1140 GACCAAGGACTCCAAGGCTTCCGCGAGATGGCATTGATTTCCAGCAAGAACACCG 1199  
Db 1794 GACCAAGGACTCCAAGGCTTCCGCGAGATGGCATTGATTTCCAGCAAGAACACCG 1853  
QY 1200 GGGCACCACCAAGATGCCCTGAACCTTGAAGATGAGGTGGATGAGTTCCTGAGCGCGTCCAT 1259  
Db 1854 GGGTGCACCAAGATGCTCTGAACCTTGAAGATGAGGTGGATGAGTTCCTGAGCGCGTCCAT 1913  
QY 1260 CGATGCGCGCAGCATGATGACGTGCGGAGGAGACCATGTGCGCGGCTTTTCTGCTACACCT 1319  
Db 1914 CGATGCGCGCAGCATGATGACGTGCGGAGGAGACCATGTGCGCGGCTTTTCTGCTACACCT 1973





Db 2126 GAACCAACTCCATCGGCGCAACCCACCACTGGGGGGCTGAGCGCCCTTCTACAACC 2185  
QY 1138 -----CGGACCAAGGACTCAAGGCCCTTCGCCAGATGGCATTGATGATTCAGCA 1189  
Db 2186 ACCTGGGTGCAACAGGCTCCAGAGAGATGAAGCGGATGGGCTTTGAAGACCCCA--- 2242  
QY 1190 AAGACAACCGGGGACCCCAAGATGCCCTGAACCCCTGAGGATGAGTGGATTCCTGA 1249  
Db 2243 ---AGGACAAGAAGCGCCAGGAGAGTGCAGAACCTGAGGATGAAGTGGATTCCTGG 2299  
QY 1250 GCCGTGCAATCGATGCCCGAGAGATGATCAGCTGCGGGAAGGACCATGTGCGCGGTTT 1309  
Db 2300 GCCGTGCCATTTAGCGCAGGAGCATGATAGGCTTCGGCTGAGCAGCTCCGCAAGTTC 2359  
QY 1310 TGCTCACTTCCAGAGAGAGATTTTGAAGAAGTACTCCCGGAAGTGGATCCCGCT 1369  
Db 2360 TCGTGACCTTACGAGGAGCTGACTTAGAAGAAGTACTCCAGCAGGATGAGACCGAT 2419  
QY 1370 TCGGAGCCTACGTTGCTGTGCCCTGTGCTCTTCTGCTTCTATCTGCTCATCCAGCTTC 1429  
Db 2420 TTGGTGCTATGCGGTGCGCTCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2479  
QY 1430 TAATTTTCCACACTACACCTGATGCTTGGGATTTATGCCAGCATCTTCTCTGCTGCTG 1489  
Db 2480 CCATCGTGCCCACTCCATATTCATGCTCAGCTTCTACCTGACCTGTTCTCTGCTGCTG 2539  
QY 1490 TAATCACCGTGCTGATCTGTGCTGTGCTACTCTCTGCTGCTTCTCTGTTCCCTAAGGCCCTGC 1549  
Db 2540 CTTGGTGGTGTGTTGCTGTGATCTACTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 2599  
QY 1550 AACGCTGTGCCGAGCATGTGCCGTCACGGGCACATAGCAGCGGATGGCATCTTTT 1609  
Db 2600 AGACCTCTCCAGGAAGCTGCGGTCCAGATGAACAGCACCTGTTGGGTGTTCA 2659  
QY 1610 CCGTCTGCTGTTGTTTACTTCTGCAATGTCGCAATGTTTACCTGTATACCAACACCCCA 1669  
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QY 1670 TAGCGAGCTGTGCGAGCGGATGCTGAATTTAACAATGCTGATGATGCTGCTGCTGCTGCT 1729  
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QY 1730 TGCAAGCAG-----CTCAATTAATCTCTCTGGGCTGGATGCTCCCTGTGTGAGGGCACCA 1783  
Db 2780 TGGCGAGTGGCGGCTCAACTACAGCTGGGCGATGAGCAGGGCTTCTGTGGCAGCCCT 2839  
QY 1784 TGCCCACTGCAAGCTTCTCTGAGGTTC 1812  
Db 2840 GGCCCACTGCAACTTCCCGGAGTACTTC 2868

RESULT 7  
US-09-925-297  
; Sequence 352, Application US/09925297  
; Patent No. US20020081659A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA105  
; CURRENT APPLICATION NUMBER: US/09/925,297  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05989  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 928  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 352  
; LENGTH: 2601  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:

; NAME/KEY: misc feature  
; LOCATION: (2520)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (2572)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-297-352  
  
Query Match 17.6%; Score 319.4; DB 10; Length 2601;  
Best Local Similarity 64.5%; Pred. No. 3.2e-76;  
Matches 515; Conservative 0; Mismatches 271; Indels 13; Gaps 2;  
  
QY 294 AGCAGAGGTGCTCTCAGCGCCAGGCTTTTCAGGAGACCCGAGTTATCATCCAGGCCCGCT 353  
Db 34 AACAGCCGCAAGCAGCCGAAGGCTTCTGGAGGCCGCCAGCTCGCTGGAGTGAAGAT 93  
QY 354 CCACCTGCGAGCATGAGAATCGGAGCAGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 413  
Db 94 GAACCTGGAGAGCAGAGCCAGCAGCAGGAGAACCTTCATGCTTTCCATCTCTGCCCAAGCA 153  
QY 414 CGTTGCCATGGAGATGAAAGAGACATCAACACA-----AAAAAGAACACAT 461  
Db 154 CGTGGCTGAGGATGCTGAAGACATGAGAAAGAGAGAGCCAGAGCCAGCAGCA 213  
QY 462 GTTCCACAAGATCTACATACAGAAAGCATGACAAATGTGACGATCCTGTTTGCAGACATTTGA 521  
Db 214 GTTCAACACCATATACATGTACCGTTCAGGAAAGCTGACGATCCTCTTTGCCGACATCGT 273  
QY 522 GGGCTTCACGAGCTGGCATCCAGTGCAGTGCAGTGCAGGAGGAGCTGCTGCTGCTGCTGCTGCTGCT 581  
Db 274 GGGCTTTACCCAGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 333  
QY 582 GCTCTTTGCCGCTTTTGAAGCTGCTGCGGAGAAATCACTGCTGAGGATCAAGATCTT 641  
Db 334 GCTCTTTGCCGCTTTTGAAGCTGCTGCGGAGAAATCACTGCTGAGGATCAAGATCTT 393  
QY 642 GGGGAGCTGTTACTACTGTGTGTCAGGGGTGCGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 701  
Db 394 GGGCGAGTGTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 453  
QY 702 CTGTGTGAGATGGGGGTAGACATGATTGAGGCCATCTCGTGGTACGTGAGGTGACAGG 761  
Db 454 CTCCATCTCTCATGGGCTGGCCATGTGTGAGGCCATCTCGTATGTGCGGGAGAGAACCA 513  
QY 762 TGTGAATGTGAACATCGCGTGGGCATCCACAGCGCGCGCTGCACTGCGGCGCTCTCTTGG 821  
Db 514 GACTGGGTGGACATCGCTGTGGGGTGCACACGCGGACCGTCTGCTGGGGCGCTCTCTGGG 573  
QY 822 CTTGCGGAATGGCAGTTGATGTGTGTCGAATGATGTGACCTTGGCCAAACACCATGGA 881  
Db 574 CCAGAAAGCGCTGGCAGTAGGAGCTGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 633  
QY 882 AGCAGAAAGCGGCTGGCGGCATCCACATCACTCCGGCAACACTGCACTGCTGCTGCTGCTGCTGCTGCT 941  
Db 634 GCGCGCGGCATCCCTTGGGCGGTGCACATCTCCAGAGACCATGGATGGCTGCTGCTGCTGCTGCTGCTGCT 693  
QY 942 GGAATACGAAGTGGAGCCAGGCGGTGGTGGCAAGCCCAACCGGCTGCTCAAGAGGAGCA 1001  
Db 694 GGAGTTGATGTGGAGCCAGGCGATGGGCGCAGCCCTGTGATTTACCTAGAGAGAAGG 753  
QY 1002 CATTGAGACTTTCCTCATCTCTGGGCGCC-AGCCAGAAAGGAAAGAGAGAAAGGATGCT 1060  
Db 754 TATTGAACCTTACCTCATCTGCTTCCAAAGCCAGAGGTGAGAGAAACAGCCACCCAGAA 813  
QY 1061 TGCCCAAGCTGCGAGCGGAC 1079  
Db 814 TGGCCTCAATGGCTCGGCC 832

RESULT 8  
US-10-121-911-2  
; Sequence 2, Application US/10121911  
; Patent No. US20020164632A1

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; GENERAL INFORMATION:
; APPLICANT: Kpeller-Libermann, Rosana
; TITLE OF INVENTION: 21529, A NOVEL ADENYLATE CYCLASE
; FILE REFERENCE: 5800-47
; CURRENT APPLICATION NUMBER: US/10/121,911
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US/09/412,210
; PRIOR FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3518
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 21529 adenylate cyclase
; NAME/KEY: CDS
; LOCATION: (247)...(3480)
; US-10-121-911-2

Query Match      15.7%; Score 284; DB 9; Length 3518;
Best Local Similarity 56.4%; Pred. No. 1.4e-66;
Matches 617; Conservative 0; Mismatches 435; Indels 42; Gaps 3;

QY 6 CGTGGTCTGGGATCTGCGGCGAGTGCAGGTCGGGGGCGCTTCGCACGACAGCCGCG 65
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DB 528 CTTGGTATGGGTCGCGCTGTAGCGCTAGGCCACGCGCTTCCTGTTACCGGGGCGGTG 587
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QY 66 CAGCCCCCTCTCGCGGCTCTGCGTGCCTGTTCTTTGTATACATCGCATACGCTCCT 125
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 588 GAGGCGCTGGGACGAGTGTCTATTCTTCCTCGTCATCTTCACGGCGTATGCCATGCT 647
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QY 126 CCCCATCCGATCGGCGCTCCGCTCTCAGCGGCGTGGGCTCTCCACCTTCGATTTGAT 185
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DB 648 GCGCTTGGGATCGGGACGCGCGTGGGCGCTCGCTCCTCACTTCGCTATCGCT 707
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QY 186 CTTGGCTGGCACTT-----NACCGTGTGATGCTTCCCTG--GAAGCAGCT 233
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DB 708 GGTCTCGGGCTGTATTCTGGGCGACAGCGGACTCAGGCGCTGCATGCTGCCGCGAGTT 767
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QY 234 CGTGTCCAATGTGCTGTCTCTGCACCAACGTCATTAGCATCTGCACACACTATCC 293
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DB 768 GGCAGCAACGAGTGTCTGCTGCGGGAACGTCGCGAGGAGTGTACCAACAGGCGCT 827
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QY 294 AGCAGAGTGTCTCAGCGCGAGGCGCTTTTCAGGAGACCCGAGTGTACATCCAGGCGCGCT 353
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DB 828 GATGGAGCGCGCTGCGGGCCAGCTTCGCGGAGGCACTCAGCTCCCTGCACCTCACGCG 887
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 354 CCACCTGCAGCATGAGAAATCGGACGAGGAGCGGCTGCTGCTGCGTATGCCCCAGCA 413
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 888 GCGGCTGGACCGCAGGAAGAACCAAGAACACCTTCTCTTGTCCATCTCTCTGCTTA 947
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 414 CGTTGCCATGAGATGAAGAAGACATCAACACAAAAAAGAG----- 457
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 948 CCGCGCGGAGAGATGAAGCAGAGATCATGCGACGCGCTGCAGGACGAGGGGTACG 1007
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 458 -----ACATGTTCCACAAGATCTACATACAGAAGCATGACAAATGTACAGCAT 503
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1008 GCCAGAGAGCACTAACAACTTCCACAGCCTCTATGTCAAGAGGCAACCGAGGAGTCAGCGT 1067
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 504 CTTGTTTTCAGACATCAGGCGCTCACCGCTGGCATCCAGTGCAGTGCAGTGCAGGAGGCT 563
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1068 GCTGTATGCTGACATCGTGGCTTCACGCGGCTGGCCAGGAGTGTTCCTTAAGAGCT 1127
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 564 GGTCAATCACCTGAATCAGCTTTTGGCCGTTTGAAGCTGGCTCGGAGAAATCACTG 623
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1128 GGTGCTCATGCTCAATGAGCTCTTTGGCAAGTTTCGACCAAGATGCCAAGGAGCATGATG 1187
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 624 CTTGAGGATCAAGATCTTTGGGAGCTTTACTACTGTGTGTACAGGCTGCCGAGGCGCG 683
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1188 CATCGGATCAAGATCTCTGGGAGCTTTACTACTGTGTCTCTGGGCTGCCACTCTCACT 1247
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 1426 TGCATTGAATGGCTTAGGCATGATAAAAGCCATCGAGCAGTTCGTGCGAGGAGAA 1485  
Qy 763 GTCAATGTGAACATGCGCTGGGTCACACAGCGGCGGTGCACATGCGGCGTCTTGGC 822  
Db 1486 GAGATGTTGAACATGCGTGTGGGTTACACAGGGGACTGTCTGTGTGGCATCTTGGC 1545  
Qy 823 TTCCGGAATGGCAGTTCGATGTGTGTCCTCAATGATGTGACCTGCGCCCAACACATGGAA 882  
Db 1546 ATCAGGAGGTTTAAATTTGATGTGTGTCCTCAACAGGATGCACTTGGCTAATCTCATGGAG 1605  
Qy 883 GCAGGAAGCGGCGTGGCGCATCCACATCACTCGGGCAACACTGCAGTACTGAACGGG 942  
Db 1606 CAGCTGGGAGTGGCTGGCAAGTTTACATATCTAGGGCCACTGCAAAATACTTAGACGAC 1665  
Qy 943 GACTAGGAATGGAGCGAGCGGCTGTGTGCAAGCGC 978  
Db 1665 AGGTATGAATGAAGATGGGAGATTATTGAGCGC 1701

RESULT 10  
US-10-071-223-1  
; Sequence 1, Application US/10071223  
; Patent No. US20020137174A1  
; GENERAL INFORMATION:  
; APPLICANT: Storm, Daniel R.  
; APPLICANT: Hacker, Beth  
; APPLICANT: Tomlinson, James E.  
; APPLICANT: COR Therapeutics, Inc.  
; APPLICANT: University of Washington  
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL  
; TITLE OF INVENTION: CYCLASE  
; FILE REFERENCE: 44481-5029-02-US  
; CURRENT APPLICATION NUMBER: US/10/071,223  
; CURRENT FILING DATE: 2002-02-11  
; PRIOR APPLICATION NUMBER: 09/473,717  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: PCI/US98/13541  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/098,559  
; PRIOR FILING DATE: 1997-07-01  
; PRIOR APPLICATION NUMBER: 08/886,440  
; PRIOR FILING DATE: 1997-07-01  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4985  
; TYPE: DNA  
; ORGANISM: human type IX adenylyl cyclase  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (17)..(3898)  
US-10-071-223-1

Query Match 11.6%; Score 209.4; DB 12; Length 4985;  
Best Local Similarity 62.1%; Pred. No. 2.3e-46;  
Matches 330; Conservative 0; Mismatches 201; Indels 0; Gaps 0;  
Qy 426 GATGAAGAAGACATCAACACAAAAAGAGACATGTTCCACAAAGATCTACATACAGAA 485  
Db 1123 GAAGAAAAAGTCTCCATCAACAAAAAGCTCTATACCTTCGCGCTTTTAAGATGCACCA 1182  
Qy 486 GCATGACATGTCAGCATCTGTTTGCAGACATTTAGGGCTTACACGCTTGGCATCCCA 545  
Db 1183 GATCAAGAAGATGACATTTATTTTGCAGATATCTGGGCTTACCAAGATGAGTGCCAA 1242  
Qy 546 GTGCACTGCGGAGGCTGTGATGACCTGAATGAGCTCTTGCCTGGTTTGACAACT 605  
Db 1243 CAACTGCTCCACGCGCTTGGTGGTCTCTGAACGATCTGTGGTCTCGACCGCT 1302  
Qy 606 GGCTCGGAGAAATCACTGCCTGAGGATCAAGATCTTGGGGGACTGTCTACTACTGTGTCTC 665  
Db 1303 GTGTGAGGAGACCAAGTGTGAGAAAAATCAGCACCTTGGGAGACTTACTACTCGGTGGC 1362

Qy 666 AGGGCTGCGGAGCGCGGCGGACCATCCACATGCTGTGTGGAGATGGGGGTAGACAT 725  
Db 1363 GGGCTGTCCGAGCGCGGCGGACCATGCTTACTGCTGATCGAGATGGGCTGGGCAT 1422  
Qy 726 GATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATCGCGGTGG 785  
Db 1423 GATCAAGGCCATCGAGCAGTCTTCCAGGAGAAAGAGAGATGGTGAACATGAGAGTCGG 1482  
Qy 786 CATCCACAGCGGCGGCTGCACTGCGGGCTCTTGGCTTGGGAAATGCGACTTTCGATGT 845  
Db 1483 GGTGCACACGGGCGCGCTCTTTCGGGCATCTGGGCATGAGGAGGTTTAAATTTTCACT 1542  
Qy 846 GTGGTCCAATGATGTGACCTGCGCCCAACACATGAACGAGGAGCGGCTGGCGCGCAT 905  
Db 1543 GTGGTCCAACAGATGTAACCTGGCCCACTCATGAGCAGCTGGGAGTGGCGCGCAAGT 1602  
Qy 906 CCACATCACTCGGCAACACTGCACTGACCTGAACGGGACTACGAAGTGA 956  
Db 1603 TCACATTTCTGAGGCGCGCGCAAAATACTTAGATGACCGGTACGAATGGA 1653

RESULT 11  
US-09-751-100B-98  
; Sequence 98, Application US/09751100B  
; Patent No. US20020142436A1  
; GENERAL INFORMATION:  
; APPLICANT: Medical Research Council  
; TITLE OF INVENTION: Human Adenylyl Cyclase and Use Therefor  
; FILE REFERENCE: P27948A  
; CURRENT APPLICATION NUMBER: US/09/751,100B  
; CURRENT FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 98  
; LENGTH: 5515  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (539)..(4600)  
; OTHER INFORMATION:  
US-09-751-100B-98

Query Match 11.5%; Score 207.8; DB 10; Length 5515;  
Best Local Similarity 62.0%; Pred. No. 6.5e-46;  
Matches 329; Conservative 0; Mismatches 202; Indels 0; Gaps 0;  
Qy 426 GATGAAGAAGACATCAACACAAAAAGAGACATGTTCCACAAAGATCTACATACAGAA 485  
Db 1645 GAAGAAAAAGTCTTCCATCCAAAAAGCTCTATAGCTTCGCGCTTTTAAGATGCACCA 1704  
Qy 486 GCATGACATGTCAGCATCTGTTTGCAGACATTTAGGGCTTACACGCTTGGCATCCCA 545  
Db 1705 GATCAAGAAGTCAAGTATTTATTTTGCAGATATCTGGGCTTACCAAGATGAGTGCCAA 1764  
Qy 546 GTGCACTGCGGAGGCTGTGTCATGACCTGAATGAGCTCTTTCGCGGTTTGAACAAGCT 605  
Db 1765 CAAGTCGCGCCACGCGCTGGTGGGTCTCTTGAACGATCTGTTCGCTCGCTTCGACCGCT 1824  
Qy 606 GGCTCGGAGAAATCACTGCCTGAGAGTCAAGATCTTGGGGGACTGTGTACTACTGTGTCTC 665  
Db 1825 GTGTGAGGAGACCAAGTGTGAGAAAAATCAGCACCTTGGGAGACTGTACTACTACTCGGTGGC 1884  
Qy 666 AGGGCTCGGAGCGCGGCGGCGGACCATGCCACTGCTGTGTGAGATGGGGGTAGACAT 725  
Db 1885 GGGCTGTCCGAGCGCGCGGCGGACCATGCTCTGTGATGAGATGGGCGCTGGGCAT 1944  
Qy 726 GATTGAGGCCATCTCGCTGTTGAGGTGACAGGTGTGAATGTGAACATGCGCGGTGGG 785  
Db 1945 GATCAAGGCCATCGAGCAGTCTTCCAGGAGAAAGAGAGATGTTGAACATGAGAGTCGG 2004  
Qy 786 CATCCACAGCGGCGCGCTGCACTCGCGCTCTTGGCTTGGGAAATGGCGAGTTTCGATGT 845

Db 2005 GGTCACACGGCCGCTCTTGGCGCATCTTGGCGCATGAGGAGTTTAAATTTGACGT 2064  
Qy 846 GTGTCCAAATGATGTACCTTGGCCACACATGGAAGAGGAGCGGCTGGCCGCAT 905  
Db 2065 GTGTCCAAATGATGTAACTTGGCCAACTCTCATGAGCAGCTGGGAGTGGCCGGAAGT 2124  
Qy 906 CCACATCACTCGGCGCAACACTGACAGTACCTGAAAGGGGAGTACCAAGTGA 956  
Db 2125 TCACATTTCTGAGGCCACCGCAAAATACCTTAGATGACCGGTACGAAATGGA 2175

RESULT 12  
US-09-764-868-182  
; Sequence 182, Application US/09764868  
; Patent No. US2002016811A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PTZ32  
; CURRENT APPLICATION NUMBER: US/09/764,868  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1510  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 182  
; LENGTH: 330  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (272)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (285)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (289)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-764-868-182

Query Match 6.9%; Score 124.4; DB 9; Length 330;  
Best Local Similarity 64.2%; Pred. No. 5.3e-24;  
Matches 185; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

Qy 669 CTGCGCGAGCGCGGCGGCGGACCATGCCACTGCTGTGTGGAGATGGGGTAGACATGAT 728  
Db 1 GCTGCCACTCTCACTGCCAGACCATGCCATCAACTGCGTGGCGCATGGGCGCTGGACATGTG 60  
Qy 729 TGAGGCCATCTCGCTGTGTGAGGTGACAGGTGTGAATGTGAACATGCCGCGTGGCGAT 788  
Db 61 CKKGCCATAGAAACTGCGGGGAGCCACCTGGCGTGGACATCAACATGCGTGTGGCGGT 120  
Qy 789 CCACAGCGGCGCGTGCATCGGCGTCTTGGCTTGGGAAATGGCAGTTTCGATGTGTG 848  
Db 121 GCACCTCAGGCGAGCTACTGTGTGGAGTCACTCGGCTGCAGAAGTGGCAGTACGACGTTTG 180  
Qy 849 GTCCATATGATGTACCTTGGCCACACCATGGAAGCAGGAGCGGCGTGGCCGCATCCA 908  
Db 181 GTCACATGATGCATCACTGGTAAACCATGAGGAGCGGCGTGTACCGGGCGAGTGCA 240  
Qy 909 CATCACTCGGCGCAACACTGACGTACCTGAACGGGAGTACCAAGTGA 956  
Db 241 CATCACAGGGGTACCTTGGCCCTGCTGGCANGGCGTTATGCTGNGGA 288

RESULT 13  
US-09-989-442-71  
; Sequence 71, Application US/09989442  
; Publication No. US20030013649A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PJZ08  
; CURRENT APPLICATION NUMBER: US/09/989,442  
; CURRENT FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/214,886  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/217,487  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,758  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/220,963  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: 60/217,496  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,447  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/218,290  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/225,757  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/226,868  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/216,647  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: 60/225,267  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/216,880  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: 60/225,270  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/251,869  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: 60/235,834  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/234,274  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: 60/234,223  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: 60/228,924  
; PRIOR FILING DATE: 2000-08-30  
; PRIOR APPLICATION NUMBER: 60/224,518  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/236,369  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/224,519  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/220,964  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: 60/241,809  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/249,299  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/236,327  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/241,785  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/244,617  
; PRIOR FILING DATE: 2000-11-01  
; PRIOR APPLICATION NUMBER: 60/225,268  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/236,368  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/251,856  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: 60/251,868  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: 60/229,344  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/234,997  
; PRIOR FILING DATE: 2000-09-25

1	PRIOR FILING DATE:	2000-11-17
2	PRIOR APPLICATION NUMBER:	60/249,217
3	PRIOR FILING DATE:	2000-11-17
4	PRIOR APPLICATION NUMBER:	60/249,211
5	PRIOR FILING DATE:	2000-11-17
6	PRIOR APPLICATION NUMBER:	60/249,215
7	PRIOR FILING DATE:	2000-11-17
8	PRIOR APPLICATION NUMBER:	60/249,264
9	PRIOR FILING DATE:	2000-11-17
10	PRIOR APPLICATION NUMBER:	60/249,214
11	PRIOR FILING DATE:	2000-11-17
12	PRIOR APPLICATION NUMBER:	60/249,297
13	PRIOR FILING DATE:	2000-11-17
14	PRIOR APPLICATION NUMBER:	60/232,400
15	PRIOR FILING DATE:	2000-09-14
16	PRIOR APPLICATION NUMBER:	60/231,242
17	PRIOR FILING DATE:	2000-09-08
18	PRIOR APPLICATION NUMBER:	60/232,081
19	PRIOR FILING DATE:	2000-09-08
20	PRIOR APPLICATION NUMBER:	60/232,080
21	PRIOR FILING DATE:	2000-09-08
22	PRIOR APPLICATION NUMBER:	60/231,414
23	PRIOR FILING DATE:	2000-09-08
24	PRIOR APPLICATION NUMBER:	60/231,244
25	PRIOR FILING DATE:	2000-09-08
26	PRIOR APPLICATION NUMBER:	60/233,064
27	PRIOR FILING DATE:	2000-09-14
28	PRIOR APPLICATION NUMBER:	60/233,063
29	PRIOR FILING DATE:	2000-09-14
30	PRIOR APPLICATION NUMBER:	60/232,397
31	PRIOR FILING DATE:	2000-09-14
32	PRIOR APPLICATION NUMBER:	60/232,399
33	PRIOR FILING DATE:	2000-09-14
34	PRIOR APPLICATION NUMBER:	60/232,401
35	PRIOR FILING DATE:	2000-09-14
36	PRIOR APPLICATION NUMBER:	60/241,808
37	PRIOR FILING DATE:	2000-10-20
38	PRIOR APPLICATION NUMBER:	60/241,826
39	PRIOR FILING DATE:	2000-10-20
40	PRIOR APPLICATION NUMBER:	60/246,475
41	PRIOR FILING DATE:	2000-11-08
42	PRIOR APPLICATION NUMBER:	60/241,786
43	PRIOR FILING DATE:	2000-10-20
44	PRIOR APPLICATION NUMBER:	60/241,221
45	PRIOR FILING DATE:	2000-10-20
46	PRIOR APPLICATION NUMBER:	60/246,475
47	PRIOR FILING DATE:	2000-11-08
48	PRIOR APPLICATION NUMBER:	60/231,243
49	PRIOR FILING DATE:	2000-09-08
50	PRIOR APPLICATION NUMBER:	60/233,065
51	PRIOR FILING DATE:	2000-09-14

Best Local Similarity 54.2%; Pred. NO. 5.3e-24;  
Matches 185; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY	569	CTGTCGGAGGCCCCGGCCGACCACTGCCCATCTGCTGTGTGGAGATGGGGGTAGACATGAT	728
Db	1	GCTGCCACTCTCACTGCCAGACATGCCATCACTCGTCGCGATCGGCTGGACATGTG	60
QY	729	TGAGGGCATCTCCCTGCTGTCAGTGTCAGAGTGTGAATGTGAACATCGCGTGGGCAT	788
Db	61	CKKGGCCATCAGAAACTGGGGCAGCCACTGGCGTGGACATCAACATCGGTGTGGCGGT	120
QY	789	CCACAGGGGCGGTGCATCGGGCGCTTCCTTGGCTTTCGGGAAATGGCAGTTCGATGTGTG	848
Db	121	GCACCTCAGGCAGCGGTACTCTGTGGAGTCATCGGGCTGTCAGAAAGTGCAGTACGACCTTGT	180
QY	849	GTCCAATGATGTACCCCTTGCSCAACACATGGAAGCAGGAACCGGGCTGCCGCATCCA	908
Db	181	GTCAATGATGTCACTGGCTTACCACATGAGGAGCGCGGTGTACCAAGGCGAGTGCA	240
QY	909	CATCACTCGGGCAACACTGCAGTACTGAACGGGGACTACGAAGTGA	956
Db	241	CATCACAGGGGTACCTGCTGCCCTGCTGGCANGGGCTTATGCTGNGGA	288

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Query Match      4.4%  Score 79.2:  DB 9:  Length 11881;
Best Local Similarity 63.4%;  Pred. No. 5.2e-11;
Matches 137;  Conservative 0;  Mismatches 78;  Indels 1;  Gaps 1;

746  TACGTGAGGTGACAGGTGTGTAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCGTGC 805
QY  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
227  TCGGGCAGCCACTGGCGTGGACATCAACATGCGTGTGGCGTGCATTCAGGCAGCGTAC 286
Db  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
806  ACTCGGGGCTCTTGGGCTTCGGAATGGCAGTTCGATGTGTTCCCAATGATGTGACCC 865
QY  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
287  TGTGTGAGTCAATCGGCTGCAGAGTGGCAGTACGACGTTTGGTCACATGATGTCAAC 346
Db  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
866  TGGCCAAACCACATGGAAGCAGGAAAGCCGGGTGGCCG -CATCCAAATCACTCGGGCAACA 924
QY  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
347  TGGCTAAACCACATGGAGCAGCGCGTGTACCAGGGTGAAGCTAGGGCCCTAGGCAGCTA 406
Db  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
925  CTGCAGTACCTGAAGGGGACTACGAAGTGAGCCA 960
QY  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  407  CAGCAGAGGCCACCGGCCTACCACAGGCTGCCA 442

Search completed: March 1, 2003, 09:04:11
Job time : 106.396 secs

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 22:03:11 ; Search time 44.382 Seconds  
(without alignments)  
12520.796 Million cell updates/sec

Title: US-09-750-240-3  
Perfect score: 1812  
Sequence: 1 gttacgtggtctggcatt.....gcagctttctgaggtgttc 1812

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2.6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2.6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2.6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2.6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2.6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1812	100.0	1812	4	US-09-008-097-3
2	1808.4	99.8	3549	4	US-09-008-097-5
3	1763	97.3	4942	4	US-09-474-076-1
4	1519.8	83.9	4046	1	US-07-793-961A-1
5	1519.8	83.9	4046	1	US-08-240-357-1
6	1437.2	79.3	4131	3	US-08-726-214-11
7	895	49.4	4523	4	US-09-473-716-1
8	858.2	47.4	3924	3	US-08-726-214-9
9	436	24.1	3978	3	US-08-726-214-1
10	393.2	21.7	1652	3	US-08-726-214-17
11	335.6	18.5	4533	3	US-08-726-214-5
12	320.6	17.7	4601	3	US-08-726-214-15
13	311.2	17.2	5199	3	US-08-726-214-13
14	286	15.8	4008	3	US-08-307-896-5
15	286	15.8	4008	3	US-08-726-214-3
16	286	15.8	4008	5	PCT-US95-11808-5
17	284	15.7	3518	4	US-09-412-210-2
18	256.2	14.1	3357	3	US-08-726-214-7
19	216.8	12.0	4473	3	US-08-894-173-1
20	216.8	12.0	4473	4	US-09-398-193-1
21	209.4	11.6	4985	4	US-09-473-717-1
22	207.8	11.5	5515	4	US-09-398-193-98
23	73	4.0	7218	1	US-08-232-463-14
24	64.4	3.6	1259	2	US-08-997-080-123
25	64.4	3.6	1259	2	US-08-997-362-123
26	64.4	3.6	1259	4	US-09-095-855-123
27	64.4	3.6	1259	4	US-09-324-542-123

28	64.4	3.6	1259	4	US-09-205-426-123	Sequence 123, App
29	64.4	3.6	2013	2	US-08-997-080-176	Sequence 176, App
30	64.4	3.6	2013	2	US-08-997-362-176	Sequence 176, App
31	64.4	3.6	2013	4	US-09-095-855-176	Sequence 176, App
32	64.4	3.6	2013	4	US-09-324-542-176	Sequence 176, App
33	64.4	3.6	2013	4	US-09-205-426-176	Sequence 176, App
34	64.4	3.6	2172	2	US-08-997-080-173	Sequence 173, App
35	64.4	3.6	2172	2	US-08-997-362-173	Sequence 173, App
36	64.4	3.6	2172	4	US-09-095-855-173	Sequence 173, App
37	64.4	3.6	2172	4	US-09-324-542-173	Sequence 173, App
38	64.4	3.6	2172	4	US-09-205-426-173	Sequence 173, App
39	43	2.4	7218	1	US-08-232-463-14	Sequence 14, Appl
40	41.8	2.3	169	4	US-09-205-995-77	Sequence 77, Appl
41	41.8	2.3	190	4	US-09-205-995-77	Sequence 77, Appl
42	41.4	2.3	3784	1	US-07-623-033-1	Sequence 1, Appl
43	39.2	2.2	2028	4	US-09-634-920-1	Sequence 1, Appl
44	39.2	2.2	2734	3	US-09-135-021-79	Sequence 79, Appl
45	39.2	2.2	2821	4	US-09-135-010A-115	Sequence 115, App

## ALIGNMENTS

RESULT 1  
US-09-008-097-3  
; Sequence 3, Application US/09008097  
; Patent No. 6306830  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, H. Kirk  
; APPLICANT: Insel, Paul A.  
; APPLICANT: Ping, Peipei  
; APPLICANT: Post, Steven R.  
; APPLICANT: Gao, Meihua  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE  
; TITLE OF INVENTION: HEART FAILURE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/008,097  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dylan, Tyler M  
; REGISTRATION NUMBER: 37,612  
; REFERENCE/DOCKET NUMBER: 22000-20567.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1812 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 1...1812  
; OTHER INFORMATION:

US-09-008-097-3

Query Match	100.0%	Score 1812	DB 4	Length 1812
Best Local Similarity	100.0%	Pred. No. 0		
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QY	1	GTTAACTGGTGTGGGCATCTCGCGCAGTCGAGGTGGGGCGCTTTTCGCAGCAGAC	60	
DB	1	GTTAACTGGTGTGGGCATCTCGCGCAGTCGAGGTGGGGCGCTTTTCGCAGCAGAC	60	
QY	61	CCGCGCAGCCCTCTGGGGCCTCTGTHGCCCCCTGTGTTTGTATATACATCGCATACAG	120	
DB	61	CCGCGCAGCCCTCTGGGGCCTCTGTHGCCCCCTGTGTTTGTATATACATCGCATACAG	120	
QY	121	CTCTCTCCCATCCGATCGCGGCTCGCGTCTCAGCGCCCTGGGCCCTTCACCTTGAT	180	
DB	121	CTCTCTCCCATCCGATCGCGGCTCGCGTCTCAGCGCCCTGGGCCCTTCACCTTGAT	180	
QY	181	TTGATCTTGGCTGGCAACTTAAACCGTGGTGATGCTTCCTCTGGAACAGCTCGGTGCC	240	
DB	181	TTGATCTTGGCTGGCAACTTAAACCGTGGTGATGCTTCCTCTGGAACAGCTCGGTGCC	240	
QY	241	AATGTGCTGCTTCCCTCTGCACCAAGTCATTAGCATCTGCACACATATCCAGCAGAG	300	
DB	241	AATGTGCTGCTTCCCTCTGCACCAAGTCATTAGCATCTGCACACATATCCAGCAGAG	300	
QY	301	GTGTCTCAGCGCCAGGCTTTCAGGAGACCGCGAGTTACATCCAGGCCCGCTCCACCTG	360	
DB	301	GTGTCTCAGCGCCAGGCTTTCAGGAGACCGCGAGTTACATCCAGGCCCGCTCCACCTG	360	
QY	361	CAGCATGAGATCCGCGAGCAGGCGGTGCTGTGCGGTATTGCCCCAGCAGCTGCC	420	
DB	361	CAGCATGAGATCCGCGAGCAGGCGGTGCTGTGCGGTATTGCCCCAGCAGCTGCC	420	
QY	421	ATGAGATGAAAGAGACATCAACACAAAAAGAACATGTTCCACAAAGATCTACATA	480	
DB	421	ATGAGATGAAAGAGACATCAACACAAAAAGAACATGTTCCACAAAGATCTACATA	480	
QY	481	CAGAAGCATGACAATGTACAGATCCTGTTCGACACATTTGAGGCTTCACCAGCCTGGCA	540	
DB	481	CAGAAGCATGACAATGTACAGATCCTGTTCGACACATTTGAGGCTTCACCAGCCTGGCA	540	
QY	541	TCCAGTGCATCGCAGGAGCTGGTCATGACCTGAATGAGCTTTGCGCGGTTTGCAC	600	
DB	541	TCCAGTGCATCGCAGGAGCTGGTCATGACCTGAATGAGCTTTGCGCGGTTTGCAC	600	
QY	601	AAGCTGCTCGGAGATCACTGCTCAGGATCAAGATCTTGGGGACTGTTACTACTGT	660	
DB	601	AAGCTGCTCGGAGATCACTGCTCAGGATCAAGATCTTGGGGACTGTTACTACTGT	660	
QY	661	GTGTCAGGCTGCGGAGGCCCGGCGACCATGCCACTGCTGTGGAGATGGGGTA	720	
DB	661	GTGTCAGGCTGCGGAGGCCCGGCGACCATGCCACTGCTGTGGAGATGGGGTA	720	
QY	721	GACATGATTGAGGCATCTCGCTGCTAGTGAGTGACAGTGTGAATGTCAACATGGC	780	
DB	721	GACATGATTGAGGCATCTCGCTGCTAGTGAGTGACAGTGTGAATGTCAACATGGC	780	
QY	781	GTGGGCATCCACAGCGGCGCGTCACTGCGGCGCTCTTGGCTTTCGCGAAATGGCAGTTC	840	
DB	781	GTGGGCATCCACAGCGGCGCGTCACTGCGGCGCTCTTGGCTTTCGCGAAATGGCAGTTC	840	
QY	841	GATGTGTGTTCCATGATGTGACCCCTGGCCAAACACATGGAAGCAGGAAGCCGGCTGGC	900	
DB	841	GATGTGTGTTCCATGATGTGACCCCTGGCCAAACACATGGAAGCAGGAAGCCGGCTGGC	900	
QY	901	CGCATCCACATCACTCGGGCAACACTCGAGTACCTGAACGGGAGTACGAAGTGGAGCA	960	
DB	901	CGCATCCACATCACTCGGGCAACACTCGAGTACCTGAACGGGAGTACGAAGTGGAGCA	960	
QY	961	GGCGTGGTGGCAAGCGCAACCGGTACCTCAAGAGCAGCATTGTAGACTTTCCTCATC	1020	
DB	961	GGCGTGGTGGCAAGCGCAACCGGTACCTCAAGAGCAGCATTGTAGACTTTCCTCATC	1020	

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RESULT 2
US-09-008-097-5
: Sequence 5, Application US/090080975
: Patent No. 6306830
: GENERAL INFORMATION:
:   APPLICANT: Hammond, H. Kirk
:   APPLICANT: Insel, Paul A.
:   APPLICANT: Ping, Peipei
:   APPLICANT: Post, Steven R.
:   APPLICANT: Gao, Meihua
:   TITLE OF INVENTION: GENE THERAPY
:   TITLE OF INVENTION: HEART FAILURE
:   NUMBER OF SEQUENCES: 9
:   CORRESPONDENCE ADDRESS:
:   ADDRESSEE: MORRISON & FOERSTER

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STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/008,097  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Dylan, Tyler M  
REGISTRATION NUMBER: 37,612  
REFERENCE/DOCKET NUMBER: 22000-20567.21  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-813-5600  
TELEFAX: 650-494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3549 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1..3501  
OTHER INFORMATION:

US-09-008-097-5

Query Match 99.8%; Score 1808.4; DB 4; Length 3549;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TAAAGTGGTGGGATCTCGGGGAGTGCAGGTGGGGGCGCTTCGCGAGAGACC 62  
DB 636 TAAAGTGGTGGGATCTCGGGGAGTGCAGGTGGGGGCGCTTCGCGAGAGACC 695

QY 63 GCGCAGCCCTCTCGGGGCTCTGGTCCCTGCTGCTTGTATACATCGCATACAGCT 122  
DB 696 GCGCAGCCCTCTCGGGGCTCTGGTCCCTGCTGCTTGTATACATCGCATACAGCT 755

QY 123 CCTCCCATCGCATGGGGTGGCGCTCCTCAGCGGCTGGGGCTCTCCACCTTGCATTT 182  
DB 756 CCTCCCATCGCATGGGGTGGCGCTCCTCAGCGGCTGGGGCTCTCCACCTTGCATTT 815

QY 183 GATCTTGGCTGGCACTTAACGTGGTGTATGCTTCTGGAAGAGAGCTCGGTGCAA 242  
DB 816 GATCTTGGCTGGCACTTAACGTGGTGTATGCTTCTGGAAGAGAGCTCGGTGCAA 875

QY 243 TGTGCTGCTGCTCTGTCACCAAGTCATTAGCATCTGCACACACTATCCAGCAGAGT 302  
DB 876 TGTGCTGCTGCTCTGTCACCAAGTCATTAGCATCTGCACACACTATCCAGCAGAGT 935

QY 303 GTCTCAGCGCCAGGCTTTTTCAGGAGACCCGAGTTACATCCAGGCGGGCTCCACCTGCA 362  
DB 936 GTCTCAGCGCCAGGCTTTTTCAGGAGACCCGAGTTACATCCAGGCGGGCTCCACCTGCA 995

QY 363 GCATGAGAAATCGGAGAGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 422  
DB 996 GCATGAGAAATCGGAGAGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1055

QY 423 GGAGATGAAAGAGACATCAACAAAAAAGAGAGATGTTCCACAGATCTACATACA 482  
DB 1056 GGAGATGAAAGAGACATCAACAAAAAAGAGAGATGTTCCACAGATCTACATACA 1115

QY 483 GAAGCATGACAATGTCTAGCATCTCTGTTTGCAGACATTTGAGGGCTTACCAGCCTGGCATC 542  
DB 1116 GAAGCATGACAATGTCTAGCATCTCTGTTTGCAGACATTTGAGGGCTTACCAGCCTGGCATC 1175

QY 543 CCAGTGCACCTCGCAGAGAGCTGTCATGACCTCAATGAGCTCTTCCCGGTTTGACAA 602  
DB 1176 CCAGTGCACCTCGCAGAGAGCTGTCATGACCTCAATGAGCTCTTCCCGGTTTGACAA 1235

QY 603 GCTGGCTCGGAGAAATCACTGCTGAGATCAAGATCTTGGGGGACTGTTACTACTGTGT 662  
DB 1236 GCTGGCTCGGAGAAATCACTGCTGAGATCAAGATCTTGGGGGACTGTTACTACTGTGT 1295

QY 663 GTCAGGGCTGCGGAGGCGGGCGGACCATGCCCCACTGCTGTGTGGAGATGGGGGTAGA 722  
DB 1296 GTCAGGGCTGCGGAGGCGGGCGGACCATGCCCCACTGCTGTGTGGAGATGGGGGTAGA 1355

QY 723 CATGATTGAGGCCATCTGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATGCCGCT 782  
DB 1356 CATGATTGAGGCCATCTGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATGCCGCT 1415

QY 783 GGGCATCCACAGCGGGCGGCTGCTGCTGGGCTTCTTGGCTTGGGAAATGGCAGTTGGA 842  
DB 1416 GGGCATCCACAGCGGGCGGCTGCTGCTGGGCTTCTTGGCTTGGGAAATGGCAGTTGGA 1475

QY 843 TGTGTGTCCAAATGATGTGACCTTGCCCAACCATGGAAGCAGAGACCGGGCTGGCGC 902  
DB 1476 TGTGTGTCCAAATGATGTGACCTTGCCCAACCATGGAAGCAGAGACCGGGCTGGCGC 1535

QY 903 CATCCACATCACTCGGGCAACACTGCACTGCTGAAACGGGGACTACGAGTGGAGCCAGG 962  
DB 1536 CATCCACATCACTCGGGCAACACTGCACTGCTGAAACGGGGACTACGAGTGGAGCCAGG 1595

QY 963 CCGTGGTGGCAAGCGCAACGCTTACCTCAAGSAGCAGACATTTGAGACTTTCCTCATCCT 1022  
DB 1596 CCGTGGTGGCAAGCGCAACGCTTACCTCAAGSAGCAGACATTTGAGACTTTCCTCATCCT 1655

QY 1023 GGGCGCCAGCCAGAAAGAGAGAGAGGATGCTGGCCCAAGCTGCAGCGAGCTCG 1082  
DB 1656 GGGCGCCAGCCAGAAAGAGAGAGAGGATGCTGGCCCAAGCTGCAGCGAGCTCG 1715

QY 1083 GGCCAACTCCATGGAAGGCTGATCCCGGATGGGTTCCTGATGCTGCTTCTCCCGGAC 1142  
DB 1716 GGCCAACTCCATGGAAGGCTGATCCCGGATGGGTTCCTGATGCTGCTTCTCCCGGAC 1775

QY 1143 CAAGSAGCTCCAAAGGCTTCCGCCAGATGGGCAATGATGATTCAGAGAAAGACACCGGG 1202  
DB 1776 CAAGSAGCTCCAAAGGCTTCCGCCAGATGGGCAATGATGATTCAGAGAAAGACACCGGG 1835

QY 1203 CACCCAGATGCCCTGAACCTGAGGATGAGGTGGATGAGTTCTTGAGCCGTCGATCGA 1262  
DB 1836 CACCCAGATGCCCTGAACCTGAGGATGAGGTGGATGAGTTCTTGAGCCGTCGATCGA 1895

QY 1263 TGCCCGCAGCATTTGATCAGCTGCGGAAGGACCATGTTGGCGCGGTTTTGCTCACCCTTCA 1322  
DB 1896 TGCCCGCAGCATTTGATCAGCTGCGGAAGGACCATGTTGGCGCGGTTTTGCTCACCCTTCA 1955

QY 1323 GAGAGAGATTTTTCAGAAAGAGTACTCCCGGAAGGTGATCCCGCTTCGGAGCCCTAGCT 1382  
DB 1956 GAGAGAGATTTTTCAGAAAGAGTACTCCCGGAAGGTGATCCCGCTTCGGAGCCCTAGCT 2015

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DB 2016 TGCCTGTGCCCTGTGTGCTTCTGCTTCACTGCTGCTTCACTCAGCTTCTTAATTTTCCACA 2075

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QY 1503 GATCTGCTGTGTACTCTGCTGCTTCTGCTTCCCTAAGGCCCTGCAACCTGCTGTCCCG 1562  
DB 2136 GATCTGCTGTGTACTCTGCTGCTTCTGCTTCCCTAAGGCCCTGCAACCTGCTGTCCCG 2195

QY 1563 CAGCATTTGCTCGGCTCAGGGCAGATAGACCCGAGTTGGCATCTTTTCCGCTCTGCTGTGT 1622

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Db 2196 CAGCATTTGTCGCTCAGGGGACATAGCACCGAGTTGGCATCTTTTCGCTCCTGCTTGT 2255
QY 1623 GTTACTCTTGGCATTTGCCAATGTTACCTGTACCCACACACCCCATACGAGCTGTGC 1682
Db 2256 GTTACTCTTGGCATTTGCCAATGTTACCTGTACCCACACACCCCATACGAGCTGTGC 2315
QY 1683 AGCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCCACTGCAGCAGCTCAA 1742
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QY 1743 TTACTCTTGGGCTGGATGCTCCCTGTGTGAGGCGACCATGCCACCTGCAGCTTTCC 1802
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QY 1803 TGAGGTGTTT 1812
Db 2436 TGAGGTGTTT 2445

RESULT 3
US-09-474-076-1
; Sequence 1, Application US/09474076
; Patent No. 6465237
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; FILE REFERENCE: 44481-5028-01-US
; CURRENT APPLICATION NUMBER: US/09/474,076
; PRIORITY FILING DATE: 1998-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4942
; TYPE: DNA
; ORGANISM: human type VI adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(3648)
US-09-474-076-1

Query Match 97.3%; Score 1763; DB 4; Length 4942;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1788; Conservative 0; Mismatches 20; Indels 3; Gaps 1;

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QY 65 GCAGCCCCCTCTGGGGCCCTCTGGTCCCTGTGTCTTGTATATACATCGCATACAGCTCC 124
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QY 125 TCCCCATCCGCATCGGGGCTGCGCTCTCAGGGGCTGCGGCTCTCCACCTTGCATTTGA 184
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QY 365 ATGAGAATCGGAGCAGGAGCGGCTGCTGCTGTGGTATTTGCCCCAGCAGCTTGCATGG 424
Db 1142 ATGAGAATCGGAGCAGGAGCGGCTGCTGCTGTGGTATTTGCCCCAGCAGCTTGCATGG 1201
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Db 1262 AGAAGCATGACAATGTGACATCTCTTTTSCAGACATTTGAGGGCTTTTACCAGCGCTGGCAT 1321
QY 542 CCCAGTGCATCGCGAGGAGCTGGTCATGACCTTGAATGAGCTCTTTGCCCGGTTTGACA 601
Db 1322 CCCAGTGCATCGCGAGGAGCTGGTCATGACCTTGAATGAGCTCTTTTGCCCGGTTTGACA 1381
QY 602 AGCTGGCTGCGGAGAAATCACTGCCTGAGGATCAAGATCTTTGGGGACTCTTACTACTGTG 661
Db 1382 AGCTGGCTGCGGAGAAATCACTGCCTGAGGATCAAGATCTTTGGGGACTCTTACTACTGTG 1441
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Db 1442 TGTGAGGCTCGCGAGGCGCGGCGGCGACCATGCCACTGCTGTGTGGAGATGGGGGTAG 1501
QY 722 ACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTAATGTGAACATCGCGG 781
Db 1502 ACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTAATGTGAACATCGCGG 1561
QY 782 TGGGATCCACAGCGGCGCTGCATCGCGGCTCTCTTGGCTTTCGGAATAGCAGTTTCG 841
Db 1562 TGGGATCCACAGCGGCGCTGCATCGCGGCTCTCTTGGCTTTCGGAATAGCAGTTTCG 1621
QY 842 ATGTGTGTTCATGATGTGACCTTGGCCCAACACATGGAAGAGAAAGCCGGGTGGCC 901
Db 1622 ATGTGTGTTCATGATGTGACCTTGGCCCAACACATGGAAGAGAAAGCCGGGTGGCC 1681
QY 902 GCATCCACATCACTCGGGCAACACTGCATGCTGAACGGGACTACGAGGTGGAGCCAG 961
Db 1682 GCATCCACATCACTCGGGCAACACTGCATGCTGAACGGGACTACGAGGTGGAGCCAG 1741
QY 962 GCCGTGGTGGCAAGCGCAACGCTCACTCAAGGAGCAGCACATTTGAGACTTTCTCATCC 1021
Db 1742 GCCGTGGTGGCAAGCGCAACGCTCACTCAAGGAGCAGCACATTTGAGACTTTCTCATCC 1801
QY 1022 TGGGCGCCAGCCAGAAACGGAAGAGGAGGATGCTGGCCAAAGCTGCAGCGGACTC 1081
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QY 1082 GGGCCAACTCCATGGAAGGGCTGATGCCCGGATGGTTCCTGATCGTGGCTTCTCCCGA 1141
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QY 1142 CCAAGGACTTCCAAAGGCTTTCGCGCAGATGGGCAATTTGATATCCAGCAAGACAACCGG 1201
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QY 1202 GCACCCAAAGATGCCCTGAACCTTGAGGATGAGTGGATGAGTTCCTGAGCCCGTGCATCG 1261
Db 1982 GCACCCAAAGATGCCCTGAACCTTGAGGATGAGTGGATGAGTTCCTGAGCCCGTGCATCG 2041
QY 1262 ATGCCCGCAGCATTTGATCAGCTGCGGAGGACCATGTCGCCCGGTTTTCCTCACCCTTC 1321
Db 2042 ATGCCCGCAGCATTTGATCAGCTGCGGAGGACCATGTCGCCCGGTTTTCCTCACCCTTC 2101
QY 1322 AGAGAGAGATTTTGAAGAAGAGTACTCCCGGAAGGTGATCCCGCTTCGAGGAGCTACG 1381
Db 2102 AGAGAGAGATTTTGAAGAAGAGTACTCCCGGAAGGTGATCCCGCTTCGAGGAGCTACG 2161
QY 1382 TTGCTGTGCCCTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCCAC 1441
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QY 542 CCCAGTGCACCTGCGCAGGAGCTGCTCATGACCTGAATGAGCTCTTTGCCCGCTTTGACA 601  
Db 1302 CCCAGTGCACCGCGCAGGAGCTGCTCATGACCTGAACGAGCTCTTCCGCCGCTTTGACA 1361  
QY 602 AGCTGGCTGCGGGAATCATCTGCTGAGGATCAAGATCTTTGGGGAGCTGTTACTACTGTG 661  
Db 1362 AGCTGGCTGCGGGAATCATCTGCTGAGGATCAAGATCTTTAGGGAGCTGTTACTACTGTG 1421  
QY 662 TGTGAGGCTGCGGAGGCGCGGCGCAGCACCATGCCACTGCTGTGTGAGATGGGGTAG 721  
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QY 722 ACATGATTGAGGCGCATCTGCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 781  
Db 1482 ACATGATTGAGGCGCATCTGCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1541  
QY 782 TGGCATCCACAGCGGCGCGGCGCAGCACCATGCCACTGCTGTGTGAGATGGGGTAG 841  
Db 1542 TGGCATCCACAGCGGCGCGGCGCAGCACCATGCCACTGCTGTGTGAGATGGGGTAG 1601  
QY 842 ATGTGTGCTCAATGATGTGACCTGCGCAGCACCATGCCACTGCTGTGTGAGATGGGGTAG 901  
Db 1602 ACGTGTGCTCAATGATGTGACCTGCGCAGCACCATGCCACTGCTGTGTGAGATGGGGTAG 1658  
QY 902 GCATCCACATCACTCGGCGCAGCACCATGCCACTGCTGTGTGAGATGGGGTAG 961  
Db 1659 GCATCCACATCACTCGGCGCAGCACCATGCCACTGCTGTGTGAGATGGGGTAG 1718  
QY 962 GCGTGTGCTCAATGATGTGACCTGCGCAGCACCATGCCACTGCTGTGTGAGATGGGGTAG 1021  
Db 1719 GCGTGTGCTCAATGATGTGACCTGCGCAGCACCATGCCACTGCTGTGTGAGATGGGGTAG 1778  
QY 1022 TGGCGCGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1081  
Db 1779 TGGCGCGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1838  
QY 1082 GGGCGCACTCCATGGAAGGCTGATGCGCGGAGTGGTTCCTGATGCTGCTGCTGCTGCTG 1141  
Db 1839 GGGCGCACTCCATGGAAGGCTGATGCGCGGAGTGGTTCCTGATGCTGCTGCTGCTGCTG 1898  
QY 1142 CCAAGGAGCTCCAGGCGCTCCGCGCAGATGGCATGATGATGATGATGATGATGATGATG 1201  
Db 1899 CCAAGGAGCTCCAGGCGCTCCGCGCAGATGGCATGATGATGATGATGATGATGATGATG 1958  
QY 1202 GCACCAAGATGCGCTGGAACCTGAGGATGAGTGGATGAGTGGATGAGTGGATGAGTGG 1261  
Db 1959 GTGCCCAAGATGCGCTGGAACCTGAGGATGAGTGGATGAGTGGATGAGTGGATGAGTGG 2018  
QY 1262 ATGCCCGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1321  
Db 2019 ATGCCCGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2078  
QY 1322 AGAGAGGAGATTTGAGAAGAGTACTCCGCGAGGAGTGGATCCCGGCTCGGAGCTTACG 1381  
Db 2079 AGAGAGGAGATTTGAGAAGAGTACTCCGCGAGGAGTGGATCCCGGCTCGGAGCTTACG 2138  
QY 1382 TTGCTGTGCGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1441  
Db 2139 TTGCTGTGCGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2198  
QY 1442 ACTCCACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1501  
Db 2199 ACTCCACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2258  
QY 1502 TGATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1561  
Db 2259 TGATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2318  
QY 1562 GCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1621  
Db 2319 GCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2378  
QY 1622 TGTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1681

Db 2379 TGTTCACCTTGCATCGCAACATGTTACCTGTAAACACACACCCCATCCGGACCTGTG 2438  
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Db 2439 CAGCCCGGATGCTGAATTTAAACACCTGCTGACATCACTGCTGCCACTGCGAGAGCTCA 2498  
QY 1742 ATTACTCTCTGGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1801  
Db 2499 ATTACTCTCTGGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2558  
QY 1802 CTGAGTGTTC 1812  
Db 2559 CTGAGTGTTC 2569  
  
RESULT 6  
US-08-726-214-11  
; Sequence 11, Application US/08726214  
; Patent No. 610706  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Wei-Jen  
; APPLICANT: Gilman, Alfred G.  
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYL CYCLASE  
; TITLE OF INVENTION: AND USES THEREFOR  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/726,214  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/005,498  
; FILING DATE: 04-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L.  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: UTSD:450  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4131 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-726-214-11

Query Match 79.3%; Score 1437.2; DB 3; Length 4131;  
Best Local Similarity 87.5%; Pred. No. 0;  
Matches 1584; Conservative 0; Mismatches 223; Indels 3; Gaps 1;  
  
QY 5 ACCTGGTGTCTGGGATCTCTGGCGCAGTGCAGGTCGGGGGGCTTTGCGACGACACCGGC 64  
Db 687 ATGTGGTCTGGGATCTCTAGCAGCGCTGCAAGTTCGGGGGTGCGCTGCGACCAACCCAC 746  
QY 65 GCAGCCCTCTGGGGGCTCTGGTGGCTCTGTTCTTTGTATACATCGCATACACGCTCC 124  
Db 747 GCAGCCCTCTGAGCAGGCTTTGGTGGCCCGCTGTTCTTCGTCTACATCACCTACACTTC 806  
QY 125 TCCCATCCGATGCGGGCTCCCGTCTCTCAGCGGCTGGGCTCTCCACCTTGCATTTGA 184

Db 807 TTCCCATTCGATGCGAGCGCGTCTCAGTGGCCCTGGGTCTTTCCACCCCTGCATTTGA 866  
QY 185 TCTTGGCCCTGGCAACTAAACCGTGGTGATGCTTCTCTCTGGAAGCAGCTCGGTGCCAATG 244  
Db 867 TTTTGGCCCTGGCATCTCAACATGGTGAGCCCTTCTCTTGGGAAGCAGCTCGGTGCTAAGC 926  
QY 245 TGTGCTGTCTCTCTGACCAACGTCATTAGCATCTGCACACACTATCCAGCAGAGGTCT 304  
Db 927 TGGTGCTCTCTCTGACCAATGCATCGGTCTGTCAGCAGCACTACCCCGCTGAAGTCT 986  
QY 305 CTCAGCGCCAGGCTTTTCCAGAGAACCCGAGATTACATCCAGGCGCGGTCTCCACCTGCACG 364  
Db 987 CTCAGCGCCAGGCTTTTCCAGAGAACCCGAGATTACATCCAGGCGCGGTCTGCACCTGCAGC 1046  
QY 365 ATGAGAAATCGGAGCAGGAGCGGCTGCTGCTGCTGGTATTGCCCCAGCAGCTTGCCATGG 424  
Db 1047 ATGAGAAATCGAGCAGGAGGAGCGGCTGCTGCTGCTGGTATTGCCCCAGCAGCTTGCCATGG 1106  
QY 425 AGATGAAAGAGACATCAACACAAAAAAGAGAC---ATGTTCCACAAGATCTACATAC 481  
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QY 482 AGAAGCATACAAATGTCAGCATCTCTGTCAGACATTCAGGCGCTTCCAGCGCTGGGCAT 541  
Db 1167 AGAAGCATACAAATGTCAGCATCTCTGTCAGACATTCAGGCGCTTCCAGCGCTGGGCCT 1226  
QY 542 CCAGTGTCACTGCGCAGGAGCTGGTGCATGACCTGTAATGAGCTCTTTGCGCGGTTTGACA 601  
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QY 602 AGCTGCTCGGAGAAATCACTGCCTGAGATCAAGATCTTTGGGGACTGTTACTACTGFG 661  
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QY 662 TGTGAGGCTCGCGAGGCGCGGCGGACCATGCCACTGCTGCTGTGGAGATGGGGGTAG 721  
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QY 722 ACATGATGAGGCGCATCTCGCTGGTACGTGAGGTGACAGGTGTAATGTAACATCCGGG 781  
Db 1407 ACATGATGAGGCGCATCTCGCTGGTACGTGAGGTGTAATGTAACATGCGCGG 1466  
QY 782 TGGCATCCACAGCGGCGCGCTGCATCGCGGCTCTTGGCTTGGCGAAATGGCAGTTGCG 841  
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QY 962 GCGGTGGTGGCAAGCGCAACCGGTACTCAAGAGCAGACATGAGACTTTCTCTCATCC 1021  
Db 1647 GCGGTGGTGGCAAGCGCAACCGGTACTCAAGAGCAGTGCATGAGACTTTCTCTCATAC 1706  
QY 1022 TGGGCGCCAGCAGCAAAACGGAAGAGGAGAAAGGATGCTGCCAGCTGCGAGCGACTC 1081  
Db 1707 TAGGAGCCAGCAGCAAAACGGAAGAGGAGAAAGGATGCTGCCAGCTGCGAGCGAGCG 1766  
QY 1082 GGGCCAACTCCATGGAAGGCTGATGCCCGCATGGGTCTCTGATGCTGCTTCTCCCGGA 1141  
Db 1767 GGGCCAACTCCATGGAAGGACTGATGCCCGCTGGGTCTCTGACCGTGCCTTCTCCCGGA 1826  
QY 1142 CCAAGACTCCAAAGGCTTTCCCGCAGATGGGCATTTGATGATTTCCAGCAAGAACCCGGG 1201  
Db 1827 CCAAGGACTCTTAAGGCTTTCCGACAGATGGGCATCGATGACTCTAGCAAGAGAACCCGGG 1886  
QY 1202 GCACCCAGATGCCCTGACCTGAGGATGAGGTGATGATGATGATGATGATGATGATGATG 1261

Db 1887 GTGCCCAAGATGCTCTGAACCCCTGAGGATGAGTGGACGAGTTTCTGGGCCGAGCCATCG 1946  
QY 1262 ATGCCCGCAGCATGATCAGCTGCGAAGCAGCATGTGTGCGCGGTTTTTGTCTCACCTTCC 1321  
Db 1947 ATGCCCGAAGCATGACACAGCTGCGTAAGAACCATGTGCGCGGTTCTCTGCTCACCTTCC 2006  
QY 1322 AGAGAGAGATTTTGAAGAAAGTACTCTCCGGAAGTGGATCCCGCTTTTCGGAGCGCTACG 1381  
Db 2007 AGAGGAGGATCTCAGAGAAGATTTACAGGAAGATAGACCCCTCGTTTCGGAGCGCTACG 2066  
QY 1382 TTGCTGTGCCCTGTGGTCTTCTGCTCTGCTCATCTGCTTCATCCAGCTTCTAAATTTCCAC 1441  
Db 2067 TCGCTGTGCCCTGTGGTCTTCTGCTCTGCTCATCTGCTTCATCCAGTTCCTCTGATTTCCAC 2126  
QY 1442 ACTCCACCCGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTTAATCACCCTGTC 1501  
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QY 1502 TGATCTGTCTGTACTCTCTGCTGCTTCTCTTCCCTAAGGCCCTTGCAACCTGTCTGTCC 1561  
Db 2187 TCATCTGTCTGTCTCTCTGCTGCTTCTTCCCAACCGCTTGACAGCGCTGTCC 2246  
QY 1562 GCAGCATGTCTCGCTCAGCGGCACATGACACCGCAGTTGGGATCTTTTCCGCTCTGCTTGG 1621  
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QY 1622 TGTTTACTTCTGCCATTTGCCAATGTTTCCACCTGTAAACCACACACCCCATACGAGCTG 1681  
Db 2307 TGTTCATCTCTGCCATTTGCCAATGTTTCCACCTGTCCAGTGCACACCCCATGAGGACTG 2366  
QY 1682 CAGCCCGGATGCTGAATTTAAACACCTGCTGACATCAGCTGCCCTGCCACCTGACAGCTCA 1741  
Db 2367 CCGCCCGGATGCTGAATTTAAACACCTGCTGACATCAGCTGCCACCTGACAGCTCA 2426  
QY 1742 ATTACTCTCTGGGCTGGATGCTCCCTGTGTGAGGCGACCATGCGCACCTGCAGCTTTC 1801  
Db 2427 ATTACTCTCTGGGACTGGAAGCTCCCTGTGTGAGGCGACCCACCCACCTGCAGCTTTC 2486  
QY 1802 CTGAGGTGTT 1811  
Db 2487 CTGAGTACTT 2496

RESULT 7  
US-09-473-716-1  
; Sequence 1, Application US/09473716  
; Patent No. 6436672  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, James  
; APPLICANT: Cor Therapeutics, Inc.  
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL  
; FILE OF INVENTION: CYCLASE  
; FILE REFERENCE: 44481-5027-01-US  
; CURRENT APPLICATION NUMBER: US/09/473,716  
; CURRENT FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: PCT/US98/13540  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/070,901  
; PRIOR FILING DATE: 1997-07-01  
; PRIOR APPLICATION NUMBER: 08/886,362  
; PRIOR FILING DATE: 1997-07-01  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4523  
; TYPE: DNA  
; ORGANISM: human type V adenylyl cyclase  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (139)..(3921)  
US-09-473-716-1

Query Match 49.4%; Score 895; DB 4; Length 4523;



Best Local Similarity 69.8%; Pred. No. 2.4e-229;  
Matches 1277; Conservative 0; Mismatches 525; Indels 27; Gaps 4;

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QY 65 GCAGCCGCTCTGCGGGGCTCTGGTGGCCCTGTGTTCTTTGTATACATCGCATACAGTCC 124
Db 1106 GCAGCGCTCTGAGGCGCTCTGGTGGACCGGTGTTCTTCACTACACCATCTACAGGTCG 1165
QY 125 TCCCATCGGATCGGGGCTCGCTCTCAGCGGCTTGGGCTCTCCACCTTGCATTGA 184
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QY 902 GCATCCACATCACTCGGGCAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 961
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QY 1138 - - -CGACCAAGAGACTTCCAAAGCCTTCCGCCAGATGGGATGGGATGATGATGATGATGATG 1189
Db 2186 ACCTGGGTGGCAACAGGTGTCCAAGGAGATGAAGCGGATGGCTTGAAGACCCCA - - - 2242
QY 1190 AAGACACCGGGGACCCAGATGCCCTGGAACCTGAGGATGAGGTGATGATGATGATGATGATG 1249
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QY 1610 CCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1669
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QY 1670 TACGAGCTGTCAGCGCGGATGCTGATTTTAAACACCTGCTGACATCACTGCTGCTGCTGCTGCTGCTG 1729
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QY 1730 TGCAGCAG - - -CTCAATTACTCTGCGGCTGAGTGTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1783
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Db 2840 GGGCCAACTGCAACTTCCCGAGTACTTC 2868
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RESULT 8  
US-08-726-214-9  
; Sequence 9, Application US/08726214  
; Patent No. 6107076  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Wei-Jen  
; APPLICANT: Gilman, Alfred G.  
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE  
; TITLE OF INVENTION: AND USES THEREFOR  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P. O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/726,214  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/005,498

FILING DATE: 04-OCT-1995

ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L.

REGISTRATION NUMBER: 37,642

REFERENCE/DOCKET NUMBER: UTSD:450

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 3924 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-726-214-9

Query Match 47.4%; Score 858.2; DB 3; Length 3924;  
Best Local Similarity 68.6%; Pred. No. 1.5e-219;  
Matches 1254; Conservative 0; Mismatches 548; Indels 27; Gaps 4;

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QY 65 GCAGCCCTCTCGGGCCCTGTGGCCCTGTCTCTTTATATACATCGATACACGCTCC 124
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 481 GCAGCCCTCTCGAGGACATCTGTGTGACCGGTGTCTTCATCATCATCATACACCTCC 540
QY 125 TCCCATCCGCGATCGGGGTGGCGTCTCAGGGGCGCTGGGCGCTCTCCACCTTGCATTGA 184
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D 541 TGCCTGTGCGATAGAGGCTGCGGTGCTCAGCGGGGTGCTTCTGTGCGGCTCTCCACTTG 600
QY 185 TCTTGGCTTGGCACTTAACGTGGTGTGATGCTTCTCTGGAAGCAGCTGGTGCCAATG 244
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QY 245 TGTCTGTGTTCTCTGCACCAACGCTCATTTAGCATCTGCACACACTATCCAGCAGAGTCT 304
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QY 305 CTCAGCGCAGGCTTTTCCAGGACCCGAGTTATACATCCAGGCGCGGCTCCACCTGCAGC 364
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QY 365 ATGAGATCGGAGCAGGAGGCTGCTGCTGCTGGTATGTCCTGATGAGCAGTGGCATGG 424
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QY 425 AGATGAAGAAGACATCAACAAAAAAGAGA---CATGTTCCAAAGATCTACATAC 481
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D 841 AGATGAACAGCAGCATCAACGCAACAGAGAGATATGATGTTCCAAAGATTTATATCC 900
QY 482 AGAAGCATGACATGTGACATCTCTGTTTTCAGACATTTGAGGCTTTCCAGGCTGGCAT 541
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QY 542 CCCAGTGCAGTGGCAGGAGCTGGTCACTGACCTGATGAGCTCTTTGGCCGGTTTGACA 601
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QY 842 ATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 901
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D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 1501 GAAACAACTCCATTTGGACACAACTCCGCTTCACTGGGGAGCTGAGCGCCCTTCTACA 1560
QY 1138 -----CGGACCAAGGACTCCAGGCGCTTCCGCGAGATGGGCAATGATGATTCAG 1189
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 1561 ACTTGGGTGGCAACAGGTGTCCAGGAATGAAGAGGATGGGCTTTGAGGACCCCA--- 1617
QY 1190 AAGACAACCGGGGCGCACCAAGATGCCCTGAACCCCTGAGGATGAGGTGGATGCTTCTGA 1249
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 1618 ---AGGACAAGAATGCCAGGAAAGTGCCACCCCTGAGGATGAAGTGGAGGAGTTCTG 1674
QY 1250 GCGGTGCCATCATGCCCGCAGCATGTAGTACGTGGGGAAGACCATGTGCGCGGTTT 1309
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 1675 GTCGAGCCATCATGCCAGGAGTATTGACAGACTTGGCATCCGAAACAGTCCGAAAGTTC 1734
QY 1310 TGTCACTTCCAGAGAGAGGATTTTGAAGAAGTACTCCCGGAAGTGGATCCCGCT 1369
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 1735 TCTTGNACCTTAGGNGGCCGACTTAGAGAGAAAGTACTCCAAAGCAGGTGGATGACCGAT 1794
QY 1370 TCGAGGCTTACGTTGCTGTGCCCTGTGGTCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 1429
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 1795 TTGGTGCCTTATGTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1854
QY 1430 TAATTTCCACACATCCACCTTGTGCTTGTGGATTTATGCCAGCATCTTCTGCTGCTG 1489
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 1855 CCATGTGCGCCACCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1914
QY 1490 TAATCACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1549
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 1915 CTTGGTGTGTTTATATCTGTGATCTAGCCTGTGTGAGCTCTTCCCTACTCCCTGCT 1974
QY 1550 AAGCTGTGTCGCGCAGCATTTCCGCTCAGGGCAGCATATGACACCGCAGTTGGCATCTTT 1609
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
D 1975 AGACACTCTCCAGGAAGATAGTGGATCCAAAGAAGAACAGCCCTGCTGCTGCTGCTGCT 2034
QY 1610 CCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1669
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QY 1670 TACGAGCTGTGCAGCGCGGATGCTGAATTTTAAACACCTGCTGACATCACTGCTGCTG 1729
D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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Query Match 21.7%; Score 393.2; DB 3; Length 1652;

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; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726.214
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/005.498
; FILING DATE: 04-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UIUSD:450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4533 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-726-214-5

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Query Match	18.5%;	Score	335.6;	DB	3;	Length	4533;
Best Local Similarity	63.6%;	Pred.	No. 7.6e-80;				
Matches 534;	Conservative	0;	Mismatches	284;	Indels	12;	Gaps
QY	220	CTCTGAAGACGCTGGTCCCAATCGCTGCTGTCTCTCGACACAGTCATTAGCATC	279				
DB	1030	CTGCTGAGGGAGATCTGGCTAACGCTCTTCTACCTGTGGCCATCATCTGGGGATC	1089				
QY	280	TGCACACATCTCCACGACGAGTGTCTCAGCGCCAGGCTTTTCAGGAGACCCGAGTTAC	339				
DB	1090	ATGTCTACTACATGSCAGACCGTAAAGCACCGAAAGGCTTCTCTGGAGGCCCGCAGTCG	1149				
QY	340	ATCCAGGCCGCGCTCCACTGCGACATCAGATCGGACGACGAGCGCTGCTCTGCTCG	399				
DB	1150	CTGGAGTGAAATGATCTGGAGAGCAGACCCACGACGACGAGAAACCTTATGCTTTCC	1209				
QY	400	GTATTGCCCCGACGCTTGCCATGGAGATGAAGAGACATCAACACA	447				
DB	1210	ATCTCTCCAAAGCATGTGGCTGACGACATGTTTGAAGGACATGAAGAAGATGAGAGTCAG	1269				
QY	448	AAAAAAGAGACATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATCTCG	507				

1270 AAGGACGAGCAGTTCACACCATGTACATGTACCGCATGAGAATGTCAGCATCCTG 1329  
508 TTTCAGACATTTAGGCGCTTACCAGCCTGGCATCCAGTGCATCGGAGGAGCTGGTC 567  
1330 TTTCAGATATTTGGCGCTTACCAGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1389  
568 ATGACCCCTGAATGAGTCTTTGGCGGCTTTCACAAAGCTGGCTGGGAGATCACTGCTG 627  
1390 AAGCTACTCAACGAGCTTTTGGCGGCTTTGACAAAGCTGGCGGCAATACACAGCTG 1449  
628 AGATCAAGATCTTTGGGGGACTGTTACTACTGTGTGTCAGGCTGGCGGAGCCGCGGC 687  
1450 AGATCAAGATCTTAGCGGACTGTTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1509  
688 GACCATGCCACATGCTGTGTGGAGATGGGGGTAGACATGATTGAGCCCATCTGCTGGTA 747  
1510 GACCATGCCATGCTGTGTGGAGATGGGGGTAGACATGATTGAGCCCATCTGCTGGTA 1569  
748 CGTGAGGTGACAGGTGTGAATGTGAACATCGCGGTGGGATCCACAGCGGCGCTGCAC 807  
1570 CGGAGAGACCAAGACCGGAGTGGACATCGGTGTGGGGTGCACACAGGACTGTGCTA 1629  
808 TGGCGGCTCTTGGCTTGGCGAATAGGACATTCGATGTGTGGTCCCAATGATGTACCCCTG 867  
1630 GGTGGGCTCTTGGCGGAGAGCGTGGCAGTATGATGTGTGTACCGATGTCACTGTG 1689  
868 GCAACACATGAGACGAGGAGCGGCTGGCGGATCCACAGCGGCGCTGCAC 927  
1690 GCAACAGATGAGGCTGGCGGATCCACAGCGGCGGTGCACATTTCCAGAGACCATG 1749  
928 CAGTACCTGAACGGGACTACGAGTGGAGCGGCGGTGGGAGCGGCGGTGCACAGCGCTAC 987  
1750 GACTGCTGAAGGGAGTTCGATGTGCAACCTGGTTCATGCTGGCAGTCTGCTGGACTAC 1809  
988 CTCAGGAGCAGCAGATTTGAGACTTTGCTCATCTGCTGGCGGCGGAGGAGGAGGAG 1047  
1810 CTAGATGAGAGGGGATCGAAGCTACCTCATCTGCTTCCCAAGCGGAGAGGTGAAGAAG 1869

RESULT 12

US-08-726-214-15

Sequence 15, Application US/08726214

Patent No. 610706

GENERAL INFORMATION:

APPLICANT: Tang, Wei-Jen

APPLICANT: Gilman, Alfred G.

TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE

TITLE OF INVENTION: AND USES THEREFOR

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P. O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: United States of America

ZIP: 77210

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/726,214

FILING DATE: Concurrently Herewith

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/005,498

FILING DATE: 04-OCT-1995

ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L.

REGISTRATION NUMBER: 37,642

REFERENCE/DOCKET NUMBER: UTSD:450

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 4601 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-726-214-15

Query Match 17.7%; Score 320.6; DB 3; Length 4601;  
Best Local Similarity 59.5%; Pred. No. 7.8e-76;  
Matches 567; Conservative 0; Mismatches 374; Indels 12; Gaps 1;

QY 79 GGCTCTGGTGGCTGTGTTCTTTGTATATACATCGCATACAGCTCCCTCCCATCCGCGATG 138  
DB 1575 GGCATAGGCTACGTGCTTTTACACCTCTCGCCACCTACAGCATGCTTCGCTGCTCTC 1634  
QY 139 CGGCTGCTGCTCCTCAGCGGCTGGGCTCTCCACCTTGCATTTGATCTTTGGCTGGCAA 198  
DB 1635 ACCTGGGCAATCTTGGCGGCTGGGCAATCTTGTGCAAGTCACACTTCAGTGCCTC 1694  
QY 199 CTTAACCGTGGTGTGATGCTTCTCTTGGAGCAGCTCGGTGCCAATGTGCTGTCTCCTC 258  
DB 1695 ATACCCAGACTAGCGGTCTTTTCCATCAACAGGCTCTGCCAGGTGGTCTCTTCATG 1754  
QY 259 TGACACCACTCATATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGC 318  
DB 1755 TGCATGAATACAGCAGCATCTTTCATCAGTTACCTTTTCAGACCGCGCCAGCGCAGGC 1814  
QY 319 TTTTCAGGAGACCGCAGTGTACATCCAGCGCGCTCCACCTGCAGCATGAGAAATCGGCAG 378  
DB 1815 TTCTTGAGAGACCGGAGGTGTGTGGAGCCAGGCTCGCTCGGAGCAGAGAACCAAGA 1874  
QY 379 CAGGAGCGGTGCTGTGCTCGGTATTGCCCCAGCAGCTTGCCTATGGAGATGAAGAAGAC 438  
DB 1875 CAGGAGCGGTGCTGTGCTCTCTGCTCCCGAGGTTTCTGCTCTAGAAATGATCAATGAC 1934  
QY 439 ATCAACACAAAAAAGAG-----ACATGTTCCACAGATCTACATACACAAG 486  
DB 1935 ATGACCAATGTGGAGGAGCAGCAGCTCAGCATCAGTTCCACCGCATCTCATCATCGC 1994  
QY 487 CATGACAATGTCAAGCATCTCTTGGAGCATTTGAGGCTTTCACAGCCTGGCATCCAG 546  
DB 1995 TAGGAGACCTCAGTATCTTTTGGAGATGTCAAAGATTTACCAACCTCTCTACGACC 2054  
QY 547 TGCACTGCGCAGGAGCTGTGATGACCTGAATGAGCTCTTTGCCCGGTTTGAACAAGTG 606  
DB 2055 TTGCTGCTCAGGAGCTTGTCAAGGATGCTCAAGCAGCTCTTTCAGATTTGATCGGCTG 2114  
QY 607 GCTGCGGAGAAATCACTGCTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGCA 666  
DB 2115 GCGCATGAGCATCTCTTTCGATTTAAATCTCGGGGAGCTGCTACTACTGTGTGCTCA 2174  
QY 667 GGGTGGCGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 726  
DB 2175 GGACTGCTGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2234  
QY 727 ATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATCGCGGCTGGG 786  
DB 2235 ATCAAAACTATCAGGTTTGTGAGGTCCAGAACGAGCATGATGTTGACATGCGAAATTTGA 2294  
QY 787 ATCCACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 846  
DB 2295 ATCCATTCAGGCTCTGCTGT 2354  
QY 847 TGGTCCAATGATGTGACCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 906  
DB 2355 TGGTCTTGGGATGTGGACATCGCAAAACAACTTGAATCTGGAGGAATCCCTGGGAGAAAT 2414  
QY 907 CACATCACTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 966

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QY	339	CATCCAGGCCCGGCTCCACCTGCAGCATGGAATCGGCAGCAGGAGGGGTGCTGCTGTC	398
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QY	399	GGTATTGCCCCAGCACGTTGCCATCGAGATGAAAAGAACATCA-----	442
Db	804	CTTGCTGCCAGCTCACATGCCATCGAGATGAAGCTGAAATCATTCAGAGGCTGCAGGG	863
QY	443	-----ACACAATAAAGAAGACATGTTCCACAAGATCTACATACAGAAGCA	488
Db	864	CCCCAAGCAGGACAGATGCGRAAACACAAACAACATCCACAATCTGTATGTCAAACGACA	923
QY	489	TGCAATGTCAGATCCTGTTTGACAGCATTTAGAGGGCTTACCAGCCTTGGCATCCCAAGT	548
Db	924	CACCAAGCTGAGCATATTATAGCGTGACATTTGTGGCTTCCACCGCCTTGCAGCGATTG	983
QY	549	CACTGGCAGGAGCTGGTCAACACCTGAATGAGCTCTTTGCCGGTTTGCACAAGCTGGC	608
Db	984	CTCCCCCTGGCACTGGTCCACATGCTGAATGAACCTCTTTGGGAAGTTTGATCAATAGC	1043
QY	609	TGCGGAGATCACTGCCTGAGGATCAAGATCTTGGGGACTGTTACTACTGTGTGCAGG	668
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QY	669	GCTGCCGAGGCCCGGGCGGACCATGCCCACTGCTGTGAGATGGGGGTAGACATGAT	728
Db	1104	GCTCCCTATATCACTCCCTTAACCATGCCAAGAACTGTCTGAAATGGGATTTGGATATGTG	1163
QY	729	TGAGGCACTCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGCAT	788
Db	1164	CGNAGCCATAAGAAGATGAGGATGCTACCGGAGTTGATATCAACATGCGGTGATAGAGT	1223
QY	789	CCACAGCGGGCGGTGCATCGCGGCTCCTTGGCTTCGGAAATGGCAGTTTCGATGTG	848
Db	1224	GCATTTCTGGGAAGCTTCTCTGTGGTGTGATTGGTCTCAGAAGTGGCATGTATGTGTG	1283
QY	849	GTCCAATGATGTGACCTTGGCCAAACCATGGAACGACGAAGCGGGCTGSCCCGATCCA	908
Db	1284	GTCTCATGATGTACTCTGGCAACCAATGGAAGCTGGAGAGTCCCTGGCGGTGTTC	1343
QY	909	CATCACTCGGGCAACACTGCATCTAAACGGGACTTACGAAGTGGAGCCAGCCGCTGG	968
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RESULT 15

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US-08-726-214-3
; Sequence 3, Application US/08726214
; Patent No. 6107076
; GENERAL INFORMATION:
; APPLICANT: Tang, Wei-Jen
; APPLICANT: Gilman, Alfred G.
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 21:13:01 ; Search time 3111.21 Seconds  
(without alignments)  
16949.756 Million cell updates/sec

Title: US-09-750-240-3  
Perfect score: 1812  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
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- 17: em.hum.\*
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- 40: em.htgo.mus.\*
- 41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1812	100.0	1812	6	AR174472	AR174472 Sequence
2	1812	100.0	1812	6	AX189759	AX189759 Sequence
3	1808.4	99.8	3549	6	AR174473	AR174473 Sequence
4	1808.4	99.8	3549	6	AX189761	AX189761 Sequence
5	1763.4	97.3	3552	6	AX189766	AX189766 Sequence
6	1763	97.3	6463	9	AF250226	AF250226 Homo sapi
7	1657.8	91.5	3582	6	AX189768	AX189768 Sequence
8	1604.2	88.5	5877	9	AB007882	AB007882 Homo sapi
9	1527.8	84.3	4046	4	DOGADENCYC	M94968 Canis fami
10	1519.8	83.9	4046	6	I29958	I29958 Sequence 1
11	1449.4	80.0	3465	10	MUSADNLNLCYC	M96653 Mus musculu
12	1437.2	79.3	4131	6	AR106659	AR106659 Sequence
13	1437.2	79.3	4131	10	RATADCYB	M96160 Rattus norv
14	1431.8	79.0	5841	6	AX305965	AX305965 Sequence
15	1431.8	79.0	5841	10	MUSADCYC	M93422 Mouse adeny
16	1427.6	78.8	6036	10	RATADC	L01115 Rattus norv
17	906.2	50.0	4995	4	OCMRADCYV	Z29371 O.cuniculus
18	886.6	48.9	4545	4	DOGADNCYC	M88649 Canis fami
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20	858.2	47.4	4847	10	RATADCYA	M96159 Rattus norv
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22	799	44.1	3137	6	AX418303	AX418303 Sequence
23	798	44.0	2554	9	AK093840	AK093840 Homo sapi
24	780	43.0	4236	5	GGA293817	AJ293817 Gallus ga
25	667.2	36.8	2429	4	DOGADCYC	M97896 Canis fami
26	436	24.1	3978	4	BOVADC	M25579 Bovine aden
27	436	24.1	3978	6	AR106654	AR106654 Sequence
28	415.2	22.9	2857	10	AF053980	AF053980 Mus muscu
29	404	22.3	3811	6	AX418306	AX418306 Sequence
30	393.2	21.7	1652	6	AR106662	AR106662 Sequence
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33	339	18.7	3563	9	AB011083	AB011083 Homo sapi
34	339	18.7	4080	9	AK027857	AK027857 Homo sapi
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37	335.6	18.5	4533	6	AR106656	AR106656 Sequence
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39	333.2	18.4	3674	10	AF458089	AF458089 Mus muscu
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42	320.6	17.7	4901	10	MMU85021	U85021 Mus musculu
43	318.2	17.6	2496	9	AK093706	AK093706 Homo sapi
44	316.6	17.5	3243	6	AX463632	AX463632 Sequence
45	316.6	17.5	6196	6	AX463638	AX463638 Sequence

ALIGNMENTS

RESULT 1	AR174472	Sequence 3 from patent US 6306830.	1812 bp	DNA	linear	PAT 17-DEC-2001
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DEFINITION	AR174472					
ACCESSION	AR174472					
VERSION	AR174472.1	GI:17914792				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 1812)					
AUTHORS	Hammond,H.Kirk., Insel,P.A., Ping,P., Post,S.R. and Gao,M.					
TITLE	Gene therapy for congestive heart failure					
JOURNAL	Patent: US 6306830-A 3 23-OCT-2001;					
FEATURES	Location/Qualifiers					

source	1. .1812	/organism="unknown"
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ORIGIN		
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Best Local Similarity	100.0%;	Pred. No. 0;
Matches 1812; Conservative	0;	Mismatches 0; Indels 0; Gaps
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Db 1	GTTAACGTGTTGCGGCATCCTCGCGGCAGTCAGGTCGGGGCGCGCTTTTCGACGACAGAC 60	
Qy 61	CCGCGCAGCCCTCTCGGGGCTCTGTCGCCCTGTGTCCTTTGTATACATCGCATACAG 120	
Db 61	CCGCGCAGCCCTCTCGGGGCTCTGTCGCCCTGTGTCGCCCTGTGTCCTTTGTATACATCGCATACAG 120	
Qy 121	CTCCTCCCCATCCGCATGCGGGTCGCCGTCTCAGCGGCTGGGCGCTCTCCACCTTTGCAT 180	
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Qy 241	AATGTGCTGCTGTTCCTCTGCACCAACGTCATTAGCATCTGCACACATATCCAGCAGAG 300	
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Qy 301	GTGTCTCAGGCCAGGCGCTTTCAGGAGACCCGCGAGTTTACATCCAGGCGCGGCTTCCACCTG 360	
Db 301	GTGTCTCAGGCCAGGCGCTTTCAGGAGACCCGCGAGTTTACATCCAGGCGCGGCTTCCACCTG 360	
Qy 361	CAGCATGAGATCGGCAGCAGGAGCGGCTGCTGCTGCTGATNTGCCACAGAGTTGCC 420	
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Db 421	ATGGAGATGAAAGAAGACATCAACACAAAAAAGAGACATGTTCCACAGAGTCTACATA 480	
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Db 481	CAGAAGCATGACAATGTTCAGCATCCTGTTTGCAGACATTCAGGGCTTCCACGCGCTGGCA 540	
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AUTHORS Hammond, H.K. and Gao, M.  
TITLE Gene therapy for congestive heart failure  
JOURNAL Patent: WO 0148164-A 3 05-JUL-2001;  
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)

FEATURES Location/Qualifiers  
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source /organism="Homo sapiens"  
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BASE COUNT 361 a 539 c 507 g 405 t  
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Query Match 100.0%; Score 1812; DB 6; Length 1812;  
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DEFINITION Sequence 5 from patent US 6308830.  
ACCESSION AR174473  
VERSION AR174473.1 GI:17914793

KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 3549)  
AUTHORS Hammond, H. Kirk., Insel, P. A., Ping, P., Post, S. R. and Gao, M.  
TITLE Gene therapy for congestive heart failure  
JOURNAL Patent: US 6306830-A 6 23-Oct-2001;  
FEATURES Location/Qualifiers  
source 1..3549 /organism="unknown"  
BASE COUNT 699 a 1025 c 1061 g 764 t  
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DEFINITION Sequence 5 from Patent WO0148164.  
ACCESSION AX189761  
VERSION AX189761.1 GI:15143135  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 3549)  
AUTHORS Hammond H.K. and Gao M.  
TITLE Gene therapy for congestive heart failure  
JOURNAL Patent: WO 0148164-A5 05-JUL-2001  
FEATURES  
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)  
Location/Qualifiers  
1..3549  
source /organism="Homo sapiens"  
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ORIGIN  
Query Match 99.8%; Score 1808.4; DB 6; Length 3549;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION AF250226
ACCESSION AF250226
VERSION AF250226.1 GI:9049782
KEYWORDS
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 6463)
AUTHORS Wicker,R., Catalan,A.G., Cailleux,A., Starenki,D., Stengel,D.,
Sarasin,A. and Suarez,H.G.
TITLE Cloning and expression of human adenylyl cyclase type VI in normal
thyroid tissues
JOURNAL Biochim. Biophys. Acta 1493 (1-2), 279-283 (2000)
MEDLINE 20435313
PUBMED 10978539
REFERENCE 2 (bases 1 to 6463)
AUTHORS Wicker,R., Gascon Catalan,A., Cailleux,A.-F., Starenki,D.,
Stengel,D., Sarasin,A. and Suarez,H.G.
TITLE Direct Submission
JOURNAL Submitted (28-MAR-2000) Lab Etude des Relations - Instabilite
genetique et Cancer UPR 2169, Institut de Recherches sur le Cancer
CNRS IFR 1221, 7 rue Guy Moquet, Villejuif 94801, France
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VERSION AX189768.1 GI:15143140  
KEYWORDS synthetic construct.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 3582)  
AUTHORS Hammond, H. K. and Gao, M.  
TITLE Gene therapy for congestive heart failure

JOURNAL Patent: WO 0148164-A 12/05-JUL-2001;  
THE-REGENTS-OF-THE-UNIVERSITY-OF-CALIFORNIA (US)  
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REFERENCE	1		
AUTHORS	Ishikawa, K., Nagase, T., Nakajima, D., Seki, N., Ohira, M., Miyajima, N., Tanaka, A., Kotani, H., Nomura, N. and Ohara, O.		
TITLE	Prediction of the coding sequences of unidentified human genes. VIII. 78 new cDNA clones from brain in which code for large proteins in vitro		
JOURNAL	DNA Res. 4 (5), 307-313 (1997)		
MEDLINE	98116655		
PUBMED	9455477		
REFERENCE	2 (bases 1 to 5877)		
AUTHORS	Ohara, O.		
TITLE	Direct Submission		
JOURNAL	Submitted (06-OCT-1997) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail: cdnainfo@kazusa.or.jp. Tel: +81-438-52-3913; Fax: +81-438-52-3914)		
COMMENT	On May 9, 2002 this sequence version replaced gi:2887418. Sequence updated (05-Jan-1998).		
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## RESULT 9

## DOGADENCYC

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## FEATURES

## source

## BASE COUNT

## ORIGIN

## Query Match

## Best Local Similarity

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## Conservative

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## Gaps 2;

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M94968.1 GI:163896

adenyllyl cyclase type VI.

Canis familiaris cardiac muscle cDNA to mRNA.

ORGANISM

Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Canidae; Canis.

1 (Bases 1 to 4046)

Katsushika, S., Chen, L., Kawabe, J., Nilakantan, R., Hainon, N.J.,

Honey, C.J., and Ishikawa, Y.

Cloning and characterization of a sixth adenyllyl cyclase isoform:

types V and VI constitute a subgroup within the mammalian adenyllyl

cyclase family

Proc. Natl. Acad. Sci. U.S.A. 89 (18), 8774-8778 (1992)

92409599

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Location/Qualifiers

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Pred. No. 0;

Mismatches 157; Indels 6; Gaps 2;

QY 5 ACGTGGTGTGGGATCTTGGGCGGAGTTCAGGTTGGGGGTCCTTGGCAGCAACCCCG 64

Db 762 ACGTGGTGTGGGATCTTGGGCGGAGTTCAGGTTGGGGGTCCTTGGCAGCAACCCCG 821

QY	65	GCAGCCCTCTGGGGCCTCTGGTGCCTCTGTGTTCTTTGTATACATCGCATACACGCTCC	124
Db	822	GCAGCCCTCTGTGGCCCTCTGGTGCCTGTGTTTTTGTCTACATCACCTTACACGCTCC	881
QY	125	TCCCAATCGCATGGGGCTGCCGTCCTCAGCGGCTGGGCTCTCCACCTTGCATTGA	184
Db	882	TACCAATCGCATTGGGGCAGCTGTCTTCAATGGCTCTGGGCTGTCCACCTCGATTGA	941
QY	185	TCTTGGCCTGGCAACTTAACCGTGGTGTATGCTTCTCTGGAAGCAGCTCGGTGCCAATG	244
Db	942	TCITTGGCTGGCAACTCAACCGCGGTGAGCCTTCTCTGGAAGCAGCTCGGTGCCAACA	1001
QY	245	TGCTGCTGTCTCTGCACCAACGCTANTAGATCTGCACACACTATCCAGCAGAGGTGT	304
Db	1002	TGCTGCTGTCTCTGCACCAACGCTANTTGGCATCTGCACACACTATCCAGCTGAGGTCT	1061
QY	305	CTCAGCGCAGGCCTTTCAGGAGACCCGAGTTACATCCAGCGCGGCTCCACTGCAGC	364
Db	1062	CTCAGCGCAGGCCTTTCAGGAGACCCGCGTTACATTGAGCCCGGCTGCACCTGCCAG	1121
QY	365	ATGAGAATCGGACGAGGCGGCTGCTGCTCGGTATTGCCCCAGCACGTTGCCATGG	424
Db	1122	ATGAGAACCGCAGCAGBAACGCTGCTGCTCGTGTGCGCTGTGCCCCAGCATTTGCCATGG	1181
QY	425	AGATGAAGAAGACATCAACACAAAAAAGAGAC- --ATGTTCCACAAGACTTACATAC	481
Db	1182	AGATGAAGAAGATATCAACACAAAAAAGAGACATGATTCCACAAGACTTACATCC	1241
QY	482	AGAAGCATGACATGTCAGCATCTCTGTTTGCAGACATTGAGGGCTTCACAGCCTGGCAT	541
Db	1242	AGAAGCATGACATGTCAGCATCTCTGTTTGCAGACATTTGAAGGCTTCACAGCCTGGCGT	1301
QY	542	CCCAGTGCACCTGGCGAGGAGCTGGTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACA	601
Db	1302	CCCAGTGCACCGCGCAGAGCTGGTCATGACCCCTGAACGAGCTCTTGCCCGGTTTGACA	1361
QY	602	AGCTGCTGGGAAGATCACTGCCTGAGGATCAAGATCTTGGGGAGCTGTTTACTACTGTG	661
Db	1362	AGCTGCTGGGAAGATCACTGCCTGAGGATCAAGATCTTAGGGGACTGTTTACTACTGTG	1421
QY	662	TGTCAGGCTCGCGAGGCGCCGGCGGACCATGCCACTGCTGTGTGGAGATGGGGTAG	721
Db	1422	TGTCAGGCTCGCGAGGCGCCGGCGGAGACCATGCCCCACTGCTGTGTGGAGATGGGGTAG	1481
QY	722	ACATGATTGAGGCCATCTCGCTGGTAGCTGAGGTGACAGGTGTGAATGTGAACATGCGCG	781
Db	1482	ACATGATCAGGCCATCTCGCTGGTGGCTGAGGTGACAGGTGTGAACGTGAACATGCGCG	1541
QY	782	TGGGCATCCACAGCGGGCGGTGCACACTCGGGCGTCCCTTGGCTTGGGAAATGCGAGTTGC	841
Db	1542	TGGGCATCCACAGCGGGCGGTGCACACTGTGTGTCTTGGCTTCGGAAATGCGAGTTGC	1601
QY	842	ATCTGTGTCCAATGATGTGACCTTGGCCACCCACATGGAAGCAGGAGCCGGGCTGGCC	901
Db	1602	ACGTGTGGTCCAATGATGATGCTTGGCCACCCATATGGAGGCGG- --CCGGGCGGGCC	1658
QY	902	GCATCCACATCACTCGGGCAACACTGCACTACTCAACGGGGACTTACGAAGTGGAGCCAG	961
Db	1659	GCATCCACATCAACCGGGCCAGCTGTGACACTCTGAACGGGGACTACGAGTGGAGCCGG	1718
QY	962	GCCGTGTGGCAAGCGCAACCGGTACCTCAAGGAGCAGCATTTGAGACTTTCTCATCC	1021
Db	1719	GCCGCGTGGCAGCGCAACCGGTACCTCAAGGAGCAGCATCGAGACCTTCTCATCC	1778
QY	1022	TGGGCGCCAGCAAGAACCGGAAGAGGAAAGGCATCTGGCCAGCTGCAGCGGACTC	1081
Db	1779	TGGGAGCCAGCAAGAACCGGAAGAGGAGGCCATCTGSCCAAGCTGCAGCGGAGCG	1838
QY	1082	GGCCAACTCCATGGAAGGCTGTATCCCGCATGGTTCTTGATCTGCTCTCCCGGA	1141
Db	1839	GGCCAACTCCATGGAAGGCTGTATGCCACGCTGGGTGCCCGACCGGCTTCTCCCGGA	1898
QY	1142	CCAAGGACTCCAAGGCTTTCGCCAGATGGGCATTGATGATTCCAGAAAGCAACCGGG	1201

Db	1899	CCAAGGACTCCAAGGCTTTCCGCCAGATGGGCATTGATGATTCACGAAAGACAAACCGGG	1958
Qy	1202	GCACCCAAAGATGCCCTGAACCCCTGAGGATGAGGTGGATGAGTTCCTGAGCCGTCGCCATCG	1261
Db	1959	GTGCCCAAGATGCCCTGAACCCCGAGGATGAGGTGATGATGAGTTCCTGGCCGCTGCCATCG	2018
Qy	1262	ATGCCCGCAGCATTTGATCATCAGCTGCGGAAGGACCATGTGCGCCGGTTTTGTGTCACTTCCTC	1321
Db	2019	ATGCCCGCAGCATCGATCAGCTACGGAAGGACCATGTGCGCCGTTCTGTGTCACTTCCTC	2078
Qy	1322	AGAGAGAGGATTTTGAGAAGAAGTACTCCGGAAGGTGGATCCCGCTTCGGAGCCCTACG	1381
Db	2079	AGAGAGAGGATTTTGAAAAGAAGTACTCAAGGAAGGTGGACCCCGCTTCGGAGGCCCTACG	2138
Qy	1382	TTGGCTGTGCCCTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCAC	1441
Db	2139	TGGCTGTGGCTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTCTCTGCTCTCCAC	2198
Qy	1442	ACTCCACCCCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTAATACCGTGC	1501
Db	2199	ACTCAACCGTGATGCTTGGGATCTACGCCAGTATCTTTGTGCTGTTGCTGATCAACCGTGC	2258
Qy	1502	TGATCTGTGCTGTGTACTCCTGTGGTTCCTGTTCCCTAAGGCCCTGCAAGCTGTGTCC	1561
Db	2259	TGACCTGTGCCGTGTACTCCTGTGGCTCTCTCTCCCAAGGCCCTGGAGCTCTTTCCC	2318
Qy	1562	GCAGCATTTGTCGCTCACGGGCATAGCAGCGAGTTGGCATCTTTTCGCTCTGCTGTG	1621
Db	2319	GCAGCATGTGCCCTCTCGGGGCACAGACACATGTGGTGGCATTTTTCAGTCTGTGTAG	2378
Qy	1622	TGTTTACTTCTGCGATTGCCAATGTTCCACCTGTAAACCACACCCCCCATACGGAGCTGTG	1681
Db	2379	TGTTCACTCTGCGCATCGCAACATGTTCACTGTAAACCACACCCCCCATCCGGACCTGTG	2438
Qy	1682	CAGCCCGGATGCTGAATTTAACAACCTGCTGACATCAGTGCCTGCCACCTGCAGCAGCTCA	1741
Db	2439	CAGCCCGGATGCTGAATGTAACACCGCTGACATCAGTGCCTGCCACCTGCAGCAGCTCA	2498
Qy	1742	ATTACTCTCTGGCCCTGGATGTCCTCCTGTGTGAGGGACCATGCCACCTGCAGCTTTC	1801
Db	2499	ATTACTCTCTGGCCCTGGATGTCCTCCTGTGTGAGGGCACCGCACCTGTCGAGCTTCC	2558
Qy	1802	CTGAGGTGTTTC	1812
Db	2559	CTGAGTACTTC	2569

[illegible]

Db 762 ACCTGGTGTGGGATCCTGCGACGGCTCAGGTTGGGGTGGCCCTGGCAGCCAAACCC 821  
QY 65 GCAGCCCTCTGCGGGGCTCTGGGTGCCCTCTGGTCTTTGTATACATGCATACACGCTCC 124  
Db 822 GCAGCCCTCTGTGGGCTCTGGTGGCCCTGTGTTTTTGTCTACATCACCTACACGCTCC 881  
QY 125 TCCCCATCCGATCGGGCTGCCCTCTCAGCGCCCTGGGCTCTCCACCTTGCAATTTGA 184  
Db 882 TACCCATCCGATCGGGGAGCTCTCTCAGTGGCCCTGGGCTCTCCACCCCTGCATTTGA 941  
QY 185 TCTTGGCTGCAACTTAAACCGTGGTGTATGCCTTCCCTTGAAGCAGCTGGTGCCCAATG 244  
Db 942 TCTTGGCTGGCACTCAACCGGGTGACGCCCTTCCCTTGAAGCAGCTCGTGCCCAACA 1001  
QY 245 TGCTGTGTTCTCTGCACCAACGTCTATTAGCATCTGCACACACTATCCAGCAGAGTGT 304  
Db 1002 TGCTGTGTTCTCTGCACCAACGTCTATTGSCATCTGCACACACTATCCAGCTGAGTCT 1061  
QY 305 CTCAGCCCGAGGCTTTTCAGGAGACCCGCGATTTACATCCAGGCGCGGCTCCACCTGCAGC 364  
Db 1062 CTCAGCCCGAGGCTTTTCAGGAGACCCGCGGTTTACATTCAGGCGCGGCTGCACCTGCAG 1121  
QY 365 ATGAGAATCGCAGCAGGCGGCTGCTGTGTCGGTATTGCCCGACGACGTTTGCCATGG 424  
Db 1122 ATGAGAACCGCAGCAGGAGCGCTGCTGTCCGTGTTGCCCGACATGTTGCCATGG 1181  
QY 425 AGATGAAGAGAGCATCAACACAAAAAAGAGAC ---ATGTTCCCAAGATCTACATAC 481  
Db 1182 AGATGAAGAGAGATATCAACACAAAGAAAGACATGATGTTCCCAAGATCTACATCC 1241  
QY 482 AGAAGCATGACATGTCAGCATCTCTGTTTCAGACATTTAGGCGTTTACCAGCGCTGCAT 541  
Db 1242 AGAAGCATGACATGTCAGCATCTCTGTTTCAGACATTTAGGCGTTTACCAGCGCTGCAT 1301  
QY 542 CCCAGTGCACCTGCGCAGGAGCTGTCATGACCTGATGAGCTCTTTGCCCGGTTTGACA 601  
Db 1302 CCCAGTGCACCGCAGGAGCTGTCATGACCTGAAAGAGCTCTTCGCGCCGGTTTGACA 1361  
QY 602 AGCTGGCTGCGGAGATCACTGCTGAGGATCAAGATCTTTGGGGGACTGTTACTACTGTG 661  
Db 1362 AGCTGGCTGCGGAAATCACTGCTGAGGATCAAGATCTTTAGGGACTGTTACTACTGTG 1421  
QY 662 TGTGAGGCTGCGCGAGGCGCGGCGACCATGCCACTGCTGTGTGGAGATGGGGTAG 721  
Db 1422 TGTGAGGCTGCGCGAGGCGCGGCGAGACCATGCCACTGCTGTGTGGAGATGGGGTAG 1481  
QY 722 ACATGATTGAGGCATCTCGCTGCTGATGAGTGAGTGAGTGAAATGTGAACATCGCG 781  
Db 1482 ACATGATGAGGCATCTCGCTGCTGATGAGTGAGTGAGTGAAATGTGAACATCGCG 1541  
QY 782 TGGGCATCCACAGCGGCGCGTGCATCGCGGCTCCTTGGGTAATGGCAGTTTCG 841  
Db 1542 TGGGCATCCACAGCGGCGGTGTCATCTGCTGCTGCTGCGCTGCGGAAATGCGAGTTTCG 1601  
QY 842 ATGTGTGTTCCATGATGTACCTCGCCCAACCATGGAAGCAGGAGCGCGGCTGGCC 901  
Db 1602 ACCTGTGGTCCATGACGTGACTCTGCGCAACCATATGAGGCGG ---CCCGGCGCGCG 1658  
QY 902 GCATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGACTACGAAGTGGAGCCAG 961  
Db 1659 GCATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGACTACGAAGTGGAGCCAG 1718  
QY 962 GCGGTGGTGGCAAGCAACGCGTACTCTCAAGGAGCAGCAGATTTGAGACTTTTCTCATCC 1021  
Db 1719 GCGCGGTGGCAGCGGAACGCGTACCTCAAGGAGCAGCAGATTTGAGACTTTTCTCATCC 1778  
QY 1022 TGGGCGCCAGCAGAAACCGGAAGAGGAGAAAGGATGCTGGCCAAAGCTGCAGCGGACTC 1081  
Db 1779 TGGGCGCCAGCAGAAACCGGAAGAGGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 1838  
QY 1082 GGGCCAACTCCATGGAAGGGCTGATGCCCGGATGGGTTCTCTGATCGCTTCTCCCGA 1141

Db 1839 GGGCCAACCTCCATGGAAGGCGCTGATGCCAGCTGGGTGGCGGACCGGCGCTTCTCCGGA 1898  
QY 1142 CCAGGACTCAAGCCCTTCGCCAGATGGGCATTTGATGATTCAGAAAACACACCGGG 1201  
Db 1899 CCAAGGACTCAAGCCCTTCGCCAGATGGGCATTTGATGATTCAGAAAACACACCGGG 1958  
QY 1202 GCACCCAAGATGCCCTGAACCCCTGAGGATGAGTGGAGTTCCTGAGCGGTGCCATCG 1261  
Db 1959 GTGCCAAGATGCCCTGAACCCCGAGGATGAGTGGATGAGTTCCTGGGCGGTGGCATCG 2018  
QY 1262 ATGCCCCAGCATTTGATCAGCTCGGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1321  
Db 2019 ATGCCCCAGCATTTGATCAGCTCGGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2078  
QY 1322 AGAGAGAGGATTTTGAAGAAGTACTCCCGGAAGTGGATCCCGGCTTCGGAGCCTACG 1381  
Db 2079 AGAGAGAGGATTTTGAAGAAGTACTCAAGGAAGTGGAGGAGGAGGAGGAGGAGGAGG 2138  
QY 1382 TTGGCTGTGCCCTGTGGTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 1441  
Db 2139 TGCCCTGTGGGCTGTGGTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 2198  
QY 1442 ACTCCACCCCTGATGCTGGGATTTATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCT 1501  
Db 2199 ACTCAACCGTGTGGGATTTATGCCAGTATCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 2258  
QY 1502 TGATCTGTGCTGTACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1561  
Db 2259 TGACCTGTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2318  
QY 1562 GCAGCATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1621  
Db 2319 GCAGCATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2378  
QY 1622 TGTGTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1681  
Db 2379 TGTGTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2438  
QY 1682 CAGCCCGGATGCTGAATTTAAACACCTGCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1741  
Db 2439 CAGCCCGGATGCTGAATTTAAACACCTGCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2498  
QY 1742 ATTACTCTTGGGCGCTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1801  
Db 2499 ATTACTCTTGGGCGCTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2558  
QY 1802 CTGAGGTGTC 1812  
Db 2559 CTGAGTACTTC 2569

RESULT 11

MUSADNLICY  
LOCUS Mus musculus adenylyl cyclase type 6 mRNA linear ROD 27-APR-1993  
DEFINITION M96653  
ACCESSION M96653  
VERSION GI:191726  
KEYWORDS adenylyl cyclase type VI  
SOURCE Mus musculus cDNA to mRNA.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 3465)  
AUTHORS Premont, R. T.  
TITLE Multiple mechanisms underlying desensitization of the liver  
adenylyl cyclase system. Structure and cAMP regulation of liver  
adenylyl cyclases  
JOURNAL Unpublished (1992)  
REFERENCE 2 (bases 1 to 3465)  
AUTHORS Premont, R. T., Jacobowitz, O. and Iyengar, R.  
TITLE Lowered responsiveness of the catalyst of adenylyl cyclase to  
stimulation by GS in heterologous desensitization: a role for  
adenosine 3',5'-monophosphate-dependent phosphorylation



QY 1502 TGATCTGCTGTGTACTCTCTGTGGTTCTCTGTGTTCCCTTAAGGCCCTGCACAGCTGTGTCC 1561  
Db 2114 TGATCTGTGGCTGTGCTCTCTGTGGTTCTCTGTGTTCCCTTAAGGCCCTGCACAGCTGTGTCC 2173  
QY 1562 GCAGCATGTCGGCTACGCGGCACATAGCAGCCGAGTTGSCATCTTTTCCGTCTCTGCTTG 1621  
Db 2174 GCATATGTTCGGCTACGTCGGGCACAGCCGCGTTGGAATCTTCTCTGCTGTCTGCTTG 2233  
QY 1622 TGTTTACTTCTGTCATGTCGCAACATGTTCACCTGTATACACACCCCATACGGAGCTGTG 1681  
Db 2234 TGTTTACTTCTGTCATGTCGCAACATGTTCACCTGTATACACACCCCATACGGAGCTGTG 2293  
QY 1682 CAGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCCACCTGCACAGCTCA 1741  
Db 2294 CAGCCCGGATGCTGAATTTAACACACAGCGATGTACCGCTGCCACCTACACAGCTCA 2353  
QY 1742 ATTACTCTGTGGCGTGGATGCTCCCTGTGTGAGGCGACCATGCCCCACCTGCAGCTTTC 1801  
Db 2354 ATTACTCTGTGGACTGGATGCTCCCTGTGTGAGGCGACCCGACCCACCTGCAGCTTTC 2413  
QY 1802 CTGAGGTGTTTC 1812  
Db 2414 CTGAGTACTTC 2424

RESULT 12  
AR106659  
LOCUS AR106659 4131 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 11 from patent US 6107076.  
ACCESSION AR106659  
VERSION AR106659.1 GI:12821189  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 4131)  
AUTHORS Tang, W.-J. and Gilman, A. G.  
TITLE Soluble mammalian adenylyl cyclase and uses therefor  
JOURNAL Patent: US 6107076-A 11 22-AUG-2000;  
FEATURES  
Location/Qualifiers  
Source 1.. 4131  
BASE COUNT 835 a 1190 c 924 t  
ORIGIN

Query Match 79.3%; Score 1437.2; DB 6; Length 4131;  
Best Local Similarity 87.5%; Pred. No. 3-2e-311;  
Matches 1584; Conservative 0; Mismatches 223; Indels 3; Gaps 1;

QY 5 ACCTGGTGTGGCATCTCTGGCGGAGTGCAAGTGTGGGGGCGCTTTCGACGACAGCCCGC 64  
Db 687 ATGTGTTCTGGGCATCTAGCAGCGGTGCAAGTGTGGGGGCGCTTTCGACGACAGCCCGC 746  
QY 65 GCAGCCCTCTCTGGGCGCTCTGTGTCCTGTGTTCTTATACATCGCATACAGCTCC 124  
Db 747 GCAGCCCTCTAGCAGCGCTTGTGTCCTGTGTCCTTATACATCGCATACAGCTCC 806  
QY 125 TCCCATCGCATGCGGGCTGCGCTCTCAGCGGCGCTGGGCGCTCTCCACCTTCATTTGA 184  
Db 807 TCCCATCGCATGCGAGCGCGTCTCAGTGGCGCTTCTTCCACCTTCATTTGA 866  
QY 185 TCTTGGCTTGGCAACTTAACCGTGGTGTGCTTCTCTGGAAGCAGCTGCGTGGCAATG 244  
Db 867 TTTTGGCTTGGCATCTCAACAATGTTGACCCCTTCTCTTGGAGCAGCTGCGTGTAAAG 926  
QY 245 TGTGCTGTCTCTCTCACCACAGTCAATAGCATCTGCACACTATCCAGCAGAGTGT 304  
Db 927 TGTGCTCTCTCTCTGACCAATGTCATCGGTGTCTGACAGCACTATCCCGCTGGAAGT 986  
QY 305 CTCAGCGCCAGCGCTTTCAGGAGACCGCGATTTACATCCAGGCGCGGCTCCACCTGCAGC 364  
Db 987 CTCAGCGCCAGCGCTTTCAGGAGACCGCGTGTGTACATCCAGGCGCGGCTGCACCTGCAGC 1046

QY 365 ATGAGAAATCGCAGCAGGAGCGGCTGCTGCTGTGCGGTATTTGCCCCACAGCATGTTGCCATGG 424  
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QY 425 AGATGAAGAGACATCAACACAAAAAAGAACAC---ATGTTCCACAAATCTACATAC 481  
Db 1107 AAATGAAGAGGATATCAACACAAAAAAGAACACATGATGTTCCACAAATTTTACATCC 1166  
QY 482 AGAAGCATGACATGTTCAGCATCTGTTTCAGACATTTAGGGCTTTCACCAAGCTTGGCAT 541  
Db 1167 AGAAGCATGACATGTTCAGCATCTGTTTCAGACATTCAGGGCTTTCACCAAGCTTGGCAT 1226  
QY 542 CCAGTGCATTCGCGAGGAGCTGCTCATGACCTGAATGAGCTCTTTTCCCGGTTTGAACA 601  
Db 1227 CCAGTGCATTCGCGAGGAGCTGCTCATGACCTTGAATGAGCTCTTTTCCCGGTTTGAACA 1286  
QY 602 AGCTGCTCGGAGAGATCATGCTGCTGAGGATCAAGATCTTTGGGGGACTGTTACTACTGTG 661  
Db 1287 AGCTGCTCGGAGAGATCATGCTGCTGAGGATCAAGATCTTTAGGAGACTGTTACTACTGTG 1346  
QY 662 TGTGAGGGCTTGGCGAGGCGCGGCGACCATGCCACCTGCTGTGAGAGATGGGGTAG 721  
Db 1347 TGTGAGGGCTTGGCGAGGCGCGGCGACCATGCCACCTGCTGTGAGAGATGGGGTAG 1406  
QY 722 ACATGATGAGGCGCATCTCGCTGTGTAGTGTGAGGTGACAGGTGTAATGTAACATGCGCG 781  
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QY 782 TGGGCATTCACAGCGGCGGCTGCACTGCGGCGTCTCTTGGCTTTCGCGAATGTCAGTTGC 841  
Db 1467 TGGGCATTCACAGCGGCGGCTGCACTGCGGCGTCTCTTGGCTTTCGCGAATGTCAGTTGC 1526  
QY 842 ATGCTGTGTCCTCAATGATGTGACCTTGGCCCAACACCATGGAAGCAGGAAGCGGCGTGGCC 901  
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QY 902 GCATCACATCACTCGGCGCAACACTGCAGTACCTGAAACGGGGACTACGAGTGGAGCCAG 961  
Db 1587 GCATCACATCACTCGGCGCAACACTGCAGTACCTGAAACGGGGACTATGAGTGGAGCCAG 1646  
QY 962 GCGTGTGTGCAAGCGCCAGCGGTACTCAAGGAGCAGACATGAGACTTTCCTCATCC 1021  
Db 1647 GCGTGTGTGCAAGCGCCAGCGGTACTCAAGGAGCAGTGCATTTGAGACTTTCCTCATAC 1706  
QY 1022 TGGGCCACAGCCAGAAACGAAAGAGAGAGCTGCTGGCCAAAGCTGCGACGCGACTC 1081  
Db 1707 TAGGACCCAGCAGAAACGAAAGAGAGAGAGCCATGCTGCTCAAGCTGCGACGCGACGC 1766  
QY 1082 GGGCCAACTCCATGGAAGGGCTGATGCCGCGATGGGTTCCTGATGCTGCTTTCCTCCGGA 1141  
Db 1767 GGGCCAACTCCATGGAAGGGCTGATGCCGCGTGGGTTCCTGACCGCTGCTTTCCTCCGGA 1826  
QY 1142 CCAAGGACTCCAGGCGCTTCCGCGCAGATGGCATTCATGATCCACGAAGACAACCGG 1201  
Db 1827 CCAAGGACTCCAGGCGCTTCCGCGCAGATGGCATTCATGATCCACGAAGACAACCGG 1886  
QY 1202 GCACCCAAAGATGCTCTGAAACCTGAGGTGAGTGCATTCCTGAGCCTGAGCGGCTCC 1261  
Db 1887 GTGCCCAAGATGCTCTGAAACCTGAGGTGAGTGCATTCCTGAGCCTGAGCGGCTCC 1946  
QY 1262 ATGCCCGCAGCATGATGATGAGCTGCGGAGAGACCATGTCGCGCGGTTTTCCTCACCTTC 1321  
Db 1947 ATGCCCGCAGCATGATGATGAGCTGCGTAAAGACCATGTCGCGCGGTTTTCCTCACCTTC 2006  
QY 1322 AGAGAGAGATTTTCAGGAAGAGTACTCCCGGAAGTGTATCCCGCTTCGAGAGCTACG 1381  
Db 2007 AGAGAGAGATTTTCAGGAAGAGTATTCAGGAAGAGTATTCAGGAAGAGTATTCGAGAGCTACG 2066  
QY 1382 TTTGCTGTGCTGTTGGTCTTCTGCTTCATCTGCTTTCATCCAGCTTCTAAATTTTCCCAC 1441  
Db 2067 TGTGCTGTGCTGCTGCTGCTTCTGCTTCATCTGCTTTCATCCAGTTCCTGCTATTTCCCAC 2126  
QY 1442 ACTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCCTGCTGCTGCTAAATCACCCTGC 1501





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QY 722 ACATGATGAGCCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATGCCGG 781
Db 1407 ACATGATCGAGCCCATCTCGCTGGTGGCTGAGGTAACTGTAACATGCCGG 1466
QY 782 TGGGATCCACAGCGGGCGCTGCACTGGGGGGTCTTGGCTTGGGAATGGCAGTTGG 841
Db 1467 TGGGATCCACAGCGGGCGTGTACACTGGGGTGTCTTGGCTTGGGAATGGCAGTTGG 1526
QY 842 ATGTGTGGTCCAAATGATGTACCTGGCCCAACACACATGGAAGCAGGAAGCGGGCTGGCC 901
Db 1527 ATGTGTGGTCCAAACATGTGACCTTGGCCCAACACATGGAAGCGGGGGGGGGGGGGGG 1586
QY 902 GCATCCACATCACTCGGCCCAACACTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAG 961
Db 1587 GCATCCACATCACTCGGGCCACACTGCAGTACCTGAACGGGGACTATGAGTGGAGCCAG 1646
QY 962 GCCGTGGTGGCAAGCGGCTACCTCAAGGACGACGACATTTAGAGCTTTCCCTCATCC 1021
Db 1647 GCCGTGGGGTGGAGCGCAACCGGTACCTCAAGGACGAGTGCATTGAGACCTTTCCCTCATAC 1706
QY 1022 TGGCGGCCAGCCAGAAACGGAAGAGGAAAGGATGCTGGCCCAAGCTGCAGCGGACTC 1081
Db 1707 TAGGAGCCAGCCAGAAACGGAAGAGGAGGACCTGCTGTGCAAGCTGCAGCGGAGCC 1766
QY 1082 GGGCCAACTCCATGGAAGGGCTGTATGCCCGGATGGGTTCTGTATGCTGCTTCTCCCGGA 1141
Db 1767 GGGCCAACTCCATGGAAGGACTGTATGCCCGGATGGGTTCTGTATGCTGCTTCTCCCGGA 1826
QY 1142 CCAAGGACTCCAAAGGCTTCCGCCAGATGGGCTATGATTCAGCAAGACACACCGGG 1201
Db 1827 CCAAGGACTCTAAGGACTTCCGACAGATGGGCTATGATTCAGCAAGACACACCGGG 1886
QY 1202 GCACCAAGATGCCCTGAACCTGAGGATGAGGTGGATGAGTCTCTGAGCGGCTGCATCG 1261
Db 1887 GFGCCCAAGATGCTCTGAACCTGAGGATGAGGTGGATGAGTCTCTGAGCGGCTGCATCG 1946
QY 1262 ATGCCCGGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1321
Db 1947 ATGCCCGGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2006
QY 1322 AGAGAGAGATTTTTCAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1381
Db 2007 AGAGAGAGATTTTCAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2066
QY 1382 TTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1441
Db 2067 TTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2126
QY 1442 ACTCCACCTGATGCTGGGATTTATGCGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1501
Db 2127 ACTCCACCTGATGCTGGGATTTATGCGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2186
QY 1502 TGATCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1561
Db 2187 TGATCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2246
QY 1562 GCAGCATTTGCGCTTCAGCGGCAATAGCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1621
Db 2247 GCAGCATTTGCGCTTCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2306
QY 1622 TGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1681
Db 2307 TGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2366
QY 1682 CAGCCCGGATGCTGAATTTAAGACCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1741
Db 2367 CAGCCCGGATGCTGAATTTAAGACCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 2426
QY 1742 ATTACTCTTGGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1801
Db 2427 ATTACTCTTGGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2486
QY 1802 CTGAGGTGTT 1811
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Db 2487 CTGAGTACTT 2496
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RESULT 14
AX305965
LOCUS AX305965 5841 bp DNA linear PAT 11-DEC-2001
DEFINITION Sequence 716 from Patent WO0188188.
ACCESSION AX305965
VERSION AX305965.1 GI:17645322
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Ishikawa,K., Asai,S., Takahashi,Y., Nagata,T. and Ishii,Y.
TITLE Method for examining ischemic conditions
JOURNAL Patent: WO 0188188-A 716 22-NOV-2001;
School Juridical Person Nihon University (JP)
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VERSION M93422.1 GI:191690
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REFERENCE
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AUTHORS Yoshimura,M. and Cooper,D.M.
TITLE Cloning and expression of a Ca(2+)-inhibitable adenylyl cyclase
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (15), 6716-6720 (1992)
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PUBMED 1379717
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Query Match 79.0%; Score 1431.8; DB 10; Length 5841;
Best Local Similarity 87.7%; Pred. No. 5.1e-310;
Matches 1588; Conservative 0; Mismatches 317; Indels 6; Gaps 2;

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Job time : 3154.21 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ORGANISM	Homo sapiens				
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AUTHORS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.				
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	97 (7)			3491-3496 (2000)
MEDLINE	20202663				
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001				

BG993320 581 bp mRNA linear EST 13-JUN-2001  
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 human.

human.  
Homo sapiens  
Eukaryota. Metazoa. Chordata. Craniata. Vertebrata: Euteleostomi:

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 581)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, J.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663

Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil

Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001

Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR3&t2=MR3-HT0999-070201-003-h04&t3=2001-02-07&t4=1>)  
Seq primer: buc 18 forward

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High quality sequence stop: 581.
Location/Qualifiers
1..581
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone_lib="HT0999"
/dev_stage="Adult"
/note="Organ: head neck: Vector: nucl8: Site 1: SmaI:"

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Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under low stringency conditions." 118 a 157 c 199 g 106 t 1 others

ch	29.8%	Score 540.2;	DB 13;	Length 581;
l Similarity	98.2%	Pred. No. 8.3e-119;		
556. Conservative	0.	Mismatches 9.	Indels 1.	Gaps 1.

[illegible]

GGGCGGACCATGCCCACTGCTGTGTGGAGATGGGGTAGACATGATTGAGGCATCTCGC 742

CGCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 135

[illegible]

GGCACTGGGGGCTCCTTGGCTTGGGAAATGGCAGTTCGATGTGTGGTCCCAATGATGTGA 862

CCCTGGGCCAACCCACATGGAGCAGGAGCCGGGCTGSCCGCATCCACATCACTCGGGCAA 922

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Db 256 CCCTGGCCAAAGCACATGGAGGAGGCGGCTGGCCGATCCACATCACTCGGGCAA 315
QY 923 CACTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAGCGCTGGTGGCAAGCGCAACG 982
Db 316 CACTGCAGTACCTGAACGGGGACTACGAAGTGGAGCCAGCGCTGGTGGGAGCGCAACG 375
QY 983 CGTACCTCAAGGAGCAGCACATGAGACTTTCCTCATCTCTGGGCGCCAGCCAGAAACGGA 1042
Db 376 CGTACCTCAAGGAGCAGCACATGAGACTTTCCTCATCTCTGGGCGCCAGCCAGAAACGGA 435
QY 1043 AAGAGGAAAGGATGCTGGCCAAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAAGGC 1102
Db 436 AAGAGGAAAGGATGCTGGCCAAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAAGGC 495
QY 1103 TGATGCGCGATGGTTCCTGATGCTGCTCTCCCGGACCAAGGACTCCAAAGCCCTTCC 1162
Db 496 TGATGCGCGCTGGTTCCTGATGCTGCTCTCTCCCGGACCAAGGACTCCAAAGCCCTTCC 555
QY 1163 GCCAGATGGCATGATGATTCAGC 1188
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RESULT 3
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LOCUS
DEFINITION 602792616F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4923890 5',
RNA sequence.
ACCESSION BG872335
VERSION BG872335.1 GI:14222875
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 565)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapps-femail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10845 row: p column: 03
High quality sequence start: 11
High quality sequence stop: 565.
FEATURES
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Location/Qualifiers
1. 565
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_SG2"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1:
NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 133 a 141 c 174 g 117 t
ORIGIN
Query Match 25.6%; Score 463.4; DB 12; Length 565;
Best Local Similarity 91.2%; Pred. No. 2.1e-100;
Matches 515; Conservative 0; Mismatches 46; Indels 4; Gaps 2;
QY 434 AAGACATCAACACAAAAAAGAGAC---ATGTTCCACAAGATCTACATACAGAAGCATG 490
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Db 1 AAGACATCAACACAAAAAAGAGAGACATGATGTTCCATAGATCTACATCCAGAAGCATG 60
QY 491 ACATGTCAGCATCCTGTTTGCAGACATTTAGGGCTTCACCAGCCTGGCATCCAGTCCA 550
Db 61 ATAATGTCAGCATCCTGTTTGCAGACATTTAGGGCTTCACCAGCCTGGCATCCAGTCCA 120
QY 551 CTGCGGAGAGCTGGTTCATGACCTGAATGAGCTCTTTGCCCGTTTGGACAAGCTGGCTG 610
Db 121 CTGCACAGAACTGGTTCATGACCTTGAATGAGCTCTTTGCCCGTTTGGACAAGCTGGCTG 180
QY 611 CGGAAATCACTGCTGAGGATCAAGATCTTTGGGGACTGTTTACTACTGTGTGTCAGGGC 670
Db 181 CGGAAATCACTGCTGAGGATCAAGATCTTTAGGAGACTGTTTACTACTGCTGTCAGGGC 240
QY 671 TGCCGGAGGCGCGGCGACCATGCCACCTGCTGTGGAGATGGGGTAGACATGATG 730
Db 241 TGCCGGAGGCGCGGCGAGATCACGCCACCTGCTGTGGAGATGGGGTAGACATGATG 300
QY 731 AGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTAATGTGAACATGCGGTGGGCATCC 790
Db 301 AAGCCATCTCGCTGGTGGTGAAGTAACAGGTGTAACGTGAACATGCGGTGGGCATCC 360
QY 791 ACAGCGGCGGTGCTACTGCGGCTCTTGGCTTTCGGAATGCGAATGCGAGTTCGATGTGGT 850
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QY 851 CCATGATGTACCTCGGCGACCATCCACATGGAGCAGGAGCCGGCTGGCGCATCCACA 910
Db 421 CAAACGATGTACCTCGGCTAAACCATGGAGCGCGGCGCGCGCATCCACA 480
QY 911 TCACTCGGGCAACACTGCAGTACCTGAACGGGGACTACGA-AGTGGAGCCAGGCGGTGGT 969
Db 481 TCACTCGGGCTACACTGCAGTACCTGAACGGGGACTATGAGGTGGAGCCAGGCGGTGGT 540
QY 970 GGCAAGCGCAACGGGTACCTCAAGG 994
Db 541 GGTGAACGCAATGGTACCTCAAGG 565

RESULT 4
BM090325
LOCUS
DEFINITION 505523 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BM090325
VERSION BM090325.1 GI:17000953
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 525)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chikko-Mckown,C.G.,
Perlea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
Keele,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
CONTACT: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCAGTCACGCG
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/lab_host="DH10B"
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Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."
BASE COUNT 112 a 162 c 133 g 117 t 1 others
ORIGIN
Query Match 24.4%; Score 442.4; DB 13; Length 525;
Best Local Similarity 91.4%; Pred. No. 2.2e-95;
Matches 480; Conservative 0; Mismatches 42; Indels 3; Gaps 1;
QY 90 CCTGTGTTCTTTGTATACATCGCATACAGCTCTCCCTCCCATCCGATCGGGCTGCCGT 149
Db 1 CCTGTGTTCTTTGTATACATCACATCACTCTCTCCATCCGATCGGGCTGCCGT 60
QY 150 COTCAGCGCCCTGGGCTCTCCACCTTGCAATTTGATCTTGGCTGGCAACTTAACCGTGG 209
Db 61 CTTTACGCGCCCTGGGCTCTCCACCTGCATTTGGTCTTGGCTGGCAGCTCAACCGTGG 120
QY 210 TGATGCTTCTTCTGGAAGCAGCTGGTCCCAATGTGCTGCTGCTCTGTCACCAACGT 269
Db 121 TGACGCTTCTTCTGGAAGCAGCTTGGAGCCCAACATGCTGCTGCTCTGTCACCAACGT 180
QY 270 CATTAGCATCTGCACACACTATCCAGCAGAGGTGCTCAGCGCCAGCGCTTTCAGGAGAC 329
Db 181 CATTGCACTCTGCACACACTATCCGGCTGAGGTGCTCAGCCCGCAGCAATTCAGAGAC 240
QY 330 CGCGATTACATCCAGGCGCGCTCCACTGCAGCATGAGATCGGCAGCAGGCGGCT 389
Db 241 CGCGGTTTACATCCAGGCGCGCTGCACCTGCAGCATGAGAACCGCGCAGCAGGCGGCT 300
QY 390 GCTGCTGTCGGTATGCCCCAGCAGCTTCCCATGAGATGAAGAGAGACATCAACACAA 449
Db 301 GCTGCTGTCGTGTGCCCCAGCATGTGCCATGAGATGAAGAGAGACATCAACACAA 360
QY 450 AAAGAAGAC---ATGTTCCACAAGATCTACATACAGAGCATGACAATGTTCAGCATCT 506
Db 361 GAAAGAAGACATGATGTTTCATAAGATCTACATCCAGAGCAGCAATGTTCAGCATCT 420
QY 507 GTTTCAGACATGAGGGCTTACCAGCTGCCATCCAGTCCAGTCCGCGCAGGAGCTGT 566
Db 421 GTTTGGGACATGGAAGGCTTACCAGCTGGCGTCCCGTCCAGTCCAGCAGCANGAGCTGT 480
QY 567 CATGACCTTGAATGAGCTCTTTGCCCGGTTTCACAAGCTGGCTGC 611
Db 481 CATGACCTTGAACGAGCTCTTTGCCCGGTTTCACAAGCTGGCTGC 525

RESULT 5
BQ180663
LOCUS BQ180663 682 bp mRNA linear EST 30-APR-2002
DEFINITION UI-M-EX0-bxb-n-18-0-UI.r1 NIH_BMAP_EX0 Mus musculus cDNA clone
IMAGE:5706065 5', mRNA sequence.
ACCESSION BQ180663
VERSION BQ180663.1 GI:20356155
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 682)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
```

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Dr. James Lin, University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)  
Seq primer: pYX-5.  
Location/Qualifiers  
1. 682  
/organism="Mus musculus"  
/strain="C57BL/6"  
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/dev\_stage="embryo 15.5 dpc"  
/lab\_host="DH10B (T1 phage resistant)"  
/Note="Organ: brain; Vector: pYX-Asc; Site\_1: EcoR I;  
Site\_2: Not I; The library was constructed according to  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured mRNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with an  
oligo-dT primer containing a Not I site. Double stranded  
cDNA was size selected according to mRNA size fraction,  
ligated with EcoR I adaptor, digested with Not I, and then  
cloned directionally into pYX-Asc vector. The library tag  
sequence located between the Not I site and the polyA tail  
is GTGCGTGAA. This library was created for the  
University of Iowa Mouse Brain Molecular Anatomy Project  
(BMAP): 'Gene Discovery in the Developing Mouse Nervous  
System', supported by National Institutes of Mental Health  
(NIMH), Hemin Chin, Ph.D., program coordinator."

BASE COUNT 142 a 195 c 187 g 156 t 2 others  
ORIGIN

Query Match 23.1%; Score 418.6; DB 14; Length 682;  
Best Local Similarity 77.9%; Pred. No. 1.2e-89;  
Matches 529; Conservative 0; Mismatches 146; Indels 4; Gaps 2;

QY 146 CGGTCTCAGCGCCCTGGGCTCTCCACTTGCCTTTGATCTTGGCTGGCAACTTAACC 205  
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QY 206 GTGGTGATGCCCTTCCTGGAAGCAGCTCGGTGCGCAATGTGCTGTGTTCTCTGCACCA 265  
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QY 266 AGTCTATTAGCATCGCACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTCAGG 325  
Db 121 ACATTGGGGTGTGTGCACTCACTACCCAGCTGAGGTCTCCAGAGACAGGCTTCCAGG 180  
QY 326 AGACCCGCGAGTTACATCCAGGCGCGCTCCACTCGACATGAGAATCGGACGAGGAGC 385  
Db 181 AGACCCGCGAGTGTATCAGGCTCGGCTCCATTCAGCGGGAGAACACAGCAGGAGC 240  
QY 386 GGCTGCTGCTGCTGATGTTGCCCGCAGCAGGTTGCCATGGAGATGAAGAAGACATCAACA 445  
Db 241 GTCTCTGCTGCTGCTCTCTCCCGCTCATGTTGCCATGGAGATGAAGAAGACATCAACG 300  
QY 446 CAAAAAAGAAGA---CATGTTCCACAAGATCTACATACAGAGCATGACAATGTCAGCA 502  
Db 301 CCNACGAGGAGATGATGTTTCCACAAGATCTATCATCAGAAAGCATGACAATGAGCA 360  
QY 503 TCCTCTTTTCGACATTTAGGGCTTTCACAGCTTGGCATCCCGATCCCGATCGCTCGCAGGAGC 562  
Db 361 TCCTCTTTTCGACATCGAGGCTTTCACAGCTTGGCTTCCAGTGTACTGCTCCCAAGAC 420  
QY 563 TGGTCATGACCCCTGAATGAGCTCTTTTGGCCGGTTTGTACAAAGCTGGCTGCGGAGATCACT 622

	Best Local Similarity Matches	96.7%; Conservative	Pred. NO. 1.4e-83; 0;	Mismatches 13;	Indels 1;	Gaps 1;
Dn	421	TGGTCATGACCCCAATAGACTCTTGC	CGCGTTTGACAAGTTGGCTCGGAGAATCACT	480		
Qy	623	GCCTGAGGATCAAGATCTTGGGGACTGT	TACTACTGTGTGTCAGGGCTGCCGGAGGCC	682		
Dn	481	GTATTACGGATTAGATCCTCGGGATGTT	ACTACTACTGCTCTCGGGCTGCTCGAAGCCA	540		
Qy	683	GGCCGACCACATGCCACTGCTGTGTGG	AGATGGGGTAGACATGATGAGGCCATCTCGC	742		
Dn	541	GAGCCGACCATGCCCACATGCTGCGT	GGAGATGGGAATGACATGATCGAGGCCATCTCGT	600		
Qy	743	TGTTACTGTAGGTGACAGGTGTCAA	TGTAACATGCGCGTGGGCATCCACACCGGGCCG	802		
Dn	601	TNGTCCGGAGGTGACAGGGGTGAAC	GTTGAACATGCGCGTGGGAATCACACGGGGAG	660		
Qy	803	TGCACTCGCGGTCTCTTGG	821			
Dn	661	T-AACTCGGTGCTCTTGG	678			
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AI905602/c						
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DEFINITION	CM-BT094-050299-173 BT094	Homo sapiens	cDNA,	mRNA sequence.		
ACCESSION	AI905602					
VERSION	AI905602.1	GI:6495989				
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,I.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.					
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags					
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	97 (7),	3491-3496	(2000)		
MEDLINE	20202663					
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/seq/gethtml.pl?tl=CM&st2=CM-BT094-173.html#t3-050299&t4=1) Seq primer: puc 18 forward. Location/Qualifiers 1. .442 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="BT094" /sex="female" /dev_stage="Adult" /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ONESTEP PCR (U.S. Letters Patent application No. 196 /716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."					
BASE COUNT	102 a	116 c	136 g	88 t		
ORIGIN						
Query Match		21.7%;	Score 393.2;	DB 9;	Length 442;	





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ACCESSION BE840138
VERSION BE840138.1 GI:10272516
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 417)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,
Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,
Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H.,
Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare
, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and
Simpson, A. J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-QV0-FN0181-280
700-321-d07&ts=2000-07-28&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence stop: 415.
FEATURES
Location/Qualifiers
1..417
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FN0181"
/dev_stage="Adult"
/note="Organ: prostate_normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT 88 a 119 c 124 g 86 t
ORIGIN
Query Match 21.4%; Score 387.8; DB 12; Length 417;
Best Local Similarity 97.8%; Pred. No. 2.6e-82;
Matches 404; Conservative 0; Mismatches 7; Indels 2; Gaps 1;
QY 1033 CAGAAACGGAAGAGAGAGCATGCTGGCCAACTGCGAGCGGACTCGGGCAACTCC 1092
Db 417 CAGAAACGGAAGAGAGAGAGGCATGCTGGCCAACTGCGAGCGGACTCGGGCAACTCC 358
QY 1093 ATGGAAGGGCTGATGCGCGGATGGGTTCCTGATCGTGCCTTCCTCCCGGACCAAGGACTCC 1152
Db 357 ATGGAAGGGCTGATGCGCGGCTGGGTTCCTGATCGTGCCTTCCTCCCGGACCAAGGACTCC 298
QY 1153 AAGGCTTCGCGCAGATGGGCAATGATGATTCAGCAAAAGACACCGGGGACCCCAAGAT 1212
Db 297 AAGGCTTCGCGCAGATGGGCAATGATGATTCAGCAAAAGACACCGGGGACCCCAAGAT 238
QY 1213 GCCTCAACCTGAGATGAGGTGGATGAGTTCCTGAGCGGTGCCATCGATGCCCGCAGC 1272
Db 237 GCCTCAACCTGAGATGAGGTGGATGAGTTCCTGAGCGGTGCCATCGATGCCCGCAGC 178
QY 1273 ATTGATCAGCTGCGGAAGACCATGTCGCCGGTGTTCCTACCTTCACAGAGAGAGGAT 1332
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QY 1393 CTGTTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTC 1445
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Db 57 CTGTTGGTCTTCTGCTTCATCTGCTTCATC--GCTTCTCATCTTCCACACTC 7
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BI873142 939 bp mRNA linear EST 11-OCT-2001
LOCUS 603397792F1 NTH_MGC_94 Mus musculus cDNA clone IMAGE:5401415 5',
mRNA sequence.
ACCESSION BI873142
VERSION BI873142.1 GI:16046817
KEYWORDS EST.
SOURCE house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 939)
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cga@rsr@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
cDNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM12023 row: h column: 24
High quality sequence stop: 638.
FEATURES
Location/Qualifiers
1..939
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/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."
BASE COUNT 208 a 271 c 256 g 204 t
ORIGIN
Query Match 20.8%; Score 377; DB 13; Length 939;
Best Local Similarity 75.6%; Pred. No. 1.1e-79;
Matches 521; Conservative 0; Mismatches 160; Indels 8; Gaps 4;
QY 133 CGATGCGGCTCCGCTCCATCGGCTCTCCACCTTCCACCTTGATTTGATCTTGCC 192
Db 12 CGATGAGGGCTCGGTGCTCAGCGGGTGCTTCTGCTGCGCTCTCCACTTGGTCACTCT 71
QY 193 TGGCAACTTAACCGTGGTGATGCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTG 252
Db 72 CTGCACACCAACCTCCCGAGGACCAAGTTTCTGCTGAAACAGCTTGTCTCCAATGTCTCATC 131
QY 253 TTCCTCTGCACCAACCTCATTCATCTGCACACTATCCACAGAGGTGTCTCAGCGC 312
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[illegible]

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DEFINITION	ACENCGOUT_8229097 Lupski_dorsal_root_ganglion Homo sapiens CDNA clone IMAGE:6182035 5' mRNA sequence.
ACCESSION	BQ881496
VERSION	BQ881496.1
KEYWORDS	GI:22273504
SOURCE	EST.
ORGANISM	human.
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1016)
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

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Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: WGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13567 row: f column: 20
High quality sequence start: 31
High quality sequence stop: 645.
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NotI; Site:2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:

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5'-TCGACCCACCGCTGG-3' and  
5'-GACTAGTCTTAGATCGGACGCCGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

BASE COUNT	186 a	297 c	268 g	265 t
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Best Local Similarity	98.7%; Pred. No. 1.8e-78;			
Matches 375; Conservative 0; Mismatches 5; Indels 0; Gaps 0;				
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Db 42	TCITCCACACTCCACCCTGATGCTTGGATCTATGCCAGCATCTTCTGCTGCTAA 101			
Qy 1493	TCACCGTGTGATGTGCTGTGTACCTCCTGTGTTCTCTGTCCCTAAGCCCTGAAC 1552			
Db 102	TCACCGTGTGATGTGCTGTGTACCTCCTGTGTTCTCTGTCCCTAAGCCCTGAAC 161			
Qy 1553	GTCGTGCCCCGACATGTCCGCTCACGGGCACATAGCAGCGAGTTGGCATCTTTCCG 1612			
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Qy 1613	TCCGTCTGTGTTTACTTCTGCCATTCGCAACATGTTCACTGTAACACACACCCCATAC 1672			
Db 222	TCCGTCTGTGTTTACTTCTGCCATTCGCAACATGTTCACTGTAACACACCCCATAC 281			
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DEFINITION	QV4-GN0122-250900-424-c07 GN0122 Homo sapiens cdna, mRNA sequence.			
ACCESSION	BF369868			
VERSION	BF369868.1 GI:11331893			
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	1 (bases 1 to 625)			
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.				
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)			
MEDLINE	20202663			
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br			

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&t2=QV4-GN0122-250900-424-c07&t3=2000-09-25&t4=1)  
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High quality sequence start: 20  
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; Site\_2: SmaI; A mini-library was made by cloning  
products derived from ORESTES PCR (U.S. Letters Patent  
application No. 196,716 - Ludwig Institute for Cancer  
Research) profiles into the puc 18 vector. Reverse  
transcription of tissue mRNA and cDNA amplification were  
performed under low stringency conditions."  
BASE COUNT 128 a 198 c 163 g 136 t  
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Db 385 GATTTAGCTCGAAGACATGACACGTGAGCATCTGTTGTCAGATCGAGGCTTCAC 444  
QY 531 CAGCTGGCATCCAGTGCACCTGCGAGGAGCTGGTGCATGACCTGAATGAGCTCTTTGC 590  
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QY 651 TTACTACTGTGTCAGGCTGGGAGCGCGGCGGAGCCATCCACCTGCTGTGTTGGA 710  
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RESULT 13

BG004182/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
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ORGANISM

REFERENCE  
AUTHORS

TITLE  
JOURNAL  
MEDLINE  
COMMENT

FEATURES  
source

BASE COUNT  
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EG004182.1 GI:12445098  
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1 (bases 1 to 611)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
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; Site\_2: SmaI; A mini-library was made by cloning  
products derived from ORESTES PCR (U.S. Letters Patent  
application No. 196,716 - Ludwig Institute for Cancer  
Research) profiles into the puc 18 vector. Reverse  
transcription of tissue mRNA and cDNA amplification were  
performed under low stringency conditions."

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QY 518 TTGAGGGCTTCCACAGCCTGGCATCCAGTGCACCTGCGCAGGAGCTGGTCAATGACCTGA 577
Db 250 TCAGGGCTTCCACAGCCTGGGCTCCAGTGCACCTGACAGCACTGATGACCTCA 191
QY 578 ATGAGCTCTTGGCCGGTTGACAGCTGGCTGCGGAGAAATCACTGCGCTGAGATCAAGA 637
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ACCESSION BQ370134
VERSION BQ370134.1 GI:21045648
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 673)
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
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; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
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; Site_2: SmaI; A mini-library was made by cloning
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application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
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Best Local Similarity 76.4%; Pred. No. 3.3e-72;
Matches 438; Conservative 0; Mismatches 132; Indels 3; Gaps 1;
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QY 582 GCTCTTTGCGCGTGTGACAACTGCTGCGGAGATCACTGCTGAGGATCAAGATCTT 641
Db 170 GCTCTTCCCGCTTGTGACAACTGCTGCGGAGAGATCACTGTTTACAGATTAAGATCT 111
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Db 110 TGGGATGTTTATTACTGCTGCGGCTGCTGCGGAGGCTGCTGAAAGCAAGGCTGACACG 51
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DEFINITION PM2-BN0080-180400-004-g02 BN0080 Homo sapiens cDNA, mRNA sequence.
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VERSION BE001572.1 GI:8261805
KEYWORDS EST.
SOURCE human.
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1 (bases 1 to 367)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
```

Search completed: March 1, 2003, 03:52:08  
Job time : 1752.49 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 21:13:01 ; Search time 6093.65 Seconds  
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16949.756 Million cell updates/sec

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

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4	3478.4	98.0	6453	9	AF250226	AF250226 Homo sapi
5	3379.2	95.2	3582	6	AX189768	AX189768 Sequence
6	3356.8	88.9	5877	9	AB007882	AB007882 Homo sapi
7	2996.8	84.4	4046	4	DOGADENCYC	M94968 Canis famill
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9	2765	77.9	5841	6	AX305965	AX305965 Sequence
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13	2743.2	77.3	6036	10	RATADCYB	L01115 Rattus norv
14	2734	77.0	3465	10	MUSADNLCYC	M96653 Mus musculu
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18	1678.8	47.3	4995	4	OCMRADCYV	Z29371 O.cuniculus
19	1655.2	46.6	4847	10	RATADCYA	M96159 Rattus norv
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21	1475.4	41.6	2743	9	AF497517	AF497517 Homo sapi
22	1431.6	40.3	4236	5	GGA293817	AJ293817 Gallus ga
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28	806.6	22.7	2429	4	DOGADCYC	M97886 Canis famill
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30	595	16.8	3978	4	BOVADC	M25579 Bovine aden
31	595	16.8	3978	6	AR106654	AR106654 Sequence
32	590.4	16.6	151706	2	AC129405	AC129405 Rattus no
33	588	16.6	108689	2	AC096835	AC096835 Rattus no
34	553.6	15.6	2857	10	AF053980	AF053980 Mus muscu
35	545	15.4	3811	6	AX418306	AX418306 Sequence
36	522.4	14.7	6193	4	BTAC11MR	Z49806 B.taurus mR
37	505.2	14.2	3518	6	AX107094	AX107094 Sequence
38	503.6	14.2	3266	9	AF497516	AF497516 Homo sapi
39	495.8	14.0	3261	6	AX457036	AX457036 Sequence
40	495.8	14.0	6470	6	AX457037	AX457037 Sequenc
41	490.4	13.8	6005	9	HSADENCYR	Z35309 H.sapiens m
42	486.4	13.7	4901	10	MMU85021	U85021 Mus musculu
43	475.2	13.4	2664	6	AX457033	AX457033 Sequence
44	475.2	13.4	5873	6	AX457034	AX457034 Sequence
45	475.2	13.4	5873	9	AB028983	AB028983 Homo sapi

ALIGNMENTS

RESULT 1	AR174473	AR174473	3549 bp	DNA	linear	PAT 17-DEC-2001
LOCUS	Sequence 5 from patent US 6306830.					
DEFINITION	AR174473					
ACCESSION	AR174473					
VERSION	AR174473.1	GI:17914793				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 3549)					
AUTHORS	Hammond,H.Kirk., Insel,P.A., Ping,P., Post,S.R. and Gao,M.					
TITLE	Gene therapy for congestive heart failure					
JOURNAL	Patent: US 6306830-A 5 23-OCT-2001;					
FEATURES	Location/Qualifiers					





Db	2041	 TTCATCTGTTTCATCCAGCTTCTAAATTTTCCACACATCCACCGTGATGCTTGGGATTTAT	2100
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Db	2101	 GCCAGCATCTTCTGCTGCTGCTAATACACCGTGTGATCTGTGCTGTGTACTCTCTGTGGT	2160
Qy	2161	 TCTCTTTCCCTTAAGSCCCTGCAAGCTGTCTCCCGCAGCATTTGCCATTTGCCAACAT	2220
Db	2161	 TCTCTTTCCCTTAAGSCCCTGCAAGCTGTCTCCCGCAGCATTTGCCATTTGCCAACAT	2220
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Db	2221	 AGCACCGCAGTTGGCATCTTTTCCGTTCTGCTTGTGTTTACTTCTGCCATTTGCCAACATG	2280
Qy	2281	 TTCACTGTGAACACACACCCCATACGGAGCTGTGCAGCCGGATGCTGAATTTAAACACCT	2340
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Db	2401	 CTGTGTGAGGGCACCATGCCCCACCTTCTGAGTGTCCTGAGTGTCCTGAGTGTCATTCGGGAACATGCTG	2460
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Db	2521	 ATCTTTGCTCTGGGGCTCATCTAATTTGGTGTGCTTCTGCTGGCTGCCCCAGCGCCATC	2580
Qy	2581	 TTTGACAACATATGACCTACTGCTTGGCTGCCATGCGCTTGGCTTCTTCCAATGAGACCTTT	2640
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Db	3061	 GAGCGGTTCGGGAGCTGGAAAAGATCAAGACGATTGTGTAGCACTACATGGCTGCCTCA	3120
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LOCUS	AX189761	3549 bp	DNA linear PAT 08-AUG-2001
DEFINITION	Sequence 5 from Patent WO0148164.		
ACCESSION	AX189761		
VERSION	AX189761.1	GI:15143135	
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 3549)		
TITLE	Hammond, H.K. and Gao, M.		
JOURNAL	Gene therapy for congestive heart failure		
FEATURES	Patent: WO 0148164-A 5 05-JUL-2001.		
source	THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)		
BASE COUNT	Location/Qualifiers		
ORIGIN	1..3549		
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Query Match	699 a 1025 c 1061 g 764 t		
Best Local Similarity	100.0%; Score 3549; DB 6; Length 3549;		
Matches 3549; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
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Qy	61	GAACCAATGGGCAGAAAGGTTTCGGGGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG	120
Db	61	GAACCAATGGGCAGAAAGGTTTCGGGGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG	120
Qy	121	CCCCGCTATATGAGTGCCTCCGGATGCAGAGCCACCCAGCCCCCTCGCGGGCCCC	180
Db	121	CCCCGCTATATGAGTGCCTCCGGATGCAGAGCCACCCAGCCCCCTCGCGGGCCCC	180
Qy	181	CCTCGGTGCCCTGGCAGGATGACGCTTTCATCCGAGGGGGGGCCCAAGGCGCAAG	240
Db	181	CCTCGGTGCCCTGGCAGGATGACGCTTTCATCCGAGGGGGGGCCCAAGGCGCAAG	240

QY 241 GAGCTGGGGCTGGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACAACGACAGCG 300  
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QY 361 CGTTTGGTGACAGTGTTCAGTCGAAGCAGTTCGCGTTCGGCCAAAGCTGGAGCGCCTGTAC 420  
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LOCUS Sequence 10 from Patent WO0148164.  
DEFINITION AX189766  
ACCESSION AX189766  
VERSION AX189766.1 GI:15143139  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 3552)  
AUTHORS Hammond, H.K. and Gao, M.  
TITLE Gene therapy for congestive heart failure  
JOURNAL Patient: WO 0148164-A 10 05-JUL-2001;  
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)  
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Location/Qualifiers  
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Hammond H.K. and Gao M.  
TITLE  
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JOURNAL  
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9455477  
REFERENCE 2 (bases 1 to 5877)  
AUTHORS Ohara, O.  
TITLE Direct Submission  
JOURNAL Submitted (06-OCT-1997) Osamu Ohara, Kazusa DNA Research Institute,  
Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba  
292-0812, Japan (E-mail: cdnainfo@kazusa.or.jp, tel: +81-438-52-3913,  
Fax: +81-438-52-3914)  
COMMENT On May 9, 2002 this sequence version replaced gi:2887418.  
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ORGANISM

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REFERENCE  
AUTHORS  
Katsushika,S., Chen,L., Kawabe,J., Nilakantan,R., Halnon,N.J.,  
Homcy,C.J. and Ishikawa,Y.

TITLE  
Cloning and characterization of a sixth adenylyl cyclase isoform:  
types V and VI constitute a subgroup within the mammalian adenylyl  
cyclase family

JOURNAL  
MEDLINE  
PUBMED  
Proc. Natl. Acad. Sci. U.S.A. 89 (18), 8774-8778 (1992)  
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1528892

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|||||  
QY 481 CTGCTACAGCGGTGCTGCTGGCTTCCAAAGCGCCAGCCCGCCCTCAGCCTGCCAT 540  
|||||  
Db 605 CTGCTACAGCGGTGCTGCTGCTAGCCTTCCATGCTGCACCTGCGCCGCTCAGCCTGCCTAC 664  
|||||

[illegible]

Qy	1618	TAC	CTCAAGGAGCAGACAT	TGAGACT	TTCC	TCTATCTCTGGGGCCAGCCAGAAACGGAAA	1677
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Db	1802	GAG	GAGAAAGGCCAT	GTGCGCAAGCTG	CAGCGSAGCGGGGCCAATCTCATGGAAGGCGTG	1861	
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Db	1922	CAG	ATGGGCAT	TGATGAT	TCAGAAAGACAACCCGGGGTGCCAAAGATG	CGCCCTGAACCCCT	1981
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Db	1982	GAG	GATCAGGTGAT	GAGTTCTTGAC	CGCGCGGTGCATCGATGCCCGCAGCAT	TCCCGCAGCAT	2041
Qy	1918	CGA	AAGGACCAT	GTGCGCGGTTTT	TGTCTCACTTCCAGAGAGAGGAT	TTTTGACAAGAAG	1977
Db	2042	CGG	AAGGACCAT	GTGCGCGCTTCT	TGTCTCACTTCCAGAGAGAGGAT	TTTTGAAAAGAAG	2101
Qy	1978	TACT	CCCGGAAGTGGAT	CCCGCTTCGGAGCT	ACGTTGGCTGTGCCCTGTGGCTTTC	2037	
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Qy	2398	CCG	CTGTGTGAGG	GCACATGCCACCT	GTGAGTCTGAGTGTCCAT	CGGGAACATG	2457
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Db	2762	TTT	GATGGCTG	CACTGTCCAGCT	GCAGGGAGGTGGCCCTCA	AAATATGACCCCTGTG	2821
Qy	2698	ATT	CTGCTGTGTT	TTCGCTGCGCTG	TATCTGATGCTCAGCAGGTG	GAATCGACCTGCC	2757



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DEFINITION	Sequence 716 from Patent WO0188188.		
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VERSION	AX305965.1 GI:17645322		
KEYWORDS	house mouse.		
SOURCE	Mus musculus		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.		
REFERENCE	1		
AUTHORS	Ishikawa,K., Asai,S., Takahashi,Y., Nagata,T. and Ishii,Y.		
TITLE	Method for examining ischemic conditions		
JOURNAL	Patent: WO 0188188-A 716 22-NOV-2001;		
FEATURES	School Juridical Person Nihon University (JP)		
	Location/Qualifiers		
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	1214 a	1558 c	1673 g 1396 t
ORIGIN			
Query Match 77.9%; Score 2765; DB 6; Length 5841;			
Best Local Similarity 87.1%; Pred. No. 0;			
Matches 3095; Conservative 0; Mismatches 445; Indels 13; Gaps 5;			
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Db	96	ATGTCATGGTTAGTGGCTCTCTGGTCCCAAGTGGATGAACGGAACAGCCTGGGGG	155
QY	61	GAACGCAATGGGAGAAAGGCTTCGGCGGCGGTGGCACTCGGGCAGGTGGCTTCTGCACG	120
Db	156	GAACGCAATGGGAGAAAGGCTTCGGCGGCGGTGGCACTCGGGCAGGTGGCTTCTGCACG	212
QY	121	CCCGCTATATGAGTGGCTTCGGGATGAGAGCCACCCAGCCCTCGGGGCC	180
Db	213	CCTCGCTATAGTGGCTTCAGAAATGCGGAGCCACCCAGCCCTCTCTGCAGCTCAC	272
QY	181	CCTCGGTGCCCTGGCAGGATGACGCTTCATCCGAGGGGGCGGCCAGGCAAG	240

Db	273	ACTCGGTGCCCTGGCAGGATGAAGCTTTCATCAGGAGGGCGGCCCGCAGGGGTGTG	332
QY	241	GAGCTGGGCTCGGGCAGTGGCCCTGGCTTCGAGGATACCGAGTGAACAGCAGCG	300
Db	333	GAGCTGGGCTCGGGCAGTGGCCCTGGCTTCGAGGATACCGAGTGAACAGCAGCG	392
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QY	361	CGTTTGGTGCAGTGTTCAGTGAAGCAGTTCCTGTTTCGGCCAAAGCTGGAGCCCTGTAC	420
Db	450	CGGCTTGTGCAGGTTTCAGTGAAGCAGTTCCTGCTCTGCCAAGCTGGAGCGGCTGTAC	509
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RESULT 10
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DEFINITION M93422
ACCESSION M93422.1 GI:191690
VERSION adenylyl cyclase; adenylyl cyclase type VI.
KEYWORDS Mus musculus cDNA to mRNA.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 5841)
AUTHORS Yoshimura,M. and Cooper,D.M.
TITLE Cloning and expression of a Ca(2+)-inhibitable adenylyl cyclase
from NCB-20 cells
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (15), 6716-6720 (1992)
MEDLINE 92357702
PUBMED 1379717
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BASE COUNT 1214 a 1558 c 1673 g 1396 t
ORIGIN

Query Match 77.9%; Score 2765; DB 10; Length 5841;
Best Local Similarity 87.1%; Pred. No. 0;
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RESULT 11

AR106659

LOCUS AR106659 4131 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 11 from patent US 6107076.

ACCESSION AR106659

VERSION AR106659.1 GI:12821189

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 4131)

AUTHORS Tang, W.-J. and Gilman, A.G.

TITLE Soluble mammalian adenylyl cyclase and uses therefor

JOURNAL Patent: US 6107076-A 11-22-AUG-2000;

FEATURES

Location/Qualifiers

source 1..4131

BASE COUNT 835 a 1190 c 1182 g 924 t

ORIGIN

Query Match 77.5%; Score 2751.2; DB 6; Length 4131;

Best Local Similarity 86.7%; Pred. No. 0;

Matches 3080; Conservative 0; Mismatches 463; Indels 11; Gaps 4;

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## RESULT 12

RATADCYB

LOCUS

Rattus norvegicus

adenylyl cyclase type VI

M96160

M96160.1

GI:202718

adenylyl cyclase; adenylyl cyclase type VI.

Rattus norvegicus (strain Sprague-Dawley) adult liver, kidney,

heart cDNA to mRNA.

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;

RATADCYB 4131 bp mRNA linear ROD 27-APR-1993

Rattus norvegicus adenylyl cyclase type VI mRNA, complete cds.

REFERENCE	Rattus.
AUTHORS	1 (bases 1 to 4131)
TITLE	Premont,R.T. Multiple mechanisms underlying desensitization of the liver adenylyl cyclase system. Structure and cAMP regulation of liver adenylyl cyclases
JOURNAL	Thesis (1992)
REFERENCE	2 (bases 1 to 4131)
AUTHORS	Premont,R.T., Chen,J., Ma,H.W., Ponnappalli,M. and Iyengar,R.
TITLE	Two members of a widely expressed subfamily of hormone-stimulated adenylyl cyclases
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 89 (20), 9809-9813 (1992)
MEDLINE	93038552
PUBMED	1409703
FEATURES	Location/Qualifiers
source	1. .4131 /organism="Rattus norvegicus" /strain="Sprague-Dawley" /db_xref="taxon:10116" /tissue_type="liver, kidney, heart" /dev_stage="adult" 14. .3556 /EC_number="4.6.1.1" /citation=[2] /codon_start=1 /evidence-experimental /product="adenylyl cyclase type VI" /protein_id="AAA40678.1" /db_xref="GI:202719" /translation="MPLPVARSGRSSMSWFSGLLVKPVKDERKTANGERNQKRRPQ AIRAGFCAPRNSCLKNVPPSPDPAARTCPWDEAFIRAGPGRGVELGRSVAL GDDTEVTPMGTAEVADTSPRSGPWHRLAQVQSKOFFSAKLERLYORYFTQM QSLTLAMVLAVLLTFAAPALPOPAVALITCASVLVFLVLLVYCNRHSFQD SMWYSVVLGILAAVOVGALANSPSAGLWCPVFVITYTLTPRMAAALVSG LGLSTLHLNLHNLNDPFLWKLQGANVLLCTNAIGCVCTHYPAEVSORAOFTFR LQIARHLHONROQERLLSVLPQHVAMEMKEDINTKEDMFKHLYIQHDNVS LRADIEGFTLSQCTAQAEVMTNLFARFKLAENHCLRIKILGDDCYCVSGLPE ARADHACVEMGDMIEAISLVREVTGVNMRVGIHSGRVHCGVILGRKWFQVWS NDVTLANHEAGGRAGRITRITATLOYLNGDYEVPEGRGNAYLKEQCIETFLILG ASOKREKEMLVKQRTANSMGLMPRPVDPAPSRGKDSKAFROMGIDDSKENR GAQDALNVEDEFLGDAIDARSIDOLRKDHVRELLTFQREDLEKKYSRKVDPRFG AVACALNVFCIFCIQFLVFPHSALILGIYAFILLLVTLVLCVSCSGSFENAL QRLRSIVSRVSHSTAVGVSFVLLVFISAIAKNTFCSTHTPLRTCAARMNLNPSDVT CHLQNYLSGLEAPLCEGTAPTSPEFVSVLSLSLASSVFLHISIGKLMTFV LGFYLLLLLPATIFDNYDLILSVHGLASSNETFDGLDPAVRGVALKYMTFVIL LVFALALYHAQVQESTARDLFWKLQATGEKEEELQAYNRLLHNLPLKDVAAHF LARERNDELYQSCVAVMEASIANSEFYVELEANNEGVECLRLNLEIADPDEI ISEERPROLEKIKTIGSTVMAASGLNASTYDQVGRSHITLADYAMRLMEQMKLINEH SPNNFQMKLGNLPGVPVAVIGARKPOYDIWNTVNVSSRMDSTGVDPRIQVTTDLQ VLAAGYQLECRGVKVKRGEMTYFLNGGPSS"
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QY	241 GAGCTGGGGCTCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGTACGAACGACAGCG 300 
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RESULT 13
LOCUS RATADC 6036 bp mRNA linear ROD 12-AUG-1994
DEFINITION Rattus norvegicus adenylyl cyclase type VI mRNA, complete cds.
ACCESSION L01115
VERSION L01115.1 GI:202712
KEYWORDS adenylylate cyclase; adenylyl cyclase; adenylyl cyclase type VI.
SOURCE Rattus norvegicus hepatoma cDNA to mRNA.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 6036)
AUTHORS Krupinski, J., Lehman, T.C., Frankenfield, C.D., Zwaagstra, J.C. and
Watson, P.A.
TITLE Molecular diversity in the adenylyl cyclase family. Evidence for
eight forms of the enzyme and cloning of type VI
J. Biol. Chem. 267 (34), 24858-24862 (1992)
MEDLINE 93077589
PUBMED 1332969
FEATURES
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ORIGIN
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Best Local Similarity 86.5%; Pred. No. 0;
Matches 3075; Conservative 0; Mismatches 468; Indels 11; Gaps 4;
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D 955 GCGCGGCTCCACCTTGCAGCATGACAAATCGGAGCAGAGAGCGGCTGCTGCTGCGTATG 1014  
QY 1039 CCCAGCAGCTTGCATCGGAGATGAAAGAGACATCAACACAAAAGAGAGAC- --ATG 1095  
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QY 1096 TTCACAAGATCTACATACAGAGCATGACAATGTACAGCATCTCTGTTGACAGCATGAG 1155  
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D 1156 GGCCTTACCAGCTGCGATCCAGTGCACGTGCGCAGAGAGCTGGTCATGACCTGAATGAG 1215  
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QY 1216 CTCTTTGCCGGTTTGACAGCTGGCTGCGAGAAATCACCTGCCTGAGGATCAAGATCTTG 1275  
D 1216 CTCTTTGCCGGTTTGACAGCTGGCTGCGAGAAATCACCTGCCTGAGGATCAAGATCTTG 1275  
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ORGANISM Unclassified.  
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AUTHORS Hammond,H.Kirk., Insel,P.A., Ping,P., Post,S.R. and Gao,M.  
TITLE Gene therapy for congestive heart failure  
JOURNAL Patent: US 6306830-A 3 23-OCT-2001;  
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Job time : 6121.65 secs

GenCore version 5.1.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 19:58:51 ; Search time 509.055 Seconds  
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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	3478.4	98.0	4942	20	AA00461 Human type VI aden
4	3379.2	95.2	3582	22	AD08568 Human modified car
5	2996.8	84.4	4046	14	AA042525 Cardiac adenyl cycl
6	2765	77.9	5841	24	AB199680 Mouse ischaemic co
7	2751.2	77.5	4131	21	AA053923 Type VI adenyl cycl
8	1808.4	51.0	1812	22	AD08562 Human partial card
9	1808.4	51.0	2127	19	AAV23246 Human adenyl cycl

10	1703.4	48.0	4523	20	AA00462 Human type V aden
11	1690	47.6	4356	16	AA095540 Cardiac adenyl cycl
12	1688.4	47.6	4356	14	AA037543 Cardiac adenyl cycl
13	1648.2	46.4	3924	21	AA053922 Type V adenyl cycl
14	843	23.8	3137	24	AD28058 Human adenyl cycl
15	595	16.8	3978	21	AA053918 Adenyl cyclase t
16	586	16.5	837	22	AA030177 DNA encoding rena
17	545	15.4	3811	24	AD28061 Human adenyl cycl
18	529.6	14.9	915	22	AA030223 cDNA encoding rena
19	529.6	14.9	915	22	AA030223 cDNA encoding nove
20	505.2	14.2	3518	22	AA02694 Human adenyl cycl
21	495.8	14.0	6470	24	AD31191 Human adenyl cycl
22	494.2	13.9	4011	22	AD06820 Human adenyl cycl
23	475.2	13.4	5873	24	AD31190 Human adenyl cycl
24	463.6	13.1	4601	21	AA053925 Type VIII adenyl cycl
25	460.2	13.0	3769	24	AD28057 Human adenyl cycl
26	459	12.9	4008	17	AA014528 Rat adenyl cyclase
27	459	12.9	4008	21	AA053919 Adenyl cyclase t
28	449.4	12.7	4827	23	AB07501 Drosophila melanog
29	446.6	12.6	3312	24	ABN89298 Human adenyl cycl
30	441.6	12.4	4533	21	AA053920 Type III adenyl cycl
31	433	12.2	5199	21	AA053924 Type VII adenyl cycl
32	428	12.1	3357	21	AA053921 Type IV adenyl cycl
33	412	11.6	4355	24	ABL39754 Human NS cDNA sequ
34	407.6	11.5	3505	24	AD34078 Human secreted pro
35	395.8	11.2	2601	21	AA053926 Human pancreatic c
36	393.2	11.1	1652	21	AA053926 Adenyl cyclase C
37	388.6	10.9	4080	22	AAH16647 Human cDNA sequenc
38	362.2	10.2	7005	23	ABL15355 Drosophila melanog
39	343.8	9.7	3239	22	AAF33100 Human secreted pro
40	295.2	8.3	314	22	AD08561 Human partial card
41	288.2	8.1	2092	17	AA014529 Human adenyl cycl
42	284.4	8.0	1180	22	AAH46933 Human secreted pro
43	277	7.8	5046	23	ABL02755 Drosophila melanog
44	273.6	7.7	320	24	ABL90026 Human polynucleoti
45	267.6	7.5	5201	23	ABL29627 Drosophila melanog

#### ALIGNMENTS

RESULT 1  
AD08563  
ID AAD08563 standard; DNA; 3549 BP.  
AC AAD08563;  
XT  
DT 04-SEP-2001 (first entry)  
XX Human cardiac adenylcyclase VI (ACVI) isoform #1 DNA.  
DE  
DE Human; cardiant; beta-adrenergic signalling protein; beta-ASP;  
KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
KW adenylcyclase; adenyate cyclase; CAMP synthetase;  
KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
KW cardiac adenylcyclase VI; ACVI isoform; beta-ASP transgene; ds.  
XX Homo sapiens.  
OS  
XX  
FH Key Location/Qualifiers  
CDS 1..3504  
FT /\*tag= a  
FT /product= "Human cardiac adenylcyclase VI isoform #1"  
FT /EC\_number= "4.6.1.1"  
FT  
XX WO200148164-A2.  
PN  
XX  
PD 05-JUL-2001.  
XX  
XX  
XX 26-DEC-2000; 2000WO-US35411.  
XX  
XX 27-DEC-1999; 99US-0472667.  
XX



```
Db 1681 GAGAAAGCATGCTGGCCAAAGCTCAGCGGACTCGGGCAACTCCATGGAAGGCTGATG 1740
Qy 1741 CCGCGATGGGTTCCTGATCGTCCCTTCTCCGGACCAAGGACTCCAAGGCTTCGCGCAG 1800
Db 1741 CCGCGATGGGTTCCTGATCGTCCCTTCTCCGGACCAAGGACTCCAAGGCTTCGCGCAG 1800
Qy 1801 ATGGGCAATTGATGATCCAGAAAGACAACCGGGGACCCAAAGATGCCCTGAG 1860
Db 1801 ATGGGCAATTGATGATCCAGAAAGACAACCGGGGACCCAAAGATGCCCTGAG 1860
Qy 1861 GATGAGTGGATGATGATTCCTGAGCCGTGCCATCGATGCCGACGATTCAGCTGGG 1920
Db 1861 GATGAGTGGATGATGATTCCTGAGCCGTGCCATCGATGCCGACGATTCAGCTGGG 1920
Qy 1921 AAGGACCATGTGCGCCGGTTTTTGGCTCACCTTCCAGAGAGAGGATTTTGAAAGAGTAC 1980
Db 1921 AAGGACCATGTGCGCCGGTTTTTGGCTCACCTTCCAGAGAGAGGATTTTGAAAGAGTAC 1980
Qy 1981 TCCCGAAGGTGGATCCCGGTTTCGGAGCCCTACGTTGCCGTGTCCTGTTGGTCTTCG 2040
Db 1981 TCCCGAAGGTGGATCCCGGTTTCGGAGCCCTACGTTGCCGTGTCCTGTTGGTCTTCG 2040
Qy 2041 TTCAATCTGCTTCATCCAGCTTCTAAATTTTCCACACTCCACCCTGATGCTTGGATTTAT 2100
Db 2041 TTCAATCTGCTTCATCCAGCTTCTAAATTTTCCACACTCCACCCTGATGCTTGGATTTAT 2100
Qy 2101 GCCAGCATCTTCCCTGCTGCTAATCACCGTGTGATCTGTGCTGTGTAATCTCTGGT 2160
Db 2101 GCCAGCATCTTCCCTGCTGCTAATCACCGTGTGATCTGTGCTGTGTAATCTCTGGT 2160
Qy 2161 TCTCTGTTCCTTAAGGCCCTGCAACGCTGTGTCGCGAGCATTTGCCCTCACGGGCACAT 2220
Db 2161 TCTCTGTTCCTTAAGGCCCTGCAACGCTGTGTCGCGAGCATTTGCCCTCACGGGCACAT 2220
Qy 2221 AGCACCCGATGTCATCTTTTCCGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
Db 2221 AGCACCCGATGTCATCTTTTCCGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
Qy 2281 TTCACCTGTAAACACACCCCATAGGAGCTGTGCAGCCGGATGCTGAATTTAACACCT 2340
Db 2281 TTCACCTGTAAACACACCCCATAGGAGCTGTGCAGCCGGATGCTGAATTTAACACCT 2340
Qy 2341 GCTGACATCACTGCTGCCACCTGACAGCTCAATTAATCTCTGGCCCTGGATGCTCCC 2400
Db 2341 GCTGACATCACTGCTGCCACCTGACAGCTCAATTAATCTCTGGCCCTGGATGCTCCC 2400
Qy 2401 CTGTGTGAGGCACCATGCCCACCTGACGCTTTCCTGAGGTGTCATCGGGAACATGCTG 2460
Db 2401 CTGTGTGAGGCACCATGCCCACCTGACGCTTTCCTGAGGTGTCATCGGGAACATGCTG 2460
Qy 2461 CTGAGTCTCTTGGCCAGCTCTGCTCTTCTGCACATACGACGATCGGGAAGTTGGCCATG 2520
Db 2461 CTGAGTCTCTTGGCCAGCTCTGCTCTTCTGCACATACGACGATCGGGAAGTTGGCCATG 2520
Qy 2521 ATCTTTGCTTGGGCTCATCTATTGCTGCTGCTTCTGCTGGTCCCGGAGGCTGCTGCTG 2580
Db 2521 ATCTTTGCTTGGGCTCATCTATTGCTGCTGCTTCTGCTGGTCCCGGAGGCTGCTGCTG 2580
Qy 2581 TTTGACAACTATGACCTACTGCTTGGGCTGCATGCGCTTGGCTTCTTCCAAATGAGACCTTT 2640
Db 2581 TTTGACAACTATGACCTACTGCTTGGGCTGCATGCGCTTGGCTTCTTCCAAATGAGACCTTT 2640
Qy 2641 GATGGCTGGACTCTCAGCTGCAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700
Db 2641 GATGGCTGGACTCTCAGCTGCAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700
Qy 2701 CTGCTGTGTTGGCTGGGCTGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2760
Db 2701 CTGCTGTGTTGGCTGGGCTGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2760
Qy 2761 CTAAACTTCTCTGGAACCTACAGGCAACAGGGGAAAGAGGAGATGGAGGACTACAG 2820
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Db 2761 CTAAACTTCTCTGGAACCTACAGGCAACAGGGGAAAGAGAGATGGAGGACTACAG 2820
Qy 2821 GCATACACCGGAGGCTGCTGCATAACATTTCTGCCAAGGACGCTGGGGCCCACTTCTCTG 2880
Db 2821 GCATACACCGGAGGCTGCTGCATAACATTTCTGCCAAGGACGCTGGGGCCCACTTCTCTG 2880
Qy 2881 GCCGGGAGGCGCCCAATGATGAATCTACTATCAGTCGTCGTGTCGTGTCGTGTCGTGTCGT 2940
Db 2881 GCCGGGAGGCGCCCAATGATGAATCTACTATCAGTCGTCGTGTCGTGTCGTGTCGTGTCGT 2940
Qy 2941 TTTGCCCTCCATGTCGCAACTTCTCTGAGTTCTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 3000
Db 2941 TTTGCCCTCCATGTCGCAACTTCTCTGAGTTCTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 3000
Qy 3001 GCCGAGTGCCTGCGGCTGCTCAACGAGATCATCTGCTGACTTTTGTATGATGATTCAGGAG 3060
Db 3001 GCCGAGTGCCTGCGGCTGCTCAACGAGATCATCTGCTGACTTTTGTATGATGATTCAGGAG 3060
Qy 3061 GAGCGGTTCCGGCAGCTGGAAGAGATCAAGACGATTTGCTAGCAGCTACATGGCTGCCTCA 3120
Db 3061 GAGCGGTTCCGGCAGCTGGAAGAGATCAAGACGATTTGCTAGCAGCTACATGGCTGCCTCA 3120
Qy 3121 GGGCTGAACGCCAGCAGCTAGCATCAGGTGGGCGCTCCACACATCACTGCCCTGGCTGAC 3180
Db 3121 GGGCTGAACGCCAGCAGCTAGCATCAGGTGGGCGCTCCACACATCACTGCCCTGGCTGAC 3180
Qy 3181 TACGCCATGCGGCTCATGAGGAGCATGAAGCACATCAATGAGCACTCCTTCAACAATTC 3240
Db 3181 TACGCCATGCGGCTCATGAGGAGCATGAAGCACATCAATGAGCACTCCTTCAACAATTC 3240
Qy 3241 CAGATGAAGATTGGGCTGAACATGGGCCAGTGTGCGAGGTGTCTAGTGTGAGGAGGCTGGAAG 3300
Db 3241 CAGATGAAGATTGGGCTGAACATGGGCCAGTGTGCGAGGTGTCTAGTGTGAGGAGGCTGGAAG 3300
Qy 3301 CCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTAGTGTGAGGAGGAGGAGGAGG 3360
Db 3301 CCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTAGTGTGAGGAGGAGGAGGAGG 3360
Qy 3361 GTCCCCAGCAGCAATCCAGGTGACCCAGCTGTACAGAGTTCTAGTGTGAGGAGGAGGAGG 3420
Db 3361 GTCCCCAGCAGCAATCCAGGTGACCCAGCTGTACAGAGTTCTAGTGTGAGGAGGAGGAGG 3420
Qy 3421 CAGCTGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3480
Db 3421 CAGCTGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3480
Qy 3481 CTCAATGGGGGCGCCAGCAGTTAACAGGGGCGCCAGCCCAAAATTCAGCTGAAGGAGGAGG 3540
Db 3481 CTCAATGGGGGCGCCAGCAGTTAACAGGGGCGCCAGCCCAAAATTCAGCTGAAGGAGGAGG 3540
Qy 3541 GTGGGCACT 3549
Db 3541 GTGGGCACT 3549
```

## RESULT 2

AAD08567

ID AAD08567 standard; DNA; 3552 BP.

XX AAD08567;

AC AC

XX 04-SEP-2001 (first entry)

XX XX

DE Human cardiac adenylylase VI (ACVI) isoform #2 DNA.

XX Human; cardiant; beta-adrenergic signalling protein; beta-ASP;

KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;

KW adenylylase; adenylylase; adenylylase; adenylylase; adenylylase;

KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;

KW cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ds.

XX Homo sapiens.

XX OS





Qy	1498	CTGCCAACCAATGGAAGAGGAGCCGGGCTGCCGCATCCACATCACTTCGGGCAACA	1557
Db	1501	CTGCCAACCAATGGAAGAGGAGCCGGGCTGCCGCATCCACATCACTTCGGGCAACA	1560
Qy	1558	CTGCAGTACCTGAACGGGACATACGAAGTGGAGCCAGCCCTGTGCGCAAGCCGCAACGCG	1617
Db	1561	CTGCAGTACCTGAACGGGACATACGAAGTGGAGCCAGCCCTGTGCGCGAGCGCAACGCG	1620
Qy	1618	TACCTCAAGGAGCAGCACATTGAGACTTTCCCTCATCTCTGGGGCCAGCAGCAAAACGAAA	1677
Db	1621	TACCTCAAGGAGCAGCACATTGAGACTTTCCCTCATCTCTGGGGCCAGCAGCAAAACGAAA	1680
Qy	1678	GAGGAAAGGCATGCTGGCCAAAGCTGCAAGGGACTCGGGCCAACTCCATGGAAGGGCTG	1737
Db	1681	GAGGAAAGGCATGCTGGCCAAAGCTGCAAGGGACTCGGGCCAACTCCATGGAAGGGCTG	1740
Qy	1738	ATCCGCGATGGGTTCCCTCATCGTGCCCTCTCCCGACCAAGGACTCCAAGGCCCTCCGC	1797
Db	1741	ATCCGCGCTGGGTTCCCTCATCGTGCCCTCTCCCGACCAAGGACTCCAAGGCCCTCCGC	1800
Qy	1798	CAGATGGGCATTGATGATTCAGCAAGAACAACCCGGGCAACCAGATGCCTGAACCCCT	1857
Db	1801	CAGATGGGCATTGATGATTCAGCAAGAACAACCCGGGCAACCAGATGCCTGAACCCCT	1860
Qy	1858	GAGATGAGTGGATGAGTTCTCTGACCGTGCCATCGATGCCGACCGAGATGATCAGCTG	1917
Db	1861	GAGATGAGTGGATGAGTTCTCTGACCGTGCCATCGATGCCGACCGAGATGATCAGCTG	1920
Qy	1918	CGAAGGACCATGTGCGCGGTTTTTGCTCACTTCCAGAGAGGATTGTGAGAAAG	1977
Db	1921	CGAAGGACCATGTGCGCGGTTTTTGCTCACTTCCAGAGAGGATTGTGAGAAAG	1980
Qy	1978	TACTCCCGAAGTGATCCCGGCTTCGGAGCTACGTTGCCTGTGCCCTGTGTTGCTCTC	2037
Db	1981	TACTCCCGAAGTGATCCCGGCTTCGGAGCTACGTTGCCTGTGCCCTGTGTTGCTCTC	2040
Qy	2038	TGCTTCACTGCTTCATCCAGCTTCTAATTTCCACACTCCACCTGATGCTTGGGATT	2097
Db	2041	TGCTTCACTGCTTCATCCAGCTTCTAATTTCCACACTCCACCTGATGCTTGGGATT	2100
Qy	2098	TATGCGCAGCATCTTCTGCTGCTAATCAACGCGTGTACTGTGCTGTGTACTCCCTGT	2157
Db	2101	TATGCGCAGCATCTTCTGCTGCTAATCAACGCGTGTACTGTGCTGTGTACTCCCTGT	2160
Qy	2158	GGTTCCTGTTCCCTAAGCCCTGCAACGCTGTGCCGACGATGTCCGCTCACGGGCA	2217
Db	2161	GGTTCCTGTTCCCTAAGCCCTGCAACGCTGTGCCGACGATGTCCGCTCACGGGCA	2220
Qy	2218	CATGACACCGCAGTTGGCATTTTCCGTCCTGCTGTGTTTACTTCTGCCATTGCCAAC	2277
Db	2221	CATGACACCGCAGTTGGCATTTTCCGTCCTGCTGTGTTTACTTCTGCCATTGCCAAC	2280
Qy	2278	ATGTTCACTGTAAACCACACCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAAAC	2337
Db	2281	ATGTTCACTGTAAACCACACCCCATACGGAGCTGTGCAGCCCGGATGCTGAATTTAAAC	2340
Qy	2338	CTGCTGACATCACTGCCCTGCCACCTGCAGCAGCTCAATTAATCTCTGGGGCTGGATGCT	2397
Db	2341	CCTGCTGACATCACTGCCCTGCCACCTGCAGCAGCTCAATTAATCTCTGGGGCTGGATGCT	2400
Qy	2398	CCCTGTGTGAGGGACCAATGCCACCTGCAGCTTTCCTGAGGTGCCATCGGGAACATG	2457
Db	2401	CCCTGTGTGAGGGACCAATGCCACCTGCAGCTTTCCTGAGTACTTCATCGGGAAATG	2460
Qy	2458	CTGCTGAGTCTCTTGGCCAGCTCTGCTTCTGTGCACATCAGCAGCATCGGGAAGTTGCC	2517
Db	2461	CTGCTGAGTCTCTTGGCCAGCTCTGCTTCTGTGCACATCAGCAGCATCGGGAAGTTGCC	2520
Qy	2518	ATGATCTTGTCTTGGGGCTCATCTAATTTGGTGCTGTCTGCTGGGTCCCGACGCGC	2577
Db	2521	ATGATCTTGTCTTGGGGCTCATCTAATTTGGTGCTGTCTGCTGGGTCCCGACGCGC	2580

RESULT 3  
AAX00461  
ID AAX  
XX

AAX00461  
ID AAX00461 standard: CDNA: 4942 BP.

XX

Qy	2578	ATCTTTGACAACTATGACCTACTGTCTGGCGTCCATAGGCTTGGCTTCTTTCAAATGAGACC	2637
Db	2581	ATCTTTGACAACTATGACCTACTGTCTGGCGTCCATAGGCTTGGCTTCTTTCAAATGAGACC	2640
Qy	2638	TTTGATGGCTGGAGCTGCACGTCAGGGAGGGTGCCCTCAAAATATATGACCCCTGTG	2697
Db	2641	TTTGATGGCTGGAGCTGTCCAGCTCAGGGAGGGTGCCCTCAAAATATATGACCCCTGTG	2700
Qy	2698	ATTCTGCTGCTGTTTTCGCTGGCGTGTATCTGCAATGCTCAGCAGGTGGAATCGACTGCC	2757
Db	2701	ATTCTGCTGCTGTTTTCGCTGGCGTGTATCTGCAATGCTCAGCAGGTGGAATCGACTGCC	2760
Qy	2758	CGCCTAAACTTCTCTGGAACCTACAGGCAACAGGGGAAAAGAGGAGATGGAGAGCTA	2817
Db	2761	CGCCTAGACTTCTCTGGAACCTACAGGCAACAGGGGAAAAGAGGAGATGGAGAGCTA	2820
Qy	2818	CAGGCATACAAACGGAGGCTGTGATATACATTCCTGCCCCAAGGAGCTGGCGGCCCACTTC	2877
Db	2821	CAGGCATACAAACGGAGGCTGTGATATACATTCCTGCCCCAAGGAGCTGGCGGCCCACTTC	2880
Qy	2878	CTGGCCCCGAGAGCGCGCAATGATGAACCTCTACTATCAGTCGTGTGAGTGTGGCTGTT	2937
Db	2881	CTGGCCCCGAGAGCGCGCAATGATGAACCTCTACTATCAGTCGTGTGAGTGTGGCTGTT	2940
Qy	2938	ATGTTTGGCTCCATTCGCAACTCTCTCAGTCTCTATGTGGAGCTGGAGGGCAAAACATGAG	2997
Db	2941	ATGTTTGGCTCCATTCGCAACTCTCTCAGTCTCTATGTGGAGCTGGAGGGCAAAACATGAG	3000
Qy	2998	GGTGCCGAGTGCTCGCGTCTCAACGAGATCATCGCTGACTTTTGATGAGATTATCAGC	3057
Db	3001	GGTGCTGAGTGCTCGCGTCTCAACGAGATCATCGCTGACTTTTGATGAGATTATCAGC	3060
Qy	3058	GAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGTTAGCACCCTACATGGCTGCC	3117
Db	3061	GAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGACGATTGTTAGCACCCTACATGGCTGCC	3120
Qy	3118	TCAGGGCTGAAGCCAGCACCCTACGATCAGGTGGCGCCGCTCCCACATCACTGCCCTGGCT	3177
Db	3121	TCAGGGCTGAAGCCAGCACCCTACGATCAGGTGGCGCCGCTCCCACATCACTGCCCTGGCT	3180
Qy	3178	GACTAGCCATGCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCCTTCAACAAT	3237
Db	3181	GACTAGCCATGCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCCTTCAACAAT	3240
Qy	3238	TTCCAGATGAAGATTGGGCTGAACATGGGCCCAAGTCGTGGCAGAGTGTCTATCGGGGCTCGG	3297
Db	3241	TTCCAGATGAAGATTGGGCTGAACATGGGCCCAAGTCGTGGCAGAGTGTCTATCGGGGCTCGG	3300
Qy	3298	AAGCCACAGTATGACATCTGGGGAAACACAGTGAATGTCCTAGTCGTTATGACAGCAGC	3357
Db	3301	AAGCCACAGTATGACATCTGGGGAAACACAGTGAATGTCCTAGTCGTTATGACAGCAGC	3360
Qy	3358	GGGGTCCCCGACCGAATCCAGGTGACCAAGGACCCTGTACCAAGTTCTAGCTGCCAAGGC	3417
Db	3361	GGGGTCCCCGACCGAATCCAGGTGACCAAGGACCCTGTACCAAGTTCTAGCTGCCAAGGC	3420
Qy	3418	TACCAGCTGGAGTGTGCGAGGGTGGTCAAGGTGAAGGCAAGGGGAGATGACCACCTAC	3477
Db	3421	TACCAGCTGGAGTGTGCGAGGGTGGTCAAGGTGAAGGCAAGGGGAGATGACCACCTAC	3480
Qy	3478	TTCTCTCAATGGGGGCCCCAGCAGTTTAAACAGGGCCCAAGCCCAAAATTCAGCTGAAGGGACC	3537
Db	3481	TTCTCTCAATGGGGGCCCCAGCAGTTTAAACAGGGCCCAAGCCCAAAATTCAGCTGAAGGGACC	3540
Qy	3538	AAGGTGGGCAT	3549
Db	3541	AAGGTGGGCAT	3552

### RESULT 3

AX00461

10

XY

AC AAX00461;  
XX  
DT 21-MAY-1999 (first entry)  
XX  
DE Human type VI adenylyl cyclase cDNA.  
XX  
KW Adenylyl cyclase type VI; human; hac6; therapy: diagnosis; ds.  
XX  
XX Homo sapiens.  
OS  
FH Key Location/Qualifiers  
FT CDS 145..3651  
FT /\*tag= a  
XX  
XX WO9901547-A1.  
XX  
XX 14-JAN-1999.  
XX  
XX 01-JUL-1998; 98WO-US13694.  
XX  
XX 01-JUL-1997; 97US-0886550.  
XX  
XX 01-JUL-1997; 97US-0070904.  
XX  
XX (CORT-) COR THERAPEUTICS INC.  
XX  
XX Tomlinson JA;  
PI  
XX WPI; 1999-106049/09.  
DR P-PSDB; AAW30599.  
DR  
XX  
XX Newly isolated and purified human type VI adenylyl cyclase (hac6)  
PT polypeptide - useful for identifying potential therapeutic agents  
PT that modulate hac6 activity, and for the diagnosis of  
PT hac6-associated diseases and disorders  
XX  
XX Claim 3; Fig 1A-I; 42pp; English.  
XX  
XX This DNA sequence encodes human type VI adenylyl cyclase (hac6, see  
CC AAW30599) that is expressed mainly in the heart and brain. hac6 has  
CC a similar putative structure to other adenylyl cyclase isoforms  
CC but, like type V, is distinguishable in that it has a larger  
CC N-terminus and a relatively shorter C-terminus as it lacks the C2b  
CC region. hac6 cDNA was initially isolated from a human heart cDNA  
CC library using an adenylyl cyclase PCR fragment as probe. It was  
CC used to design primers that were used in a PCR-based RACE to obtain  
CC the full-length cDNA sequence. The invention relates to the hac6  
CC gene, methods for the recombinant production of purified hac6 and  
CC the proteins made by these methods, antibodies against hac6,  
CC vectors, probes and host cells (especially HEK-293) transformed by  
CC genes encoding polypeptides having hac6 activity, along with  
CC diagnostic and therapeutic uses for these various reagents. hac6  
CC can be used as a tool to screen for agonists and antagonists that  
CC stimulate/inhibit hac6. Such compounds have therapeutic utility  
CC in treating diseases caused by aberrant activity of this enzyme,  
CC and diseases whose symptoms can be ameliorated by stimulating or  
XX inhibiting the activity of hac6.  
XX  
XX Sequence 4942 BP; 953 A; 1404 C; 1512 G; 1073 T; 0 other;  
SQ  
Query Match 98.0%; Score 3478.4; DB 20; Length 4942;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 3513; Conservative 0; Mismatches 36; Indels 3; Gaps 1;  
Oy 1 ATGTCATGGTTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGAAACACCGCTGGGGT 60  
Db 145 ATGTCATGGTTAGTGGCTCTCTGGTCCCTAAAGTGGATGAACGAAACACCGCTGGGGT 204  
Oy 61 GAACCAATGGGCAAGAGCTTCGGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 120  
Db 205 GAACCAATGGGCAAGAGCTTCGGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 264  
Oy 121 CCCGCTATATAGTGGCTCGGGATGCAGAGCCACCCAGCCCTCGGGGGCCCC 180  
Db 1345 GTCATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACAAAGCTGGCTGGGAGAAATCACTGC 1404

Db 265 CCCGCTATATAGTGGCTCTCGGGATGCAGAGCCACCCAGCCCAACCCCTCGGGCCCC 324  
Oy 181 CTCTGGTCCCTGGCAGGATGACGCCCTTCATCCGAGGGGGGCCAGGCAAGGCAAG 240  
Db 325 CTCTGGTCCCTGGCAGGATGACGCCCTTCATCCGAGGGGGGCCAGGCAAGGCAAG 384  
Oy 241 GAGCTGGGGCTTCGGGGCAGTGGCCCTTGGGCTTCGAGGATACCGAGGTGACACGACGCG 300  
Db 385 GAGCTGGGGCTTCGGGGCAGTGGCCCTTGGGCTTCGAGGATACCGAGGTGACACGACGCG 444  
Oy 301 GCGGGAGCGCTGAGGTGGCGCCGACGCGGTGCCAGGAGTGGCGGATCTCTGCTGGCGC 360  
Db 445 GCGGGAGCGCTGAGGTGGCGCCGACGCGGTGCCAGGAGTGGGAGATCTCTGCTGGCGC 504  
Oy 361 CGTTGGTGCAGGTGTTCCAGTGAAGCAGTTCCTTCGGCAAGCTGAGAGCGCTGTAC 420  
Db 505 CGTCTGGTGCAGGTGTTCCAGTGAAGCAGTTCCTTCGGCAAGCTGAGAGCGCTGTAC 564  
Oy 421 CAGCGGTACTTTTCCAGATGAACAGAGACGCTGACGCTGCTGGTGGCGGTGCTGGT 480  
Db 565 CAGCGGTACTTTTCCAGATGAACAGAGACGCTGACGCTGCTGATGGCGGTGCTGGT 624  
Oy 481 CTGCTCAGAGCGGTGCTGCTGGCTTTCCAGCGCGCACCCGCCCTCAGCCTGCCTAT 540  
Db 625 CTGCTCAGAGCGGTGCTGCTGGCTTTCCAGCGCGCACCCGCCCTCAGCCTGCCTAT 684  
Oy 541 GTGCACTGTTGGCTGTGCGCGCGCCCTGTTGCTGGGGCTCATGTTGGTGTGTAAACGG 600  
Db 685 GTGCACTGTTGGCTGTGCGCGCGCCCTGTTGCTGGGGCTCATGTTGGTGTGTAAACGG 744  
Oy 601 CATAGCTTCCGCCAGGACTCCATGTGGTGTGTGAGTAAAGTGGTGTGGGCTCCTGGCG 660  
Db 745 CATAGCTTCCGCCAGGACTCCATGTGGTGTGTGAGTAAAGTGGTGTGGGCTCCTGGCG 804  
Oy 661 GCAGTGCAGGTGCGGGGGCGCTTTCGCACAGACACCGCGCGCCCTCTGCGGGGCTCTGG 720  
Db 805 GCAGTGCAGGTGCGGGGGCGCTTTCGCACAGACACCGCGCGCCCTCTGCGGGGCTCTGG 864  
Oy 721 TGCCCTGTGTTCTTTGTATACATGCATACAGCTCCCTCCCATCCGATCGGGGCTGCC 780  
Db 865 TGCCCTGTGTTCTTTGTATACATGCATACAGCTCCCTCCCATCCGATCGGGGCTGCC 924  
Oy 781 GTCTCAGCGGCTGGGCTCTCCACCTTGCATTTGATTTGGCTTGGCACTTAAACCGT 840  
Db 925 GTCTCAGCGGCTGGGCTCTCCACCTTGCATTTGATTTGGCTTGGCACTTAAACCGT 984  
Oy 841 GGTATGCTTCTCTGGAAGCAGCTCGGTGCCATGTGCTGCTTCTCTGCACCAAC 900  
Db 985 GGTATGCTTCTCTGGAAGCAGCTCGGTGCCATGTGCTGCTTCTCTGCACCAAC 1044  
Oy 901 GTCATTAGCATCTGCACACACTATCCACAGAGGTGTCTCAGCGCGAGGCTTTTCAGGAG 960  
Db 1045 GTCATTAGCATCTGCACACACTATCCACAGAGGTGTCTCAGCGCGAGGCTTTTCAGGAG 1104  
Oy 961 ACCCGAGTTATATCCAGGCGCGCTCCACCTGCAGCATGAGAATCGGACGAGGAGCGG 1020  
Db 1105 ACCCGAGTTATATCCAGGCGCGCTCCACCTGCAGCATGAGAATCGGACGAGGAGCGG 1164  
Oy 1021 CTGCTGTGTCGGTATTGCCCGCAGCAGCTTGCATGGAGATGAAGAAGACATCAACACA 1080  
Db 1165 CTGCTGTGTCGGTATTGCCCGCAGCAGCTTGCATGGAGATGAAGAAGACATCAACACA 1224  
Oy 1081 AAAAAAGAGAC --- ATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAAGCATC 1137  
Db 1225 AAAAAAGAGACATGATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAAGCATC 1284  
Oy 1138 CTGTTTGCAGACATTGAGGGCTTCAACAGCTTGGCATCCCACTGCCAGTGCAGGAGCTG 1197  
Db 1285 CTGTTTGCAGACATTGAGGGCTTCAACAGCTTGGCATCCCACTGCCAGTGCAGGAGCTG 1344  
Oy 1198 GTCATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACAAAGCTGGCTGGGAGAAATCACTGC 1257  
Db 1345 GTCATGACCCCTGAATGAGCTCTTTGCCCGGTTTGACAAAGCTGGCTGGGAGAAATCACTGC 1404

Qy	1258	CTGAGGATCAAGATCTTTGGGGAGCTGTTACTACTGTGTGTGTCAGGGCTGCCGGAGAGCCCGG	1317
Db	1405	CTGAGGATCAAGATCTTTGGGGAGCTGTTACTACTGTGTGTGTCAGGGCTGCCGGAGAGCCCGG	1464
Qy	1318	GCCGACCATGCCACATGCTGTGTGGAGATGGGGGTAGACATGATTTGAGGCCATCTCGCTG	1377
Db	1465	GCCGACCATGCCACATGCTGTGTGGAGATGGGGGTAGACATGATTTGAGGCCATCTCGCTG	1524
Qy	1378	GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGCGCGCTG	1437
Db	1525	GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGCGCGCTG	1584
Qy	1438	CACTGCGGCGTCTTGGCTTGGGAAATGGCAGTTTCGATGTGTGGTCCAATGATGTGACC	1497
Db	1585	CACTGCGGCGTCTTGGCTTGGGAAATGGCAGTTTCGATGTGTGGTCCAATGATGTGACC	1644
Qy	1498	CTGCCAACACATGGAAGCAGGAAGCCGGGCTGGCCGATCCACATCCTCGGGCAACA	1557
Db	1645	CTGCCAACACATGGAAGCAGGAAGCCGGGCTGGCCGATCCACATCCTCGGGCAACA	1704
Qy	1558	CTGCAGTACTGAACGGGAGCTACGAAGTGGAGCAGGCCGCTGTGGCAAGCGACGCG	1617
Db	1705	CTGCAGTACTGAACGGGAGCTACGAAGTGGAGCAGGCCGCTGTGGCAAGCGACGCG	1764
Qy	1618	TACTCAAGGAGCAGCACATTGAGACTTTCCCTCATCTCTGGGCGCCAGCCAGAAACGGAAA	1677
Db	1765	TACTCAAGGAGCAGCACATTGAGACTTTCCCTCATCTCTGGGCGCCAGCCAGAAACGGAAA	1824
Qy	1678	GAGGAAAGGCATGCTGGCCAAAGTGCAGCGGACTCGGGGCCAACTCCATGGAAGGGCTG	1737
Db	1825	GAGGAAAGGCATGCTGGCCAAAGTGCAGCGGACTCGGGGCCAACTCCATGGAAGGGCTG	1884
Qy	1738	ATGCCGGATGGGTTCTTGATCGTGGCTTCTCCCGGACCAAGGACTCCAAGGCGCTTCGCG	1797
Db	1885	ATGCCGGCTGGGTTCTTGATCGTGGCTTCTCCCGGACCAAGGACTCCAAGGCGCTTCGCG	1944
Qy	1798	CAGATGGGCATTGATGATTTCCAGCAAGAACAACCGGGGCACCCAAAGATGCCCTCAACCGT	1857
Db	1945	CAGATGGGCATTGATGATTTCCAGCAAGAACAACCGGGGCACCCAAAGATGCCCTCAACCGT	2004
Qy	1858	GAGATGAGGTGGATGAGTTCCTGAGCCGTGCCATCGATGCCCGCAGCATTTGATCAGCTG	1917
Db	2005	GAGATGAGGTGGATGAGTTCCTGAGCCGTGCCATCGATGCCCGCAGCATTTGATCAGCTG	2064
Qy	1918	CGGAAGGACCATGTGCGCGGTTTTTGCTCACCTTCCAGAGAGAGGATTTTGAGAAAG	1977
Db	2065	CGGAAGGACCATGTGCGCGGTTTTTGCTCACCTTCCAGAGAGAGGATTTTGAGAAAG	2124
Qy	1978	TACTCCCGAAGTGGATCCCGCTTCGGAGGCTACGTTGGCTGTGCCCTGTGGCTTTC	2037
Db	2125	TACTCCCGAAGTGGATCCCGCTTCGGAGGCTACGTTGGCTGTGGCTTTC	2184
Qy	2038	TGCTTCATCTGCTTCAATCCAGCTTCTAATTTTCCACACTCCACCCCTGATGTTGGGATT	2097
Db	2185	TGCTTCATCTGCTTCAATCCAGCTTCTAATTTTCCACACTCCACCCCTGATGTTGGGATT	2244
Qy	2098	TATGCCAGCATCTTCTGCTGCTGCTAATCACCCTGCTGATCTGTGCTGTGCTACTCCTGT	2157
Db	2245	TATGCCAGCATCTTCTGCTGCTGCTAATCACCCTGCTGATCTGTGCTGTGCTACTCCTGT	2304
Qy	2158	GGTTCTCTGTTCCCTAAGGCCCTGCAACGCTGTGCCGACGATTTGCCGTACAGGGCA	2217
Db	2305	GGTTCTCTGTTCCCTAAGGCCCTGCAACGCTGTGCCGACGATTTGCCGTACAGGGCA	2364
Qy	2218	CATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCTGTGTTTACTTCTGCCATTTGCCAAC	2277
Db	2365	CATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCTGTGTTTACTTCTGCCATTTGCCAAC	2424
Qy	2278	ATGTTCACTGTAAACACACACCCCATACGGAGCTGTGAGCCCGCGGATGCTGAATTTAAACA	2337
Db	2425	ATGTTCACTGTAAACACACACCCCATACGGAGCTGTGAGCCCGCGGATGCTGAATTTAAACA	2484

Qy	2338	CCTGCTGACATCACTACTGCTGCCACCTGCGACGAGCTCAATTA	CTCTCTCTGCGGCTCGGATGCT	2339
Db	2485	CCTGCTGACATCACTACTGCTGCCACCTGCGACGAGCTCAATTA	CTCTCTCTGCGGCTCGGATGCT	2544
Qy	2398	CCCTGTGTGAGGGCACCATTGCCCCACTGCGCTTCTGAGGTGCT	CTCCATCGGGAACAATG	2457
Db	2545	CCCTGTGTGAGGGCACCATTGCCCCACTGCGCTTCTGAGTCTT	CATTCGGGNAACATG	2604
Qy	2458	CTGTGAGTCTCTTTGGGCCAGCTCTGTCTTCCTGCGACATCAG	ACAGCATCGGGAAGTTGGCC	2517
Db	2605	CTGTGAGTCTCTTTGGGCCAGCTCTGTCTTCCTGCGACATCAG	CAGCAGCATCGGGAAGTTGGCC	2664
Qy	2518	ATGATCTTTTGTCTGGGGTCATCTATTTTGGTGTGCTTCTGCT	TGCTGCCCGCAGCGCC	2577
Db	2665	ATGATCTTTTGTCTGGGGTCATCTATTTTGGTGTGCTTCTGCT	TGCTGCCCGCAGCGCC	2724
Qy	2578	ATCTTTTACAACTATGACCTACTGCTGTGGCTGCCATGGCTTG	GGCTTTCCTTCCAAATGAGACC	2637
Db	2725	ATCTTTTACAACTATGACCTACTGCTGTGGCTGCCATGGCTTG	GGCTTTCCTTCCAAATGAGACC	2784
Qy	2638	TTTGATGGCTTGGACTGTCCAGTGCAGGGAGGGTGGCCCTCAA	ATATATATGACCCCTGTG	2697
Db	2785	TTTGATGGCTTGGACTGTCCAGTGCAGGGAGGGTGGCCCTCAA	ATATATGACCCCTGTG	2844
Qy	2698	ATTCTGCTGCTGTTTGGCTTGGGGCTGTATCTGCGATGCTCAG	CAGGTTGGAATTCGACTGCC	2757
Db	2845	ATTCTGCTGCTGTTTGGCTTGGGGCTGTATCTGCGATGCTCAG	CAGGTTGGAATTCGACTGCC	2904
Qy	2758	CGCTTAACTTCCTCTGGAACTTACAGGCAACAGGGGAAAAGAG	AGAGATGGAGAGGACTA	2817
Db	2905	CGCTTAACTTCCTCTGGAACTTACAGGCAACAGGGGAAAAGAG	AGAGATGGAGAGGACTA	2964
Qy	2818	CAGGCATACAACCGGAGGCTGTGCTACATAACATTCCTCCCA	AGGACGTGGCGCCCACTTC	2877
Db	2965	CAGGCATACAACCGGAGGCTGTGCTACATAACATTCCTCCCA	AGGACGTGGCGCCCACTTC	3024
Qy	2878	CTGGCCCGGAGCGCCCAATGATGAACCTACTATCAGTCTGTG	AGTGTGTGGCTGTT	2937
Db	3025	CTGGCCCGGAGCGCCCAATGATGAACCTACTATCAGTCTGTG	AGTGTGTGGCTGTT	3084
Qy	2938	ATGTTTGCCCTCAATGCGCAACTTCTCTGAGTTCATATGTGAG	CTGTGAGCTGGAGGCAACAATGAG	2997
Db	3085	ATGTTTGCCCTCAATGCGCAACTTCTCTGAGTTCATATGTGAG	CTGTGAGCTGGAGGCAACAATGAG	3144
Qy	2998	GGTGCCGAGTGCCCTGCGGCTGTCTCAACGAGATCATCGCTGA	CTTTGATGAGATTATCAGC	3057
Db	3145	GGTGCCGAGTGCCCTGCGGCTGTCTCAACGAGATCATCGCTGA	CTTTGATGAGATTATCAGC	3204
Qy	3058	GAGGAGCGGTTCCGGCAGCTGGAAAAGATCAGACGATTTGGT	TAGCACCTACATGGCTGCC	3117
Db	3205	GAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGAGGATTTGG	TAGCACCTACATGGCTGCC	3264
Qy	3118	TCAGGGCTGAACCGCAGCAGCTACGATCAGGTGGGCGCTCCCA	TCATCAGTCCCTGGCT	3177
Db	3265	TCAGGGCTGAACCGCAGCAGCTACGATCAGGTGGGCGCTCCCA	TCATCAGTCCCTGGCT	3324
Qy	3178	GACTTACGCCATGGGGTCTATGGAGCAGATGAAGACACATCAAT	TGAGCAGCTCCCTTCAACAAT	3237
Db	3325	GACTTACGCCATGGGGTCTATGGAGCAGATGAAGACACATCAAT	TGAGCAGCTCCCTTCAACAAT	3384
Qy	3238	TTCCAGATGAAGATTTGGGCTGAACATGGGCCAGTCTGTGGCAG	GTGTATCGGGGCTCGG	3297
Db	3385	TTCCAGATGAAGATTTGGGCTGAACATGGGCCAGTCTGTGGCAG	GTGTATCGGGGCTCGG	3444
Qy	3298	AAGCCACAGTATCAGATCTGGGGGAACACAGTGAATGCTCTCT	AGTCGTATGAGCAGCAGC	3357
Db	3445	AAGCCACAGTATCAGATCTGGGGGAACACAGTGAATGCTCTCT	AGTCGTATGAGCAGCAGC	3504
Qy	3358	GGGTCCTCCGACCGAATCCAGGTGACCGGACCTGTACCAAGTT	CTAGCTTCTAGCTGCCAAGGGC	3417
Db	3505	GGGTCCTCCGACCGAATCCAGGTGACCGGACCTGTACCAAGTT	CTAGCTTCTAGCTGCCAAGGGC	3564
Qy	3418	TACCAGCTGGAGTGTGCGAGGGGTGGTTCGAAGGTTGAAGGCA	AGGGGAGATGACCACTAC	3477

|||||  
Db 3565 TACCAGCTGGAGTGTGCGAGGGGTGCTCAAGGTGAAGGGCAAGGGGAGATGACACCTAC 3624  
Qy 3478 TTCCCTCAATGGGGGCCCGCAGCAGTTTAAACAGGGGCCCGCAGCCACAAATTCAGCTGAAGGGACC 3537  
Db 3625 TTCCCTCAATGGGGGCCCGCAGCAGTTTAAACAGGGGCCCGCAGCCACAAATTCAGCTGAAGGGACC 3684  
Qy 3538 AAGGTGGGCACT 3549  
Db 3685 AAGGTGGGCATT 3696  
|||||  
RESULT 4  
AAD08568  
ID AAD08568 standard; cDNA: 3582 BP.  
XX  
XX  
AC AAD08568;  
XX  
DT 04-SEP-2001 (first entry)  
XX  
DE Human modified cardiac adenylylase VI (ACVI) isoform cDNA.  
XX  
KW Human; cardiant; beta-adrenergic signalling protein; beta-ASP;  
KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
KW adenylylase; adenylylase; adenylylase; adenylylase; adenylylase;  
KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
KW cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 22..3525  
FT /\*tag= a  
FT /product= "Human modified cardiac ACVI isoform"  
XX  
PN WO200148164-A2.  
XX  
XX  
PD 05-JUL-2001.  
XX  
PF 26-DEC-2000; 2000WO-US35411.  
XX  
XX 27-DEC-1999; 99US-0472667.  
PR  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Hammond HK, Gao M;  
PI  
XX  
DR WPI; 2001-418260/44.  
DR P-PSDB; AAE04312.  
XX  
PT Novel polynucleotide encoding a modified adenylylase polypeptide  
PT useful for enhancing cardiac function in mammalian hearts, and for  
PT treating heart disease, especially congestive heart failure -  
XX  
PS Claim 4; Page 143-150; 153pp; English.  
XX  
XX The present invention relates to methods and compositions for enhancing  
CC cardiac function in mammalian hearts by inserting transgenes encoding  
CC beta-adrenergic signalling proteins (beta-ASP) which increase  
CC beta-adrenergic responsiveness within the myocardium using in vivo  
CC gene therapy. The beta-ASPs of the invention include beta-adrenergic  
CC receptors (beta-AR), adenylylases (also referred to as adenylylase,  
CC adenylylase cyclase and CAMP synthetase) and G-protein receptor kinase  
CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function  
CC in mammalian hearts and for treating heart disease, especially  
CC congestive heart failure. The present cDNA sequence encodes human  
CC modified cardiac adenylylase VI (ACVI) isoform which is used for  
CC generating a beta-ASP transgene, used in the exemplification of the  
XX invention.  
XX  
XX Sequence 3582 BP; 703 A; 1036 C; 1067 G; 776 T; 0 other;

Query Match 95.2%; Score 3379.2; DB 22; Length 3582;  
Best Local Similarity 97.4%; Pred. No. 0;  
Matches 3458; Conservative 0; Mismatches 88; Indels 6; Gaps 2;  
Qy 1 ATGTCATGTTAGTGGGCTCTGCTGCTTAAAGTGGATGAACGGAACACCCCTGGGT 60  
Db 22 ATGTCATGTTAGTGGGCTCTGCTGCTTAAAGTGGATGAACGGAACACCCCTGGGT 81  
Qy 61 GAAACCAATGGGCAAGCGTTTCGGGGCGCGTGCACCTCGGGCAGGTGCTTCTGCAG 120  
Db 82 GAAACCAATGGGCAAGCGTTTCGGGGCGCGTGCACCTCGGGCAGGTGCTTCTGCAG 141  
Qy 121 CCCCCTATATAGCTGCTCCGGGATGAGAGCCACCCAGCCACCCCTCGGGCCCC 180  
Db 142 CCCCCTATATAGCTGCTCCGGGATGAGAGCCACCCAGCCACCCCTCGGGCCCC 201  
Qy 181 CCTCGGTGCCCTGGCAGGATGACCCCTTCATCCGGAGGGGGGGCCAGGCGCAAG 240  
Db 202 CCTCGGTGCCCTGGCAGGATGACCCCTTCATCCGGAGGGGGGGCCAGGCGCAAG 261  
Qy 241 GAGCTGGGGCTCGGGCAGTGGCCCTTCGAGGATACCGAGTGAACAACGACAGCG 300  
Db 262 GAGCTGGGGCTCGGGCAGTGGCCCTTCGAGGATACCGAGTGAACAACGACAGCG 321  
Qy 301 GCGGGACGGCTGAGTGGGGCGCCGACGCGTGCAGAGTGGCGATCTCTGCTGGCG 360  
Db 322 GCGGGACGGCTGAGTGGGGCGCCGACGCGTGCAGAGTGGCGATCTCTGCTGGCG 381  
Qy 361 CGTTTGGTGCAGGTCTTCAGTGAAGAGTTCCTTTCGGCCAAAGCTGAGGCGCTGTAC 420  
Db 382 CGTCTGGTGCAGGTCTTCAGTGAAGAGTTCCTTTCGGCCAAAGCTGAGGCGCTGTAC 441  
Qy 421 CAGCGGTACTTTTCCAGATGAACAGAGCAGCCCTGCTGCTGTCGCGGTGCTGTCG 480  
Db 442 CAGCGGTACTTTTCCAGATGAACAGAGCAGCCCTGCTGCTGTCGCGGTGCTGTCG 501  
Qy 481 CTGCTCACAGGGTCTGCTGGCTTTTCCAGCGCCAGCCCGCCCTCAGCCTGCCTAT 540  
Db 502 CTGCTCACAGGGTCTGCTGGCTTTTCCAGCGCCAGCCCGCCCTCAGCCTGCCTAT 561  
Qy 541 GTGGCAGTGTGGCTGTGCGCGCCCTGCTGCTGGGGCTCATGCTGTTGTTAACCGG 600  
Db 562 GTGGCAGTGTGGCTGTGCGCGCCCTGCTGCTGGGGCTCATGCTGTTGTTAACCGG 621  
Qy 601 CATAGCTTCGCGCAGGACTCCATGTGGTGTGAGTAACTGCTGCTGGCATCTCTGGCG 660  
Db 622 CATAGCTTCGCGCAGGACTCCATGTGGTGTGAGTAACTGCTGCTGGCATCTCTGGCG 681  
Qy 661 GCAGTGCAGGTGGGGGCGCTTTCGACAGACCGCGAGCCCTCTGCGGGCTCTCTGG 720  
Db 682 GCAGTGCAGGTGGGGGCGCTTTCGACAGACCGCGAGCCCTCTGCGGGCTCTCTGG 741  
Qy 721 TGCCCTGTGTTCTTTGATATACATCCATACAGCTTCTTCCCATCCGATCGGCGTGC 780  
Db 742 TGCCCTGTGTTCTTTGATATACATCCATACAGCTTCTTCCCATCCGATCGGCGTGC 801  
Qy 781 GTCCCTCAGCGGCTGGGCTCTCCACCTTGCATTTGATCTTGGCTTGGCACTTAACCGT 840  
Db 802 GTCCCTCAGCGGCTGGGCTCTTCCACCTTGCATTTGATCTTGGCTTGGCACTTAACCGT 861  
Qy 841 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTTCTCTGTCACCAAC 900  
Db 862 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTTCTCTGTCACCAAC 921  
Qy 901 GTCATTACATCTGCACACACTATCCACAGAGGTGCTCAGCGCCAGGCTTTTCAGAG 960  
Db 922 GTCATTGCACTCTGCACACACTATCCACAGAGGTGCTCAGCGCCAGGCTTTTCAGAG 981  
Qy 961 ACCCGCAGTTACATCCAGGCGCGGCTCCACCTGACAGCATGAGAATCGGACGAGGGG 1020  
Db 982 ACCCGCAGTTACATCCAGGCGCGGCTCCACCTGACAGCATGAGAATCGGACGAGGGG 1041  
Qy 1021 CTGCTGCTGTCGGTATTCGCCCGACGACGCTTGCCTGGAGATGAAGAAGACATCAACACA 1080

Db 1042 CTGCTGCTGTCGTAATGCCCCAGCAGTTCGCCATGAGATGAAGAAGACATCAACACA 1101  
QY 1081 AAAAAAGAGAC---ATGTTCCACAAGATCTACATACAGAGCATGACAAATGTCAGCATC 1137  
Db 1102 AAAAAAGAGAGATGATGTTTCCACAAGATCTACATACAGAAGCATGACAAATGTCAGCATC 1161  
QY 1138 CTGTTTGCAGACATTTAGGGCTTTCACCCAGCCTGCCATCCCAAGTGCATCGCCAGGAGCTG 1197  
Db 1162 CTGTTTGCAGACATTTAGGGCTTTCACCCAGCCTGCCATCCCAAGTGCATCGCCAGGAGCTG 1221  
QY 1198 GTCATGACCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGCTGCGGAGAAATCACTGC 1257  
Db 1222 GTCATGACCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGCTGCGGAGAAATCACTGT 1281  
QY 1258 CTGAGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGGAGGCCCGG 1317  
Db 1282 CTGAGATCAAGATCTTAGAGACTGTTACTACTGCTGTCAGGGCTGCCCGAGGCCCGG 1341  
QY 1318 GCCGACCATGCCACCTGCTGTGTGGAGATGGGGGTAGACATGATGAGGCCATCTCGCTG 1377  
Db 1342 GCAGATCACGCCACCTGCTGTGTGGAGATGGGGGTAGACATGATCGAAGCCATCTCGCTG 1401  
QY 1378 GTACGTGAGGTGACAGGTGTGAATGTGAACATCGCGGTGGGATCCACAGCGGGCGGGTG 1437  
Db 1402 GTGCGTGAAGTAACAGGTGTGAACGTGAACATGCTGTGGGCATCCACAGCGGACGTGTG 1461  
QY 1438 CACTGGGGCTGCTTGGCTTGGCGAAATGCGAGTTCGATGTGTGGTCCCAATGATGTGACC 1497  
Db 1462 CATTGGGGCTGCTTGGCTTACCGAATGGCAGTTTGTATGCTGTGGTCAACAGATGTGACC 1521  
QY 1498 CTGGCCAAACACATGGAAGCAGGAAGCCGGGCTGGCGCATCCACATCACTCGGGCAACA 1557  
Db 1522 CTGGCTAACACATGGAGGCCGGGGC---GGCCGGCGCATCCACATCACTCGGGCTACA 1578  
QY 1558 CTGCAGTACCTGAACGGGGACTAGGAAGTGGAGCGCAGCGCGTGGTGGCAAGCCCAAGCG 1617  
Db 1579 CTGCATACTTGAACGGGGACTATGAGTGGAGCGCAGCGCGTGGTGAACGCAATGCG 1638  
QY 1618 TACCTCAAGGAGCAGCACATTTAGACTTTCCTCATCTGGCGGCCAGCCAGCAAGAACGGAAA 1677  
Db 1639 TACCTCAAGGAGCAGTGATTTAGACCTTCCTCATACTTGGCGCCAGCCAAACCGGAAA 1698  
QY 1678 GAGGAAAGGCATGTGGCCAAAGCTGCAGCGGACTCGGSCCAACTCCATGGAAGGGCTG 1737  
Db 1699 GAGGAAAGCCATGCTGGCCAAAGCTTCAGCGGACAGCGGCCAACTCCATGGAAGGACTG 1758  
QY 1738 ATGCCGGATGGTTCCTGATGCTGCTTCTCCGGACCAAGACTCCCAAGGCTTCCCGC 1797  
Db 1759 ATGCCCGCTGGGTTCCTGACCTGGCTTCTCCCGGACCAAGGACTCTAAGGCAATTCGCG 1818  
QY 1798 CAGATGGGCATTTGATGATTCACAAAGACAACCCGGGGCACCAAGATGCCCTGAACCCCT 1857  
Db 1819 CAGATGGGCATTTGATGATTTACAAAGACAACCCGGGGTCCCAAGATGCTGTAACCCCT 1878  
QY 1858 GAGGATCAGGTGATGAGTTCCTGAGCCGTGCCATCGATGCCCGCAGCAATTTGATCAGCTG 1917  
Db 1879 GAAGATCAGGTGATGAGTTCCTGGCCGAGCCATCGATGCCCGCAGCAATTTGATCAGCTG 1938  
QY 1918 CGAAGAGACCATGTGGCCGGTTTTTGTCTACACCTTCAGAGAGAGGATTTTGAGAAGAAG 1977  
Db 1939 CGAAGAGACCATGTGGCCGGTTTTGCTCACCCTTCACAGAGAGAGATCTTTGAGAAGAAG 1998  
QY 1978 TACTCCGGAAGTGGATCCCGCTTCGGAGCCTAGTTCGCTGTCCTGTTGGTCTTC 2037  
Db 1999 TACTCCGGAAGTGGATCCCGCTTCGGAGCCTAGTTCGCTGTCCTGTTGGTCTTC 2058  
QY 2038 TGCTTCATCTGCTTCATCCAGCTTCTAATTTTCCCACTCCACCTGATGCTTGGGATT 2097  
Db 2059 TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCCACTCCACCTGATGCTTGGGATC 2118  
QY 2098 TATGCCAGCATCTTCTGCTGCTGCTTAATCACCGTGTGCTGATCTGCTGTGTACTCCTGT 2157

Db 2119 TATGCCAGCATCTTCTGCTGCTGCTAATCACCGTGTGATGCTGTGCTGTACTCCTGT 2178  
QY 2158 GGTTCCTCTGTTCCCTTAAGGCCCTGCAACGCTCTGCCGAGCATGTGCCCTCACGGGCA 2217  
Db 2179 GGTTCCTCTGTTCCCTTAAGGCCCTGCAACGCTGTGCCGAGCATGTGCCCTCACGGGCA 2238  
QY 2218 CATAGCACCGCAGTTGGCACTTTTTCCGCTGCTGCTGTTTACTTCTGCAATTTGCCAAC 2277  
Db 2239 CATAGCACCGCAGTTGGCACTTTTTCCGCTGCTGTTTACTTCTGCAATTTGCCAAC 2298  
QY 2278 ATGTTTCACTGTAACACACACCCCATACGAGCTGTGCAGCCGGATGCTGAATTTAACA 2337  
Db 2299 ATGTTTCACTGTAACACACACCCCATACGAGCTGTGCAGCCGGATGCTGAATTTAACA 2358  
QY 2338 CTTGCTGACATCACTGCTGCCACCTGCGAGCTCAATTAATCTCTGCGGCTTGATGCT 2397  
Db 2359 CTTGCTGACATCACTGCTGCCACCTGCGAGCTCAATTAATCTCTGCGGCTTGATGCT 2418  
QY 2398 CCCTGTGTGAGGCAACCATGCCCCACTGCACTTCTCTGAGGTGTCATCGGGAACATG 2457  
Db 2419 CCCTGTGTGAGGCAACCATGCCCCACTGCACTTCTCTGAGTACTTTCATCGGGAACATG 2478  
QY 2458 CTGCTGAGTCTCTTGGCCAGCTCTGCTTCTCTGCACATCAGCAGCATCGGGAAGTTGGCC 2517  
Db 2479 CTGCTGAGTCTCTTGGCCAGCTCTGCTTCTCTGCACATCAGCAGCATCGGGAAGTTGGCC 2538  
QY 2518 ATGATCTTCTGTTGGGGCTCATCTATTGCTGCTGCTTCTGCTGGTCCCGCAGCGCC 2577  
Db 2539 ATGATCTTCTGTTGGGGCTCATCTATTGCTGCTGCTTCTGCTGGTCCCGCAGCGCC 2598  
QY 2578 ATCTTTGACAACATATGACCTTACTGCTTGGCTCCATGGCTTGGCTTCTTCCAATGAGACC 2637  
Db 2599 ATCTTTGACAACATATGACCTTACTGCTTGGCTCCATGGCTTGGCTTCTTCCAATGAGACC 2658  
QY 2638 TTTGATGGGCTGAGCTGTCCAGCTGAGGAGGGTGGCCCTCAAAATATATGACCCCTGTG 2697  
Db 2659 TTTGATGGGCTGAGCTGTCCAGCTGAGGAGGGTGGCCCTCAAAATATATGACCCCTGTG 2718  
QY 2698 ATTCTGCTGCTGTTGGCTGGCGCTGATCTGATGCTCAGCAGGTGGAATGACATGCC 2757  
Db 2719 ATTCTGCTGCTGTTGGCTGGCGCTGATCTGATGCTCAGCAGGTGAGTGCATGCC 2778  
QY 2758 CGCCTAAACTTCTCTGGAACCTACAGGCAACAGGGGAAAAGAGAGATGGAAGAGCTA 2817  
Db 2779 CGCCTAGACTTCTCTGGAACCTACAGGCAACAGGGGAGAAGGAGAGATGGAAGAGCTA 2838  
QY 2818 CAGGCATACAACCGGAGGCTGCTGCATAACATTCGCCCAAGGACGTGGCGGCCCACTTC 2877  
Db 2839 CAGGCATACAACCGGAGGCTGCTGCATAACATTCGCCCAAGGACGTGGCGGCCCACTTC 2898  
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QY 2938 ATCTTTGCCCTCCATTTGCCAACTTCTCTGAGTTCATGTGAGCTGGAAGCAAAATGAG 2997  
Db 2959 ATCTTTGCCCTCCATTTGCCAACTTCTCTGAGTTCATGTGAGCTGGAAGCAAAATGAG 3018  
QY 2998 GGTGCGGAGTGCCTGCGGCTGCTCAGGAGATCATCGCTGACTTTGATGAGATTTATCAGC 3057  
Db 3019 GGTGCGGAGTGCCTGCGGCTGCTCAGGAGATCATCGCTGACTTTGATGAGATTTATCAGC 3078  
QY 3058 GAGGAGCGGTTCCGGCAGCTGGAAGATCAAGACGATTTGATGACCTACATGCGCTGCC 3117  
Db 3079 GAGGAGCGGTTCCGGCAGCTGGAAGATCAAGACGATTTGATGACCTACATGCGCTGCC 3138  
QY 3118 TCAGGGCTGAACCCAGCAGCTTACGATCAGGTGGCGGCTCCCAACATCACTGCGCTGGCT 3177  
Db 3139 TCAGGGCTGAACCCAGCAGCTTACGATCAGGTGGCGGCTCCCAACATCACTGCGCTGGCT 3198  
QY 3178 GACTACGCCATGCGGCTTCATGGAGCAGATGAAGCACATCAATGAGCAGCTCTCTTCAACAAT 3237  
Db 3199 GACTACGCCATGCGGCTTCATGGAGCAGATGAAGCACATCAATGAGCAGCTCTCTTCAACAAT 3258

```
QY 3238 TTCCAGATGAAGATTGGGCTGAACATGGGCCAGTCGTGGCAGGTGTCATCGGGGCTCGG 3297
|||||
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|||||
QY 3298 AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGCTCTAGTCGTATGACAGCAGG 3357
|||||
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|||||
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|||||
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|||||
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|||||
QY 3538 AAGGTGGGCACCT 3549
|||||
Db 3559 AAGGTGGGCACCT 3570
|||||
```

## RESULT 5

```
AAQ42525
ID AAQ42525 standard; DNA; 4046 BP.
```

```
XX AAQ42525;
```

```
AC AAQ42525;
```

```
DT 14-SEP-1993 (first entry)
```

```
XX Cardiac adenylyl cyclase gene.
```

```
DE Regulation; cardiac function; heart; heart failure; ss.
```

```
XX Canis familiaris.
```

```
XX Key Location/Qualifiers
```

```
FT CDS 131..3627
```

```
FT /*tag= a
```

```
XX EP543137-A.
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XX 26-MAY-1993.
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XX 12-OCT-1992; 92EP-0117374.
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XX 18-NOV-1991; 91US-0793961.
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XX (AMCY ) AMERICAN CYANAMID CO.
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XX PA
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XX Ishikawa Y;
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XX WPI; 1993-168873/21.
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DR P-PSDB; AAR37309.
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XX Purified DNA encoding cardiac adenylyl cyclase - useful to screen
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PT for cpds. which stimulate activity of the cyclase
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XX Claim 1; Fig 2; 34pp; English.
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XX A canine heart cDNA library was constructed in lambda gt10 and was
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CC screened with a 970 bp AatI-HincII fragment from type I adenylyl
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CC cyclase cDNA probe (encodes the first cytoplasmic domain of adenylyl
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CC cyclase, which has significant homology to other previously known
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CC types of adenylyl cyclase). One positive clone, of 5.4 kb was obtd.
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CC Positive colonies were subcloned into pUC18 and further subcloned
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CC and sequenced bidirectionally. The 5.4 kb clone was used to
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CC rescreen the library and on overlapping clone contg. the 5' end of
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CC the gene was isolated. Together the two clones cover the complete
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CC canine cardiac adenylyl cyclase gene. The gene is suspected of
CC being involved in the regulation of cardiac function and it is thought
CC that decreased activity of adenylyl cyclase in the heart may be a
CC major factor in the development of heart failure. Thus the adenylyl
CC cyclase gene is useful to screen cpds. which stimulate the activity
CC of the cyclase.
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XX
SQ Sequence 4046 BP; 743 A; 1206 C; 1254 G; 843 T; 0 other;
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Query Match 84.4%; Score 2996.8; DB 14; Length 4046;
Best Local Similarity 91.0%; Pred. No. 0;
Matches 3233; Conservative 0; Mismatches 307; Indels 12; Gaps 4;
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QY 1 ATGTCTATGTTTGTAGTGGCTCTCTGTCTCCCTAAAGTGGATGAACGGAACACAGCTGGGGT 60
|||||
Db 131 ATGTCTGTTTGTAGTGGCTCTCTGTCTCCCAAGTGGATGAACGGAACACAGCTGGGGT 190
|||||
QY 61 GAACCAATGGGCAGAAAGGTTTCGGGGCCCTGCAGCTCGGGCAGGTGCTTCATGTCACG 120
|||||
Db 191 GAACCAATGGGCAGAAAGGTTTCGGGGCCCTGCAGCTCGGGCAGGTGCTTCATGTCACG 247
|||||
QY 121 CCCCCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGCCACCCCTCGGGCCCC 180
|||||
Db 248 CCCCCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGTCCACCCCTCGGGCTCCC 307
|||||
QY 181 CCTCGTGCCTTGGCAGGATGACGCTTTCATCCGGAGGGCGGCCAGGCAAGGGCAAG 240
|||||
Db 308 CCTCGTGCCTTGGCAGGATGAGGCTTTCATCCGGAGGGCGGCCAGGCAAGGGCAAG 367
|||||
QY 241 GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACAGCAGCG 300
|||||
Db 368 GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAGGACACTGAGG---CCATGTCAGCG 424
|||||
QY 301 GCGCGGACGGCTGAGGTGCGCGCCGACGCGTCCAGAGTGCGGAGTGCGGATCTCTGCGCGC 360
|||||
Db 425 GTTGGGCGAGCTGAGGTGGCCCTGACGTGACCCCGGAGTAGCGATCTCTGCTGGGCG 484
|||||
QY 361 GCTTTGGTGCAGGTGTTCCAGTGAAGCAGTTTCCCTTCGGCCAAAGTGGAGCGCTGTAC 420
|||||
Db 485 CGTCTGGGCCAGGTGTTCCAGTGAAGCAGTTTCCCTTCGGCCAAAGTGGAGCGCTGTAC 544
|||||
QY 421 CAGCGGTACTTTTCCAGATGAACACAGACAGCCCTGAGCGTCTGCTGGCGGTGCTGGTG 480
|||||
Db 545 CAGCGGTACTTTTCCAGATGAACACAGACAGCCCTGAGCGTCTGCTGGCGGTGCTGGTG 604
|||||
QY 481 CTGCTCACAGGGTGTCTGTGGCTTTTCAAGCCGACACCGCCGCTCAGCTGCCTAT 540
|||||
Db 605 CTGCTGACAGCGGTGCTGTAGCTTCCATGCTGACCTGCGCCGCTCAGCTGCCTAC 664
|||||
QY 541 GTGGCAGTGTGGGCTGTGCGCGCCCTGTTGCTGGGGCTCATGGTGTGTAAACCGG 600
|||||
Db 665 GTGGCCCTGTGGCTGTGCGGCCACCTCTTCTGCTGGGCTCATGGTGTGTAAACCGG 724
|||||
QY 601 CATAGCTTCCGCCAGGACTTCCATGTGGTGTGAGTACGTGGTCTGGGCATCTGGCG 660
|||||
Db 725 CACAGCTTTCGCCAGGACTTCCATGTGGTGTGAGTACGTGGTCTGGGCATCTGGCA 784
|||||
QY 661 GCAGTGCAGGTGCGGGGCGCTTTCGACGACAGCCGCGCAGCCCTCTGCGGGCTCTGG 720
|||||
Db 785 GCGGTTCAGTTGGGGGTGCGCCCTGGCAGCCAAACCCCGCAGCCCTCTGCTGGGCTCTGG 844
|||||
QY 721 TGCCCTGTGTTTGTATATACATGACATACAGCTTCTCCCATCCCATCCGATGGGCGTCC 780
|||||
Db 845 TGCCCTGTGTTTGTATATACATACATACAGCTTCTCCCATCCCATCCGATGGGCGTCC 904
|||||
QY 781 GTCCTCAGCGGCTGGGCTCTCCACCTTGCATTTGATCTGGGCTGGCAACTTAAACGT 840
|||||
Db 905 GTCCTCAGTGGCGTGGGCTGTCCACCTGTCATTTGATCTTGGGCTGGCAACTTAAACGC 964
|||||
QY 841 GGTGATGCTTCTCTGGAAGCAGCTGCGTGCATATGCTGCTGCTTCTCTGCAACCAAC 900
|||||
Db 965 GGTGAGCGCTTCCCTCTGGAAGCAGCTGCGTGCATATGCTGCTGCTTCTCTGCAACCAAC 1024
|||||
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[illegible]



Db 3182 GAGGAGCGGTTCCGCGACGTGGAGAAATCAAGACGATCGGTAGACGCTACATGCGTGGC 3241  
Qy 3118 TCAGGGCTGAAGCGCCAGCACCTACGATCAGGTGGCGCGCTCCACATCACTACCTGCGCT 3177  
Db 3242 TCGGGGCTGAAGCGCCAGCACCTACGATCAGCGCGCGCTCCACATCACTACCTGCGC 3301  
Qy 3178 GACTACGCCATCGCGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCCTTCAACAAT 3237  
Db 3302 GACTATGCCATCGCGCTCATGGAGCAGATGAACACATCAACGAGCACTCCCTTCAACAAC 3361  
Qy 3238 TTCCAGATGAAGTGGGCTGAACATGGGCGCCAGTCGTCGGCAGGTGTATCGGGGCTCGG 3297  
Db 3362 TTCCAGATGAAGTGGGCTGAACATGGGCGCCAGTTGTGGCAGGCGTCAATTGGGGCTCGG 3421  
Qy 3298 AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTTAGTCGTATGGACAGCAGC 3357  
Db 3422 AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTTAGTCGTATGGACAGCAGC 3481  
Qy 3358 GGGTTCGCCGACCGAATCCAGGTGACACGAGCACTGTACCAAGTGTCTAGCTGCCAAGGGC 3417  
Db 3482 GGGGTTCCTGACCGAATCCAGGTGACACGAGCACTGTACCAAGTGTCTAGCTGCCAAGGGC 3541  
Qy 3418 TACCAGCTGGAGTGTGAGGGGTGCTCAAGGTGAAGGCAAGGGGAGATGACCACTTAC 3477  
Db 3542 TACCAGCTGGAGTGTGAGGGGTGCTCAAGGTGAAGGCAAGGGGAGATGACCACTTAC 3601  
Qy 3478 TTCTCAATGGGGGCCCCAGCAGTTAACAGGGCCCCAGCACCACAAATTCAGCTGAAGGGACC 3537  
Db 3602 TTCTCAATGGGGGCCCCAGCAGTTAGCAGACGCCAGCTACAAGTTCAAGTGTACAGGACC 3661  
Qy 3538 AAGTGGGCACT 3549  
Db 3662 AAGTGGGCACT 3673

RESULT 6

AB199680  
ID AB199680 standard; cDNA; 5841 BP.  
XX  
AC AB199680;  
XX  
DT 07-MAR-2002 (first entry)  
XX  
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:716.  
XX  
KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;  
KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.  
XX  
OS Mus musculus.  
XX  
PN W0200188188-A2.  
XX  
PD 22-NOV-2001.  
XX  
PF 18-MAY-2001; 2001WO-JP04192.  
XX  
PR 18-MAY-2000; 2000JP-0145977.  
XX  
PA (UVNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
XX  
PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;  
XX  
DR WPI; 2002-034733/04.  
DR P-PSDB; ABB57257.  
XX  
PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring  
PT expression levels of particular genes defined in the specification or  
PT by determining the expression profile of a gene group comprising these  
PT genes -  
XX  
PS Claim 2; Page 1771-1780; 2690pp; English.  
XX  
CC The present invention describes a method for examining ischaemic

CC conditions, comprising measuring the expression levels of particular  
CC genes (I) in a test sample or determining the expression profile of a  
CC gene group in the sample comprising genes selected from (I). The method  
CC is useful for examining the ischaemic condition (e.g. compressive  
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring  
CC expression levels of particular genes (AB199202 to AB199912, encoding  
CC the protein sequences in ABB57020 to ABB57374) or by determining the  
CC expression profile of a gene group comprising these genes. The  
CC expression levels or expression profiles produced by these genes are  
CC used as an indicator when screening for ischaemic condition-improving  
CC drugs or therapeutics for ischaemic diseases. AB199913 and AB199914  
CC represent PCR primers for a mouse ischaemic condition related sequence,  
CC which are used in the exemplification of the present invention.  
XX  
SQ Sequence 5841 BP; 1214 A; 1558 C; 1673 G; 1396 T; 0 other;  
  
Query Match 77.98; Score 2765; DB 24; Length 5841;  
Best Local Similarity 87.18; Pred. No. 0;  
Matches 3095; Conservative 0; Mismatches 445; Indels 13; Gaps 5;  
  
Qy 1 ATGTCATGTTAGTGGCTCTCTGTCCTAAAGTGGATGAACGAAACAGCCCTGGGGT 60  
Db 96 ATGTCATGTTAGTGGCTCTCTGTCCTAAAGTGGATGAACGAAACAGCTGGGGG 155  
Qy 61 GAACGCAATGGGCAAGACGTTTCGGCGCGCTGTCGCACTCGGGAGGTGGCTTTGTCAG 120  
Db 156 GAACGCAATGGGCAAGACG---CCACGCCACGCAATCGACGACGTCGCTTCTGCGCA 212  
Qy 121 CCCGCTATATGAGTGCCTCCGGGATGACAGCACCACCCAGCCCTCTGCGGGCCCC 180  
Db 213 CTGCTACATGAGTGCCTCAAGAAATCGGAGGCCACCCAGCCCTCTGCGACTCAC 272  
Qy 181 CTGCGTCCCTTGGCAGGATGACGCTTCATCCGGAGGGCGGCCAGCAAGGCAAG 240  
Db 273 ACTCGTCCCCCTGGCAGGATGAAGCTTCATCAGGAGGGCGGCCGCGAGGGGTGTG 332  
Qy 241 GAGCTGGGGCTGGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGGTGACACGACAGC 300  
Db 333 GAGCTGGGGCTGGGGTCACTGGGCTTGGGGTTGACGACACTGAGGTGACACACCGATG 392  
Qy 301 GCGGGACGCTGAGTGGCGCCGCGAGCGGTGCCAGAGTGGCGCATCTGCTGGCGC 360  
Db 393 GGC---ACAGCTGAAGTGGCACCGGATACATCGCTCGAGCGGTCCCTCTGCTGGCAC 449  
Qy 361 CGTTGGTGCAGGTGTTCCAGTGAAGCAGTTCGCTTCGGCCAAAGCTGAGCGCTGTAC 420  
Db 450 CGGCTGTGCAAGTGTTCAGTCTAAGCAGTTCGCTCTGCAAGCTGAGCGGCTGTAC 509  
Qy 421 CAGCGTACTTTTCCAGATGAACGAGACGCTGAGCGCTGCTGGTGGCGGTGCTGTG 480  
Db 510 CAGCGTACTTTTCCAGATGAACGAGACGCTGAGCGCTGCTGCTGCTGCTGTG 569  
Qy 481 CTGCTCACAGCGGTGCTGCTGCTTCCAAAGCGCCAGCCCGCCCTCAGCTGCTGCTAT 540  
Db 570 CTGCTCATGGCTGTACTGTTGACTTTCCAGCTGGCGCTGCCAGCTCAGCTGCTTAC 629  
Qy 541 GTGCACTGTTGGGCTGTGCGCGCGCCCTGTTGCTGGGGCTCATGGTGGTGTAAACGG 600  
Db 630 GTGGCCCTGCTGACTGTGCGCTCTGCTCTTTTGTGGTACTCATGTTGTGTAAACGA 689  
Qy 601 CATAGCTTCCGCGAGGACTCCATGTGGTGTGAGTACGAGTGGTGGTGGGATCTGCGG 660  
Db 690 CACAGCTTCCGCGAGGACTCCATGTGGTGTGAGTATGTGGTGTGGGATCTCTAGCA 749  
Qy 661 GCAGTGCAGGTGGGGGCGCTTCGACAGCAGCCGCGCCAGCCCTCTGCGGGCTCTGG 720  
Db 750 GCCGTGAAGTGGGGGTGCGCTGGCAGCAATCCACAGCCCTCGCGGGGCTTTGG 809  
Qy 721 TGCCCTGTCTTGTATACATGCAATGCACTGCTCCCTCCCATCCGATCGGGGCTGCC 780  
Db 810 TGCCCCGTGTTCTCGTCTACATCACCTACACTCTTCTTCCATTCGATCGGACCCGA 869  
Qy 781 GTCCTCAGCGGCTGGGCTCTCCACCTTGCATTTGATCTTGGGCTGGCAACTTAACCGT 840



Db 870 GTACTCAGCGCCTGGCCCTCTACTCTGCAATTTGATTTGGCCTGCAGCTCAACAGC 929  
QY 841 GGTGATCCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTGTTCCCTCTGCACCAAC 900  
Db 930 AGCAGCCCTTCCTTTTGGGAAGCAGCTCGGTGCTAAAGTGTGCTTCCCTCTGCACCAAT 989  
QY 901 GTCAATTAGCATCTGCACACACTATCCAGCAGAGGTGCTCAGGGCCAGGCGTTTTCAGGAG 960  
Db 990 GCCATCGGTCTGSCACACACTACCTGCTGAAGTGTCTCAGCGCCAAAGCTTTCAGGAG 1049  
QY 961 ACCCGCATTTACATPCAGGCCCGGCTCCACTCGAGCATGAGAAATCGGCAGCAGGAGCGTG 1020  
Db 1050 ACCCGAGTTTACATPCAGGCCCGGCTGCACCTGCAGCATGAGAACCCTCAGCAGGAACGG 1109  
QY 1021 CTGCTGCTGTGCGTATTGCCCCAGCAGCTTGCCATGAGATGAAGAGATCAACACACA 1080  
Db 1110 CTGCTGCTATTGCGGTGTGCCCCAGCAGCTTGCCATGAGATGAAGAGATCAACACACA 1169  
QY 1081 AAAAAAGAAAGAC---ATGTTCCACAAGATCTACATACAGAAGCATGACAATGTCAAGCATC 1137  
Db 1170 AAAAAAGAGACATGATGTTCCATAGATCTACATCCAGAAGCATGATATGTCAAGCATC 1229  
QY 1138 CTGTTTGCAGACATGAGGCGCTTCACCAGCTTGGCATCCCAAGTCCACTGCGCAGGAGCTG 1197  
Db 1230 CTGTTTGCAGACATGAGGCGCTTCACCAGCTTGGCGCTGCCCTGCCCTGCCAGGAACTG 1289  
QY 1198 GTCATGACCTGTAATGAGCTCTTTGCCCGTTTGACAAAGCTGGTGGGAGAAATCACTGC 1257  
Db 1290 GTCATGACCTTGAATGAGCTCTTTGCCCGTTTGACAAGCTGGCTGCGGAGAAATCACTGT 1349  
QY 1258 CTGAGGATCAAGATCTTTGGGGGACTGTACTACTGTGTGTCAGGGCTGCCGGAGGCCGG 1317  
Db 1350 CTGAGGATCAAGATCTTTAGGAGACTGTACTACTGCTGTCAAGGCTGCCCGAGGCCGG 1409  
QY 1318 GCCGACCATGCCACTGCTGTGTGGAGATGGGGGTAGACATGATGATGAGGCCATCTCGCTG 1377  
Db 1410 GCAGATCACGCCCACTGCTGTGTGGAGATGGGGGTAGACATGATCGAAGCCATCTCGCTG 1469  
QY 1378 GTACGTGAGGTGACAGGTGTAATGTGAACATGGCGTGGGCATCCACACGGCGCGGTG 1437  
Db 1470 GTGCGTGAAGTACAGGTGTGAAGTGTGAACATGCGTGTGGGCATCCACACGGAGCGTGTG 1529  
QY 1438 CACTGCGGCCTCCTTGGCTTGCAGAAATGGCAGTTGCATGTGTGGTCCCAATGATGTGACC 1497  
Db 1530 CATTTGCGCGCTCCTTGGCCTTACGGAATGSCAGTTTGATGTCTGGTCAACAGATGTGACC 1589  
QY 1498 CTGGCCAAACCACATGGAAGCAGGAAGCCGGGCTGGCGGCATCCACATPACTCGGGCAACA 1557  
Db 1590 CTGGCTAAACCACATGGAAGCCGGGCGG---GGCCGGCGCATCCACATPACTCGGGCTACA 1646  
QY 1558 CTCAGTACCTGAACGGGGACTAGGAAGTGGAGCCAGGCCGTGGTGGCAAGCGCCAGCGG 1617  
Db 1647 CTCAGTACTTGAACGGGGACTATGAGGTGGAGCCAGGCCGTGGTGGTGAACCAATGGC 1706  
QY 1618 TACCTCAAGGAGCAGTGCATTGAGACCTTCTCATCTACTTTGGCGCCAGCCAAAACGGAAA 1677  
Db 1707 TACCTCAAGGAGCAGTGCATTGAGACCTTCTCATCTACTTTGGCGCCAGCCAAAACGGAAA 1766  
QY 1678 GAGGAGAAAGGATGTGTGGCCAAAGCTGCAGCGGACTCGGGGCCAATCTCCATGGAAGGCGTG 1737  
Db 1767 GAGGAGAAAGCCATGTGTGGCCAAAGCTTCAAGCGGACACGGGCCAACTCCATGGAAGGACTG 1826  
QY 1738 ATGCCGGATGGGTTCCTGATCTGCTTCTCCCGGACCAAGGACTCCCAAGGCCCTTCCCG 1797  
Db 1827 ATGCCCGCTGGGTTCCTGACCGTGCTTCTCCCGGACCAAGGACTTCAAGGCATTCCCG 1886  
QY 1798 CAGATGGGCATTGATGATTCAGCAAGACAAACCGGGGCAACCGGAGTGCCTGAAACCTT 1857  
Db 1887 CAGATGGGCATTGATGATTCAGCAAGACAAACCGGGGTCCCAAGATGCTGTGAAACCTT 1946  
QY 1858 GAGGATGAGGTGATGATTCCTGAGCCGTGCGCATCGATGCCCGCAGCATTTGATCAAGCTG 1917  
Db 1917 GAGGATGAGGTGATGATTCCTGAGCCGTGCGCATCGATGCCCGCAGCATTTGATCAAGCTG 1917

Db 1947 GAAGATGAGGTGATGAGTTCTCTGGGCGGAGCCATCGATGCCCGAGCATCGACCAACTG 2006  
QY 1918 CGGAAGACCATATGCGCGCGGTTTTCCTCACCCTTCAGAGAGAGGATTTTGAAGAAAG 1977  
Db 2007 CGTAAGACCATATGCGCGCGGTTCCCTGCTCACCTTCAGAGAGAGGATCTTTGAAGAAAG 2066  
QY 1978 TACTCCCGGAAGGTGGATATCCCGCTTCGGAGCCCTACCTTGCCTGTGCCCCCTGTTGCTTTC 2037  
Db 2067 TATTCAGGAAAGTAGATCCTCGCTTCGGAGCCCTACGTGCGCTGTGCCCCCTCTGGTTTTT 2126  
QY 2038 TGCTTCATCTGCTTCATCCAGCTTCTAAATTTTCCCAACATCCACCCTGATGCTTGGGATTT 2097  
Db 2127 TGCTTCATCTGCTTTCATCCAGCTTCTGCTTCCCATACTCCACCCTGATACTCGGATTT 2186  
QY 2098 TATGCCAGCATCTTCCTGCTGCTGCTAAATCACCCGTGCTGATCTGCTGTACTGCTCTGT 2157  
Db 2187 TATGCCCTATCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2246  
QY 2158 GGTTCCTGTTTCCCTTAAGGCCCTGCAACGCTGTGCTCCCGCAGCATTTGCTCCGCTCACGGCCA 2217  
Db 2247 GGTTCCTTCTCCCAAGGCCCTGCAACGCTGTGCTCCCGCAATATTTGCTCCGCTCACGGGTG 2306  
QY 2218 CATAGCACCGAGTTGGCATCTTTTCCGCTCCTGCTGTGTTTACTTCTGCTGCTGCTGCTGCT 2277  
Db 2307 CACAGCACCGCGGTTGGAATCTTCTCGGTTCTGCTTGTGTTTCTCATCTGCTGCTGCTGCTGCT 2366  
QY 2278 ATGTTACCTGTAAACACACACCCCATACAGGAGCTGTGCAGCCCGGATGCTGAATTTAAACA 2337  
Db 2367 ATGTTTACCTGTAAATCACACCCCAATAAGAACCTTGCGCGCCGGATGCTGAACTTTAAACA 2426  
QY 2338 CTTGCTGACATCTACTGCTGCCACTGTCAGCAGCTCAATTTACTTCTCTGGGCTGGATGCT 2397  
Db 2427 CCAGCGGATGTCACCGCTGCCACCTACACAGCTCAATTTACTTCTCTGGGACTGGATGCT 2486  
QY 2398 CCCCCTGTGTGAGGCGCACCATGCCCCACCTGACGCTTTTCTGAGGTGTCATCGGGAACATG 2457  
Db 2487 CCCCCTGTGTGAGGCGCACCGCACCCACCTGACGCTTCCCTGAGTACTTCTGCTGCGGAACGTG 2546  
QY 2458 CTGCTGAGTCTCTTGGCCAGCTGCTGCTTCTGTCACATACAGCAGCATCGGMAAGTTGGCC 2517  
Db 2547 CTGCTGAGTCTCTTAGCCAGCTGCTGCTTCTCTACATACAGCAGCATCGGCAAGCTGGCC 2606  
QY 2518 ATGATCTTTCTTGGGGCTCATCTATTGTTGCTGCTTCTGTTGGTCCCGCCAGCGGCC 2577  
Db 2607 ATGACCTTTCATCTTGGGGTTCACTTACTTGTGCTGCTTGTGTTGCTGCTGCTGCTGCTGCT 2666  
QY 2578 ATCTTTGAACAATATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACC 2637  
Db 2667 ATCTTTGAACAATATGATCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACC 2726  
QY 2638 TTTGATGGGCTGGACTGCTCCAGCTGCAGGAGGCTGGCCCTCAAATATATGACCCCTGTG 2697  
Db 2727 TTTGATGGGCTGGACTGCCAGCTGTGGGAGGAGTACGCTCAAATATATGACCCCTGTG 2786  
QY 2698 ATTCTGCTGTTGTTGCTGCGGCTGATCTGCTGCTCAGCAGGTGGAATGACCTGSCC 2757  
Db 2787 ATTCTGCTGTTGTTGCTGCGGCTGACCTTACTTGTGCTGCTTGTGTTGCTGCTGCTGCTGCTGCT 2846  
QY 2758 CGCCTAAACTTCTCTGGAACCTACAGGCAACAGGGGAAAAGAGAGATGAGGAGAGCTA 2817  
Db 2847 CGCCTGAGCTTCTGTGGAAGTTACAGGCAACAGGGGAGAGGAGAGATGAGGAGAGCTA 2906  
QY 2818 CAGGCATACAAACCGAGGCTGCTGCAATAACATTTCTGCCCAAGGACGTGGCGGCCACTTC 2877  
Db 2907 CAGGCATACAAACCGAGGTTGCTGCAATAACATTTCTCCCAAGGACGTGGCGGCCACTTC 2966  
QY 2878 CTGSCCGGGAGCGCCGAATGATGAACCTTACTATCAGTCTGTTGAGTGTGTGGCTGTGTT 2937  
Db 2967 CTGSCCGGGAGCGCCGACAGATGAGTGTACTACAGTCTGTGTAATGTGTGGCTGTGTC 3026  
QY 2938 ATGTTTGCCTTCCATGTCGAACCTTCTCTGAGTTCTATGTGAGCTGGAGGCAACAATGAG 2997  
Db 3027 ATGTTTGCCTTCCATGTCGAACCTTCTCTGAGTTCTTACGTGGAGTTCGAGGCAACAACGAG 3086





Db 2810 CGCTGGACTTCTGTGGAACATGCGAGGCACAGGGGAGAAGGAGGAGATGGAGGATGG 2869  
QY 2818 CAGGCATACAAACGGAGGCTGTGCATACATCTCTGCCAAGGACGTGGCGCCCACTTC 2877  
Db 2870 CAGGCCTACACCGCGGCTGTGCATACATCTCTGCCAAGGACGTGGCGCCCACTTC 2929  
QY 2878 CTGGCCGGGAGCGCGCAATGATGAACCTCTACTATCATCTGTCGTGTGTGGCTGTT 2937  
Db 2930 CTGGCCGGGAGCGCGCAAGGAGCTGTACTACCAATCTTGGCAGTGGCTGTCTGTC 2989  
QY 2938 ATGTTTGCCTTCATTCGCCAACTTCTGTAGTTCATGTGTGGAGTGAGGCAACAATGAG 2997  
Db 2990 ATGTTTGCCTTCATTCGCCAACTTCTGTAGTTCATGTGTGGAGTGAGGCAACAATGAG 3049  
QY 2998 GTGCGGAGTGGCTGGCGTGTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC 3057  
Db 3050 GCGTGGAGTGGCTGGCGTGTCAATGAGATCATCGCGGACTTTGATGAGATTATCAGT 3109  
QY 3058 GAGGAGCGGTTCGGCAGCTGGAAGAATCAAGACGATTGGTAGCACCTTACATGGCTGCC 3117  
Db 3110 GAGGAGAGTTCGGCAGCTGGAGAGATCAAGACCATCGGTAGCACTTACATGGCGCC 3169  
QY 3118 TCAGGCTGAACGCCAGCACCTACGATAGTGGGCGCTGCCACATCACTGCCCTGGCT 3177  
Db 3170 TCGGGCTAAATGCCAGCACCTATGACCAAGTTCGGCGCTCGCACATCACCGCCCTGGCA 3229  
QY 3178 GACTACGCCATGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCTTCAACAT 3237  
Db 3230 GACTACGCCATGGCGTTATGGAGCAATGAACACATCAAGCAACACTCTTCAACAC 3289  
QY 3238 TTCAGATGAAGATTGGGTGAACATGGCGCCAGTGGTGCAGGTGTATCGGGGCTCGG 3297  
Db 3290 TTCAGATGAAGATCGGTTGAACATGGTTCGGTTGTAGCAGGTGTATGGGCGCG 3349  
QY 3298 AAGCCACATGATACATCTGCGGGAACACAGTGAATGTCTTAGTCTGATGACAGCAG 3357  
Db 3350 AAGCCACATGATACATCTGCGGGAACACAGGTGAATGTTCAGCGCTGATGACAGCACA 3409  
QY 3358 GGGTCCCGACCGAATCCAGGTGACACGAGCTGACCGACCTGACAGGTCTAGCTGCCAGGCG 3417  
Db 3410 GAGTTCCTGACCGAATACAGGTGACACGAGTCTACCGATCTTACAGGTTCTAGCTGCCAAGGCG 3469  
QY 3418 TACAGCTGGAGTGTGAGGGGTGTCAAGGTGAAGGCAAGGGGAGATGACCACTAC 3477  
Db 3470 TACCAACTGGAGTGTGAGGGGTGTCAAGGTGAAGGAAAGGGGAGATGACCACTAC 3529  
QY 3478 TTCCTCAATGGGGCCCCAGCAGTTAACAGGGCCCA--GCCACAAATTCAGCTGAGGGA 3535  
Db 3530 TTCCTCAATGGGGCCCCAGCAGTTAGCAGAGCGCACAGTGGAAATTCACCAAGGGA 3589  
QY 3536 CCAAGTGGGCACT 3549  
Db 3590 CCAAGTGGGCACT 3603

RESULT 8  
ID AAD08562  
XX AAD08562 standard; cDNA; 1812 BP.  
AC AAD08562;  
XX  
DT 04-SEP-2001 (first entry)  
DE Human partial cardiac adenylylase VI (ACVI) isoform #2 cDNA.  
XX  
KW Human; cardiant; beta-adrenergic signalling protein; beta-ASP;  
KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;  
KW adenylylase; adenylylase; adenylylase; adenylylase;  
KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;  
KW cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ss.  
OS Homo sapiens.

XX Key Location/Qualifiers  
FH 1..1812  
FT /\*tag= a  
FT /product= "Human partial cardiac ACVI isoform #2"  
FT /note= "CDS does not include start and stop codon"  
FT /EC\_number= "4.6.1.1"  
XX WO200148164-A2.  
XX 05-JUL-2001.  
XX 26-DEC-2000; 2000WO-US35411.  
XX 27-DEC-1999; 99US-0472667.  
XX (REGC ) UNIV CALIFORNIA.  
XX Hammond HK, Gao M;  
XX WPI: 2001-418260/44.  
XX P-PSDB; AAE04309.  
XX Novel polynucleotide encoding a modified adenylylase polypeptide useful for enhancing cardiac function in mammalian hearts, and for treating heart disease, especially congestive heart failure -  
XX Example 5; Page 115-119; 153pp; English.  
XX The present invention relates to methods and compositions for enhancing cardiac function in mammalian hearts by inserting transgenes encoding beta-adrenergic signalling proteins (beta-ASP) which increase beta-adrenergic responsiveness within the myocardium using in vivo gene therapy. The beta-ASPs of the invention include beta-adrenergic receptors (beta-AR), adenylylases (also referred as adenylylase, adenylylase and cAMP synthetase) and G-protein receptor kinase (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function in mammalian hearts and for treating heart disease, especially congestive heart failure. The present cDNA sequence encodes human partial cardiac adenylylase VI (ACVI) isoform which is used for generating a third beta-ASP transgene, used in the exemplification of the invention.

XX SQ Sequence 1812 BP; 361 A; 539 C; 507 G; 405 T; 0 other;  
Query Match 51.0%; Score 1808.4; DB 22; Length 1812;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 636 TAACGTGGTGTGGGCATCTGGCGCAGTGCAGGTGGGGCGCTTTCGACAGACCC 695  
Db 3 TAACGTGGTGTGGGCATCTGGCGCAGTGCAGGTGGGGCGCTTTCGACAGACCC 62  
QY 696 GCGCAGCCCTCTGGGGCTCTGGTGCCTGTGTCTTTGTATACATCGCATACAGCT 755  
Db 63 GCGCAGCCCTCTGGGGCTCTGGTGCCTGTGTCTTTGTATACATCGCATACAGCT 122  
QY 756 CTCCCATCCGATCGGGCTGCGTCTCAGCGGCTGGGCTTCCACCTTGCATTT 815  
Db 123 CTCCCATCCGATCGGGCTGCGTCTCAGCGGCTGGGCTTCCACCTTGCATTT 182  
QY 816 GATCTTGGCTGGCAACTTAACCGTGGTGTGATGCCCTTCTCTGGAAGAGCTCGGTGCCAA 875  
Db 183 GATCTTGGCTGGCAACTTAACCGTGGTGTGATGCCCTTCTCTGGAAGAGCTCGGTGCCAA 242  
QY 876 TGTGTGCTGTCTCTGACCAACGATCATTAGCATCTGCACACATATCCAGCAGAGT 935  
Db 243 TGTGTGCTGTCTCTGACCAACGATCATTAGCATCTGCACACATATATCCAGCAGAGT 302  
QY 936 GTCTCAGGCCAGGCTTTTCAGGAGACCGCAGTTACATCCAGGCCGCTCCACTGCA 995  
Db 303 GTCTCAGGCCAGGCTTTTCAGGAGACCGCAGTTACATCCAGGCCGCTCCACTGCA 362

QY 996 GCATGAGAAATCGCAGCAGAGCGGCTGCTGCTGTGGTATTGCCCCAGCAGCTTGCCAT 1055  
|||||  
Db 363 GCATGAGAAATCGCAGCAGAGCGGCTGCTGCTGTGGTATTGCCCCAGCAGCTTGCCAT 422  
|||||  
QY 1056 GGAGATGAAGAAGACATCAACACAAAAAAGAACACATGTTCCACAAGATCTACATACA 1115  
|||||  
Db 423 GGAGATGAAGAAGACATCAACACAAAAAAGAACACATGTTCCACAAGATCTACATACA 482  
|||||  
QY 1116 GAAGCATGACAATGTACAGCATCCTGTTTGCAGACATTTAGGGCTTACCAGCCTGGCATC 1175  
|||||  
Db 483 GAAGCATGACAATGTACAGCATCCTGTTTGCAGACATTTAGGGCTTACCAGCCTGGCATC 542  
|||||  
QY 1176 CCAGTGCATCGCAGGAGCTGGTCATGACCTGTAATGAGCTTTTGGCCGGTTTGACAA 1235  
|||||  
Db 543 CCAGTGCATCGCAGGAGCTGGTCATGACCTGTAATGAGCTTTTGGCCGGTTTGACAA 602  
|||||  
QY 1236 GCTGGCTGGGAGATCACTGCTGAGGATCAAGATCTTTGGGGACTGTTACTACTGTGT 1295  
|||||  
Db 603 GCTGGCTGGGAGATCACTGCTGAGGATCAAGATCTTTGGGGACTGTTACTACTGTGT 562  
|||||  
QY 1296 GTGAGGGCTGCGGGAGCGCGGCGGACCATGCCACTGCTGTGTGGAGATGGGGTAGA 1355  
|||||  
Db 663 GTGAGGGCTGCGGGAGCGCGGCGGACCATGCCACTGCTGTGTGGAGATGGGGTAGA 722  
|||||  
QY 1356 CATGATTGAGGCATCTCGCTGGTAGGTGAGGTGACAGGTGTAATGTGAACATGGCGCT 1415  
|||||  
Db 723 CATGATTGAGGCATCTCGCTGGTAGGTGAGGTGACAGGTGTAATGTGAACATGGCGCT 782  
|||||  
QY 1416 GGGCATCCACAGCGGCGGTGCTGCTGCGCGCTGCTTGGCTTGGGAAATGGCAGTTCCA 1475  
|||||  
Db 783 GGGCATCCACAGCGGCGGTGCTGCTGCGCGCTGCTTGGCTTGGGAAATGGCAGTTCCA 842  
|||||  
QY 1476 TGTGTGGTCCAAATGATGTGACCTGCGCCAAACACATGGAAGCAGGAAGCGGGCTGGCGG 1535  
|||||  
Db 843 TGTGTGGTCCAAATGATGTGACCTGCGCCAAACACATGGAAGCAGGAAGCGGGCTGGCGG 902  
|||||  
QY 1536 CATCCACATCACTCGGGAACACTGAGTACCTGAACGGGGACTACGAAGTGGAGCCAGG 1595  
|||||  
Db 903 CATCCACATCACTCGGGAACACTGAGTACCTGAACGGGGACTACGAAGTGGAGCCAGG 962  
|||||  
QY 1596 CCGTGTGGCAGCGCAACCGCTACTCTCAAGGAGCAGCATTGAGACTTTCTCATCT 1655  
|||||  
Db 963 CCGTGTGGCAGCGCAACCGCTACTCTCAAGGAGCAGCATTGAGACTTTCTCATCT 1022  
|||||  
QY 1656 GGGCGCCAGCCAGAAACGAGAGAGAAAGGCATGCTGGCCAAAGCTCAGCGACTCG 1715  
|||||  
Db 1023 GGGCGCCAGCCAGAAACGAGAGAGAAAGGCATGCTGGCCAAAGCTCAGCGACTCG 1082  
|||||  
QY 1716 GGGCAACTCCATGGAGGCTGATCGCGGATGGGTTCCTGATCGTGCCTTCTCCCGGAC 1775  
|||||  
Db 1083 GGGCAACTCCATGGAGGCTGATCGCGGATGGGTTCCTGATCGTGCCTTCTCCCGGAC 1142  
|||||  
QY 1776 CAAGGACTCCAAGGCTTCCGCCAGATGGCATTTGATGATTCAGCAAGACAACCGGGG 1835  
|||||  
Db 1143 CAAGGACTCCAAGGCTTCCGCCAGATGGCATTTGATGATTCAGCAAGACAACCGGGG 1202  
|||||  
QY 1836 CACCAAGATGCCCTGAACCTGAGGATGAGGTGATGATGTTCTGAGCCGTGCCATCGA 1895  
|||||  
Db 1203 CACCCNAGATGCCCTGAACCTTGAAGATGAGGTGATGATGTTCTGAGCCGTGCCATCGA 1262  
|||||  
QY 1896 TGCCGCGCAGCATTTGATCAGCTCGGAAGGACCATGTGCGCGGTTTTTGTCTCACCTTCCA 1955  
|||||  
Db 1263 TGCCGCGCAGCATTTGATCAGCTCGGAAGGACCATGTGCGCGGTTTTTGTCTCACCTTCCA 1322  
|||||  
QY 1956 GAGAGGAGATTTGAGAAGAAGTACTCCCGGAAGTGGATCCCGCTTCGGAGCCCTACGT 2015  
|||||  
Db 1323 GAGAGGAGATTTGAGAAGAAGTACTCCCGGAAGTGGATCCCGCTTCGGAGCCCTACGT 1382  
|||||  
QY 2016 TGCCTGTGCCCTTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAAATTTCCACCA 2075  
|||||  
Db 1383 TGCCTGTGCCCTTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAAATTTCCACCA 1442  
|||||  
QY 2076 CTCCACCCTGATGCTTGGGATTATGCCAGCATCTTCTGCTGCTTAATCACCGTGTCT 2135

Db 1443 CTCCACCCTGATGCTTGGGATTATGCCAGCATCTTCCTGCTGCTTAATCACCGTGTCT 1502  
|||||  
QY 2136 GATCTGTGCTGTGTACTCTCTGTGGTCTCTGTTCCTTAAGGCCCTGCACAGCTGTCCCG 2195  
|||||  
Db 1503 GATCTGTGCTGTGTACTCTCTGTGGTCTCTGTTCCTTAAGGCCCTGCACAGCTGTCCCG 1562  
|||||  
QY 2196 CAGCATTTGCCCTCACGGGCACATAGCAGCCGAGTTGGCATCTTTTCCGTCTCTGCTTGT 2255  
|||||  
Db 1563 CAGCATTTGCCCTCACGGGCACATAGCAGCCGAGTTGGCATCTTTTCCGTCTCTGCTTGT 1622  
|||||  
QY 2256 GTTTACTTCTGCGCATGCGCAACATGTTACCTGTAAACACACACCCCATACGAGAGCTGTGC 2315  
|||||  
Db 1623 GTTTACTTCTGCGCATGCGCAACATGTTACCTGTAAACACACACCCCATACGAGAGCTGTGC 1682  
|||||  
QY 2316 AGCCGGGATGCTGAATTTAAACACCTGCTGACATCACTGCTGCCACCTGCAGCAGCTCAA 2375  
|||||  
Db 1683 AGCCGGGATGCTGAATTTAAACACCTGCTGACATCACTGCTGCCACCTGCAGCAGCTCAA 1742  
|||||  
QY 2376 TTACTCTCTGGCCCTGGATGCTCCCTGTGTGAGGGCAGCATGCCCACCTGCAGCCTTTCC 2435  
|||||  
Db 1743 TTACTCTCTGGCCCTGGATGCTCCCTGTGTGAGGGCAGCATGCCCACCTGCAGCCTTTCC 1802  
|||||  
QY 2436 TGAGGTGTCC 2445  
|||||  
Db 1803 TGAGGTGTTC 1812  
|||||  
RESULT 9  
AAV23246  
ID AAV23246 standard; cDNA; 2127 BP.  
XX  
AC AAV23246;  
XX  
DT 17-JUL-1998 (first entry)  
XX  
DE Human adenylyl cyclase isoform VI encoding cDNA.  
XX  
KW Human; adenylyl cyclase VI; AC-VI; beta-adrenergic signalling protein;  
KW transgene; gene therapy; congestive heart failure; cardiac function;  
KW adenovirus; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
CDS 1..2127  
FT /\*tag= a  
FT /product= "adenylyl cyclase isoform VI"  
FT /transl\_except= (pos:229..231,aa:Xaa)  
FT /transl\_except= (pos:315..317,aa:Xaa)  
FT /note= "no stop codon given; Xaa = unknown"  
FT misc\_difference 315  
FT /\*tag= b  
FT /note= "n indicates a gap of about 0.5 kb"  
FT  
XX  
PN W09810085-A2.  
XX  
PD 12-MAR-1998.  
XX  
PF 05-SEP-1997; 97WO-US15610.  
XX  
PR 16-JUN-1997; 97US-0048933.  
PR 05-SEP-1996; 96US-0708661.  
XX  
XX (COLL-) COLLATERAL THERAPEUTICS.  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Gao M, Hammond HK, Insel PA, Ping P, Post SR;  
XX  
XX WPI; 1998-193633/17.  
DR P-PSDB; AAW53345.  
XX  
PT Vectors containing transgene(s) encoding beta-adrenergic signalling

PT proteins - useful for gene therapy of congestive heart failure

xx Claim 60; Fig 12A; 114pp; English.

xx  
CC The present sequence encodes human adenylyl cyclase isoform VI (AC-VI) from the present invention. The present invention describes a recombinant replication-defective viral particle (I) comprising a gene encoding a beta-adrenergic signalling protein (beta-ASP) operably linked to a promoter. Also described are: (1) a recombinant pro-viral plasmid (Ia) comprising a gene encoding a beta-ASP, as above, operably linked to a promoter and further comprising a replication-defective viral genome; (2) a (mammalian) cell transfected with (1) or (Ia); (3) an isolated polynucleotide comprising a sequence encoding a human adenylyl cyclase isoform VI (AC-VI), or a variant having AC activity; (4) a human AC-VI encoded by (3); (5) an isolated polynucleotide sequence which hybridises at high stringency to (3); and (6) a vector comprising the polynucleotide of (3). (1) can be used to form a filtered adenovirus particle preparation. (1) is used to enhance cardiac function in mammals.

xx  
SQ Sequence 2127 BP; 421 A; 637 C; 615 G; 452 T; 2 other;

Query Match 51.08; Score 1808.4; DB 19; Length 2127;  
Best Local Similarity 99.94; Pred. No. 0;  
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	636	TAACTGTGCTGGGCATCTCTGGCGCAGTCAGGTGGGGCGCTTTTCGACGACAGCC	695
Db	318	TAACTGTGCTGGGCATCTCTGGCGCAGTCAGGTGGGGCGCTTTTCGACGACAGCC	377
Qy	696	CGCAGCCCCCTCTGGGGCCCTCTGGTGCCTCTGTCTTTGTATACATCGCATACACGCT	755
Db	378	CGCAGCCCCCTCTGGGGCCCTCTGGTGCCTCTGTCTTTGTATACATCGCATACACGCT	437
Qy	756	CCTCCCATCCGATCGAGGTGGCTGCTCTCAGCGGCGTGGCCCTCCACCTTGCACTTT	815
Db	438	CCTCCCATCCGATCGAGGTGGCTGCTCTCAGCGGCGTGGCCCTCTCCACCTTGCACTTT	497
Qy	816	GATCTTGGCCCTGGCACTTAACCGTGTGATGCCTTCTCTGGAAGCAGCTCGGTGCCAA	875
Db	498	GATCTTGGCCCTGGCACTTAACCGTGTGATGCCTTCTCTGGAAGCAGCTCGGTGCCAA	557
Qy	876	TGTGCTGCTGTCTCTCGCAACAGCTCATTTAGCATCTGCACACATTCACGACAGGT	935
Db	558	TGTGCTGCTGTCTCTCGCAACAGCTCATTTAGCATCTGCACACATTCACGACAGGT	617
Qy	936	GTCTCAGCGCCAGGCTTTTCAGGAGACCGCAGTTTACATCAGGCGCGGCTCCACCTGCA	995
Db	618	GTCTCAGCGCCAGGCTTTTCAGGAGACCGCAGTTTACATCAGGCGCGGCTCCACCTGCA	677
Qy	996	GCATGAGAAATCGGCAGCAGGCGGCTGCTGCTGTCGGTATTGCCCCAGCAGCTTGCCAT	1055
Db	678	GCATGAGAAATCGGCAGCAGGCGGCTGCTGCTGTCGGTATTGCCCCAGCAGCTTGCCAT	737
Qy	1056	GGAGATGAAGAAGACATCACACAAAAAAGACATGTTCCACAAAGATCTACATACA	1115
Db	738	GGAGATGAAGAAGACATCACACAAAAAAGACATGTTCCACAAAGATCTACATACA	797
Qy	1116	GAAGCATCACAAATGTCAGCATCTCTTTTGACAGACATTCAGGCGCTTCACACGCTGGCATC	1175
Db	798	GAAGCATCACAAATGTCAGCATCTCTTTTGACAGACATTCAGGCGCTTCACACGCTGGCATC	857
Qy	1176	CCAGTGCACTCGCAGGAGCTGGTCATGACCCCTGAATGAGCTCTTTGGCCGCTTTGACAA	1235
Db	858	CCAGTGCACTCGCAGGAGCTGGTCATGACCCCTGAATGAGCTCTTTGGCCGCTTTGACAA	917
Qy	1236	GCTGGCTCGGAGAAATCACTGCTGAGGATCAAGATCTTTGGGGGACTGTTACTACTGTT	1295
Db	918	GCTGGCTCGGAGAAATCACTGCTGAGGATCAAGATCTTTGGGGGACTGTTACTACTGTT	977
Qy	1296	GTCAGGGCTGCGGAGGCGCGGCGGACCATGCCACATGCTGTGTGGAGATGGGGGTAGA	1355
Db	978	GTCAGGGCTGCGGAGGCGCGGCGGACCATGCCACATGCTGTGTGGAGATGGGGGTAGA	1037

Qy	1356	CATGATTGAGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATCGCGGT	1415
Db	1038	CATGATTGAGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTGAACATCGCGGT	1097
Qy	1416	GGGCATCCACAGCGGGCGGTGTCACCTGCGGGCTCTTGGCTTGGGAAATGCGAGTTGCA	1475
Db	1098	GGGCATCCACAGCGGGCGGTGTCACCTGCGGGCTCTTGGCTTGGGAAATGCGAGTTGCA	1157
Qy	1476	TGTGTGTTCCAATGATGTGACCCCTGGCCCAACACCATGGAAGCAGGAACCGGGCTGGCG	1535
Db	1158	TGTGTGTTCCAATGATGTGACCCCTGGCCCAACACCATGGAAGCAGGAACCGGGCTGGCG	1217
Qy	1536	CATCCACATCACTCGGGCAACACCTGACCTGTAACGGGACTACGAAGTGGAGCCAGG	1595
Db	1218	CATCCACATCACTCGGGCAACACCTGACCTGTAACGGGACTACGAAGTGGAGCCAGG	1277
Qy	1596	CCGTGTTGGCAAGCGCAACGCGTACCTCAAGAGCAGACATGTAGACTTTCTCATCCT	1655
Db	1278	CCGTGTTGGCAAGCGCAACGCGTACCTCAAGAGCAGACATGTAGACTTTCTCATCCT	1337
Qy	1656	GGCGCCAGCCAGAACGGAAGAGGAGAAAGGCATGCTGCCAGCTGCAGCGGACTCG	1715
Db	1338	GGCGCCAGCCAGAACGGAAGAGGAGAAAGGCATGCTGCCAGCTGCAGCGGACTCG	1397
Qy	1716	GGCCAACTCCATGGAAGGGCTGATGCCCGATGGGTTCTCTGATCGTGCCTTCTCCCGAC	1775
Db	1398	GGCCAACTCCATGGAAGGGCTGATGCCCGATGGGTTCTCTGATCGTGCCTTCTCCCGAC	1457
Qy	1776	CAAGGACTCCAAAGCCCTTCCGCCAGATGGCATTTGATGATTCACAGAAAGAACCGGG	1835
Db	1458	CAAGGACTCCAAAGCCCTTCCGCCAGATGGCATTTGATGATTCACAGAAAGAACCGGG	1517
Qy	1836	CACCCAGATCCCTGAAACCTGAGGATGAGTGGATGAGTTCCTGAGCCGTGCCATCGA	1895
Db	1518	CACCCAGATCCCTGAAACCTGAGGATGAGTGGATGAGTTCCTGAGCCGTGCCATCGA	1577
Qy	1896	TGCCCGCAGCATTTGATCAGCTGCGGAAGGACCATGTGCGCGGTTTGTGCTCACCTTCCA	1955
Db	1578	TGCCCGCAGCATTTGATCAGCTGCGGAAGGACCATGTGCGCGGTTTGTGCTCACCTTCCA	1637
Qy	1956	GAGAGAGGATTTTGAGAAGAAGTACTCCCGAAGGTGATCCCGCTTCGGAGCCTAGGT	2015
Db	1638	GAGAGAGGATTTTGAGAAGAAGTACTCCCGAAGGTGATCCCGCTTCGGAGCCTAGGT	1697
Qy	2016	TGCCTGTGCCCTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAAATTTTCCACA	2075
Db	1698	TGCCTGTGCCCTGTGGTCTTCTGCTTCATCTGCTTCATCCAGCTTCTAAATTTTCCACA	1757
Qy	2076	CTCCACCCCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCT	2135
Db	1758	CTCCACCCCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCT	1817
Qy	2136	GATCTGTGCTGTACTCCTGTTCTGTTCTGTTCCCTAAGGCCCTGCAACGCTGTGCTCGG	2195
Db	1818	GATCTGTGCTGTACTCCTGTTCTGTTCTGTTCCCTAAGGCCCTGCAACGCTGTGCTCGG	1877
Qy	2196	CAGCATTGTGCTGCTCACGGGACATAGCACCGCAGTTGGCATCTTTTCCGCTCTGCTGT	2255
Db	1878	CAGCATTGTGCTGCTCACGGGACATAGCACCGCAGTTGGCATCTTTTCCGCTCTGCTGT	1937
Qy	2256	GTTTACTTCTGCCATGTCACACATGTTTACCTGTAAACACACACCCCATACGAGAGTGTGC	2315
Db	1938	GTTTACTTCTGCCATGTCACACATGTTTACCTGTAAACACACACCCCATACGAGAGTGTGC	1997
Qy	2316	AGCCCGGATGCTGAATTTAAACCTGCTGACATCACTGCTGCCACCTGCAGAGCTCAA	2375
Db	1998	AGCCCGGATGCTGAATTTAAACCTGCTGACATCACTGCTGCCACCTGCAGAGCTCAA	2057
Qy	2376	TTACTCTCTGGGCTGGATGCTGCCCTGTGTGAGGGACCATGCCACCTGCAGCTTTCC	2435
Db	2058	TTACTCTCTGGGCTGGATGCTGCCCTGTGTGAGGGACCATGCCACCTGCAGCTTTCC	2117

[illegible]



Db 1762 ATGGACATGATCGAGGCCATCTCGTTGGTCCGGGAGGTGACAGGGGTGAACGTGAACATG 1821  
Qy 1411 CCGCTGGGCATCCACAGCGGGCGCTGCACCTGCGCGCTCTTGGCTTCGGAAATGGCAG 1470  
Db 1822 CGTGTGGGAATTCACAGCGGGCGATACACTGCGGTGCTTGGTCTCAGGAAGTGGCAG 1881  
Qy 1471 TTCGATGTGTGCTCAATGATGTGACCTGCGCCACACACATGGAAGCAGGAAGCGGCT 1530  
Db 1882 TTCGACGTGTGGTCTAAGCATGTCTACGCTAGCCACACACATGAGGCGTGGGGCAAGCA 1941  
Qy 1531 GSCCGCATCCACATCCTCGGCAACACTGCGATGACCTGCAAGCGGAGTACGAAGTGGAG 1590  
Db 1942 GGACGATCCACATCACCAGAGCTACACTCAACTACCTGAAATGGGGATACGAGGTGGAG 2001  
Qy 1591 CCAGCCGTGTGGCAAGCGCAACCGTACCTTCAAGGAGCAGCACATTTGAGACTTTCCTC 1650  
Db 2002 CCAGGCTGTGGGGCGAGCGCAACCGCTACCTCAAGGAGCAGATATCGAGACCTTCCTC 2061  
Qy 1651 ATCCTGGGCGCAGCCGAAGAACGGAAGAGGAGAAAGCATGCTGGCCAAAGCTGCAGCGG 1710  
Db 2062 ATCTCTGCGCTGCACCCAGAAGCGGAAGAGAGAGAGGCATGATCGCCAAAGATGAACGC 2121  
Qy 1711 ACTCGGGCCAACTCCATCGAAGGGCTGATGCGCGCATGGTTCTCGATCGTCCCTTCTCC 1770  
Db 2122 CAGAGAACCACTCCATCGGCGACAACCCACCACTGGGGGCTGAGCGCCCTTCTAC 2181  
Qy 1771 -----CGGACCAAGGACTCCAAAGGCCTTCCGCCAGATGGGCATTTGATGATTC 1818  
Db 2182 AACCACCTGGGTGGCAACCGAGTGTCCAAGGAGATGAAGCGGATGGGCTTTGAAGACCC 2241  
Qy 1819 AGCAAGACACACCGGGGCACCGAAGATGCCCTGGAACCTGAGGATGAGGTGATGATTC 1878  
Db 2242 A-----AGGACAAGAACGCCACGAGAGAGTGCGAACCTCGAGGATGAAGTGGATGAGTTT 2295  
Qy 1879 CTGAGCGCTGCATCGATGCGCGAGCATTTGATCAGCTGCGGAAGGACCATGTGGCGCGG 1938  
Db 2296 CTGGCGGTGCCATTGACGCCAGGAGCATTGNATGGCTTCGGTCTGAGCACGTCGCGAAG 2355  
Qy 1939 TTTTGTCTACCTTCCAGAGAGAGATTTTGAGAGAAGTACTCCCGAAGGTGGATCCC 1998  
Db 2356 TTCTCTCTGACCTTCAGGAGGAGCTGACTTAGAGAAGAAGTACTCCAAGCAGGTAGACAG 2415  
Qy 1999 CGCTTCGAGCGTACGTGCGCTGCGCTGTGGTCTTCTGCTTCTCATCTGCTTCATCCAG 2058  
Db 2416 CCAATTTGGTGCCTATGTGGCGTGTGCTCGCTGCTTCTTCTTCTTCTTCTTCTTCTCAG 2475  
Qy 2059 CTCTTAATTTTCCACACTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCCCTGCTG 2118  
Db 2476 ATCACCATCGTGCCCACTCCATATTCATGCTCAGCTTCTACCTGACCTGTTCCTGCTG 2535  
Qy 2119 CTGCTAATCAGCGTCTGATCTGTGCTGTACTCCTGTGCTTCTTCTTCTTCTTCTTCTTCT 2178  
Db 2536 CTGACCTTGGTGGT 2595  
Qy 2179 CTGCAACGCTGTCCCGCAGCATTTCTCGCTCAGCGGCACATAGACACCGATGGGCATC 2238  
Db 2596 CTGACAGCCCTCTCAGGAAGATCTGCGGTCCAAAGATGAACAGCAGCCCTGTTGGGGTG 2655  
Qy 2239 TTTTTCCTGCTGCTGT 2298  
Db 2656 TTCACCATCACCCTGGTGTCTTCTGCGGCTTTTGTCAACATGTTCACTGCAACTCCAG 2715  
Qy 2299 CCCATACGAGGTGTGACGCGCGGATGCTGAATTTAAACACCTGCTGACATCACTGCCTGC 2358  
Db 2716 GACCTGCTGGGTGCTTGGCAGAGGACACACATCAGCGGAGCGCAGTCAACCGCTGT 2775  
Qy 2359 CACCTGACAGCAG-----CTCAATTTACTCTCTGGGCTTGGATGCTCCCTGTGAGGGC 2412  
Db 2776 CACGTGGGCGAGTCCGCGCTCAACTACAGCCTGGGCGATGAGCAGGGCTTCTGTGGCAGC 2835  
Qy 2413 ACCATGCCACCTGACGCTGCTTCTGAGGTGTCATCGGGAACATGCTGCTGAGTCTCTTG 2472  
Db 2836 CCCTGGCCCACTGCAACTTCCCGAGTACTTCACTTACAGCGGTGCTGCTCAGCGCTGCTG 2895

Qy 2473 GCCAGCTCTGTTCTCTGCATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGCTTG 2532  
Db 2896 GCCTGCTCCGTGTTCTCTGCAGATCAGCTGCACTCGGAAGCTGGTCTCATGCTGCCATC 2955  
Qy 2533 GGGCTCATCTATTGTTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2592  
Db 2956 GAGCTCATCTA---CGTGTCTATCTGAGGTGCGAGGTGTCACGCTCTCGACACGCC 3012  
Qy 2593 GACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACCTTTGATGGGCTGGAC 2652  
Db 3013 GACCTGCTGGTACCGCCCAACGCCATAGACTTCTTCA---ACAAGGAGACCTCCAGTGC 3069  
Qy 2653 TGTCCAGCTCAGGGAGGTGGCCCTCAATATATATAGCCCTGTGATCTGCTGCTGCTT 2712  
Db 3070 CCTGAGCATGCAACCAAGTGCATTTGAAGTGGTGGACGCCATCATCTCATCTCTT 3129  
Qy 2713 GCGCTGGCGCTGTATCTCATGCTCAGCAGTGGAAATGACTGCTGCTGCTGCTGCTGCTGCTGCT 2772  
Db 3130 GTGCTGGCCTGTACTGACGCCCAGCAGGTGGAGTCCACTGCGCGCTCGACTTCCTC 3189  
Qy 2773 TGGAAACTACAGGCAACAGGGAAGAGGAGATGGAGGAGCTACAGGCATACAAACGG 2832  
Db 3190 TGGAAACTGCAAGCCACAGAGGAAGAGAGATGGAGGAGCTCAGGCCCTACAAACGG 3249  
Qy 2833 AGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCACTTCTTGGCCCGGAGCGC 2892  
Db 3250 CGGCTGCTGCACAACATCTGCCCAAGGACGTGGCGCGCTACTTCTGCGCGGAGCGG 3309  
Qy 2893 CGCAATGATGACTCTACTATCAGTCTGTGAGTGTGGCTGTGATTTGCTGCTCCTCAT 2952  
Db 3310 CGCAATGATGACTCTACTATCAGTCTGTGAGTGTGGCGGCTCATGTTGCTGCTCCTC 3369  
Qy 2953 GCCAACTTCTGAGTCTTCTATGAGCTGGAGGCAACAAATGAGGCTGCGGAGTGCCTG 3012  
Db 3370 GCCAACTTCTCGAGTCTTCTGAGTGGAGCTGGAGGCAACAAATGAGGCTGCGGAGTGCCTG 3429  
Qy 3013 GCGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTTATCAGCAGGAGGCTTCCGG 3072  
Db 3430 CGGCTACTCAATGAGATCATCGCTGACTTTGATGAGATCATCAGCAGGAGTCCGGTCCGG 3489  
Qy 3073 CAGCTGGAAGAAATCAACAGCATTTGATGAGCTACATGAGTGTGCTGAGGCTGAGGCTGAACGCC 3132  
Db 3490 CAGCTGGAGAAGATCAAGACCATCGGAGCAGCTACATGAGTGTGCTGCGCTCAGGAC 3549  
Qy 3133 AGCAGCTACGATCAGTGGCGGCTCCACATCACTGCGCTGGCTGAGTACGCCATGGG 3192  
Db 3550 TCTACCTAGCACAGGTGGGCAAGACCCACATCAAGGACCTGGCGGACTTTGCCATGAG 3609  
Qy 3193 CTCATGGAGCAGATGAAGCAGCATCAATGAGCAGCTCTTCAACAATTTCCAGATGAAGAT 3252  
Db 3610 CTGATGGACAGATGAAGTACATCAATGAGCAGCTCTTCAACAATTTCCAGATGAAGATC 3669  
Qy 3253 GGGCTGACATGGGCCCCAGTGTGCGAGGTGTATCGGGGCTCGGAAGCCACAGTATGAC 3312  
Db 3670 GGGCTCAACATCGGCCCCGTGGTGGCGGGTGTAGGGGCAAGAAACCCCTCAGTACGAC 3729  
Qy 3313 ATCTGGGGGAACACAGTGAATGTCTCTAGTGTATGAGCAGCAGCGGGGTCCCCAGCAG 3372  
Db 3730 ATCTGGGCAATACCGTGAACGTGGCCAGCGCATGAGCAGCAGCGGTGTATCCCGACGC 3789  
Qy 3373 ATCCAGGTGACCGGAGCTGTACAGGTCTTAGCTGCCAAGGGCTACAGGTGAGGTGT 3432  
Db 3790 ATCCAGGTGACCGAGACATGTACCAGTGTGGCTGCCAAGCAGTACAGGTGAGGTGC 3849  
Qy 3433 CGAGGGTGTCAAGGTGAAGGGCAAGGGGAGATGACCACTTCTTCTCAATGGGGGC 3492  
Db 3850 CGGGCGTGGTCAAGGTCAAGGGCAAGGGGAGATGATGATGATGATGATGATGATGATGATGAT 3909  
Qy 3493 CCC 3495  
Db 3910 CCC 3912



RESULT 11	165	CACCCCTGCGGGCCCTCGGTGCCCTGGCAGGATGAGCCCTTATCCGGAGGGCGG	224
AAQ95540	Db		
AAQ95540 standard; DNA; 4356 BP.			
XX			
AC			
AAQ95540;			
XX			
31-JAN-1996 (first entry)			
XX			
Cardiac adenyllyl cyclase gene.			
XX			
Cardiac adenyllyl cyclase; effector enzyme; ss.			
XX			
Homo sapiens.			
XX			
Key			
Location/Qualifiers			
148..3702			
FT			
/*tag= a			
XX			
TW243453-A.			
XX			
21-MAR-1995.			
XX			
02-JUL-1992; 92TW-0105242.			
XX			
12-JUN-1992; 92US-0899068.			
XX			
(AMCY ) AMERICAN CYANAMID CO.			
XX			
WPI; 1995-214006/28.			
DR			
P-PSDB; AAR78519.			
XX			
Cardiac adenyllyl cyclase and corresp. DNA - having specified			
sequences			
XX			
Claim 1; Fig 2; 45pp; Chinese.			
XX			
AAQ95540 encodes AAR78519, the novel effector enzyme cardiac adenyllyl			
CC			
cyclase.			
XX			
Sequence 4356 BP; 836 A; 1372 C; 1373 G; 775 T; 0 other;			
SQ			
Query Match	47.6%;	Score 1690;	DB 16; Length 4356;
Best Local Similarity	70.1%;	Pred. No. 0;	
Matches 2348; Conservative	0;	Mismatches 980;	Indels 20; Gaps 5;
QY	165	CACCCCTGCGGGCCCTCGGTGCCCTGGCAGGATGAGCCCTTATCCGGAGGGCGG	224
Db	346	CGCCCTGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG	405
QY	225	CCAGGCAAGGGCAAGGAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCCAGGATACCGA	284
Db	406	CTCGTGGAGCTGGCTGGACAGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGG	465
QY	285	GGTGACACAGACAGGGGGGACGGCTGAGTGGGGCGGGCGGGCGGGCGGGCGGGCGGG	342
Db	466	GGCCGAGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG	525
QY	343	GGCGGATCTGCTGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG	402
Db	526	CCGGCGGCTGCTGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG	585
QY	403	AAGCTGGAGGGCTGTACCAAGCGGTACTTTTCCAGATGAACACAGACAGCAGCTGAGCGTG	462
Db	586	AAGCTGGAGGGCTGTACCAAGCGGTACTTTTCCAGATGAACACAGACAGCAGCTGAGCGTG	645
QY	463	CTGGTGGCGGTGCTGTGCTGCTACAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	522
Db	646	CTATGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	705
QY	523	CGCCCTCAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	582
Db	706	CGCTGGGGTGGCCCACTGGGGCGGTGCTGGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG	765





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Db 1956 GGAGGCAACCAAGGTGTCACAGAGATGATGAAGCCATGCGGCTTCGAAGACCCCAAGACAAAG 2025
Qy 1838 -----CCCAAGATGCCCTGAACCCCTGAGGATGAGTGGATGAGTTCTCTGAGCGGTGCCATC 1893
Db 2026 RACGCCCAAGGAAGTGCAGACCCCTGAGGATGAGTGGATGAATTTCTGGCGCGGCCAATT 2085
Qy 1894 GATGCCCGCAGATGATGATCAGCTGCGGGAAGGACCAATGTCGCGGGTTTTTGTCTACCTTC 1953
Db 2086 GACGCCAGGAGCATCGACAGGCTGGGTCGGAGCAGCTCCGCAAGTTCTCTGACCTTC 2145
Qy 1954 CAGAGAGAGGATTTTGAAAGAGTACTCCCGGAAGTGGATCCCGCTTCGGAGCCCTAC 2013
Db 2146 AGGGAGCTGACTTAGAAAAGAGTACTCCAAGCAGCTGGGATGACCGATTCGGTGCCTAC 2205
Qy 2014 GTTGCTGTGCCCTGTGGTCTTCTGCTTCATCTCTCATCCAGCTTCTAATTTTCCCA 2073
Db 2206 GTGGCATGTGCTCGTGTCTTCTCTCTTCATCTGCTTTGTCCAGATCACCATCGTACCC 2265
Qy 2074 CACTCCACCCGTATGCTTTGGGATTTATGCCAGCATTTCTCTGCTGCTCTAATCACCCGTG 2133
Db 2266 CACTCCGTGTTTCATGTTGAGTTTCTACTTGAACCTGTTTCTCTGCTGCTGACGTTGGTGTA 2325
Qy 2134 CTGATCTGTGCTGCTACTCTCTGTTGTTCTCTGTTCCCTAAGGCCCTGCAAGCTGTGTC 2193
Db 2326 TTTGTGTCGGTGATCTATTCTGCTGGTGAAGCTCTTCCCGGGCCCGCTCCAGAGCCTCTCG 2385
Qy 2194 CGCAGCATTTGCCGTACGGGCACATAGCACCGAGTTGCACTCTTTTCCGTCTGCTT 2253
Db 2386 AGGAATCGTGGCTCCAAGACCACAGACCCCTGGTCTGGGGTGTTCACCATCACCCGTG 2445
Qy 2254 GTGTTTACTTGTGCAATTTGCCAATGTTTACCTGTATACCAACACCCCATACGGAGCTGT 2313
Db 2446 GTGTTCTGTGGCTTTCGTCAACATGTTTCATGTGTAACTCCGAGGACCTGTGTTGGCTGC 2505
Qy 2314 GCAGCCGGATGCTGAATTTAACACCTCTGTACATCACTGCTGCCACCT-----CGAG 2367
Db 2506 CTGGCGGAGAGACAAACATCAGACCCGGGTCAACGGCTGACAGCTGGCGGCGCTG 2565
Qy 2368 CAGCTCAATTAATCTCTGCGGCTGGATGCTCCCTGTGTGAGGACCACTGCCACCTGC 2427
Db 2566 GCGGCAACCTCAGCTTGGCGACGAGCAGGCTTCTGCGGCACGCCCTGGCCGAGCTGC 2625
Qy 2428 AGCTTCTGTAGGTGTCATCGGGACATGCTGCTGAGTCTCTTGGCCAGCTCTGTCTTC 2487
Db 2626 AACTTCTCCCGAGTACTTACCTACAGCTGCTGTCTGCTCAGCCCTGCTGCGCTGCTCCGTG 2685
Qy 2488 CTGCATCAGCAGCATCGGGAAGTTGGCCATGATCTTGTGTTGGGCTCATCTATTG 2547
Db 2686 CTGCAGATCAGCTGCATCGGAAGCTGTGTCTATGCTGGCCATGAGCTCATATA---C 2742
Qy 2548 GTGCTGCTTCTGCTGGGTCCCGGACCGCCCATCTTTGACAACTATGACCTACTGCTTGGC 2607
Db 2743 GTGCTCGCTCGAGGTGCCCGGGTCACTGTTTGAACAAGCTGACCTGCTGTGTCACC 2802
Qy 2608 GTCCATGCTTGGCTTCTTCAATGAGACCTTTGATGGCGTGGAGCTGTCAGCTGCAGGG 2667
Db 2803 GCCAACGCCATAGACTTCAACAACAACAACCGGAGCTCGCAGTGGCTTCTGAGCAGCGCAC 2862
Qy 2668 AGGTGGCGCTCAATATATGACCCCTGTGATCTCTGCTGGTGTGTTGCGCTGGCGCTGAT 2727
Db 2863 AAGTGGCGCTGAAGTGGTGAACCCCATCATCTCCGTCTGCTGCTGCGCTGTAC 2922
Qy 2728 CTGCATGCTCAGCAGGTGGAATGCACTGCCCGCTTAACTTCTCTGGAATACTACAGCA 2787
Db 2923 CTGCATGCCCAAGCAAGTGGAGTCCACCGCCCGCTCGACTTCTCTGGAATACTGAGGCC 2982
Qy 2788 ACAGGGAAAGAGGAGATGGAGAGCTACAGGCATACACCGGAGGCTGCTGCATAAC 2847
Db 2983 ACAGGAGAGAGGAGATGGAGAGCTGACGGCTTCAACACCGCGGCTGCTGCACAA 3042
Qy 2848 ATTGCCCCAAGGAGCTGGCGGCCACTTCTCTGGCGGGAGCGCCGCAATGATGAATC 2907
Db 3043 ATCTGTGCCCAAGGAGCTGGCTGCCACTTCTGTGCCCCGTGAGCGACGACGAGCTC 3102
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Qy 2908 TACTATCAGTCTGTGAGTGTGTGCTGTTATGTTTGGCTTCCATTTGCCAACTTCTCTGAG 2967
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Qy 2968 TTTATGTGGAGCTGGAGGCAACAATGAGGTTGCCGAGTGCCTGCGGCTGCTCAACAG 3027
Db 3163 TTTACGTGGAGCTTTGAGGCCAACAATGAGGTTGTCGAGTGCCTGCGGCTGCTCAATGAG 3222
Qy 3028 ATCATCGTCTGTTGATGAGATATACGAGGAGCGGTTCCGCGACGTGGAAGAATC 3087
Db 3223 ATCATCGTCTGATTTGATGAGATCATCAGGAGGATCGGTTTCAAGCAGCTGGAGAATC 3282
Qy 3088 AAGACGATTGTAGCACCTACATGCTGCCCTCAGGCTGGAACGCCAGCACCTACGATCAG 3147
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Qy 3148 GTGGCCGCTCCACATACACTGCCCCGTGCTGACTACGCCATGCGGCTCATGAGCAGATG 3207
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Qy 3208 AAGCACATCAATGAGCACTCCTTCAACAATTTCCAGATGAAGATTGGGCTGAACATGGC 3267
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Qy 3268 CCAGTCTGGCAGGTGTTCATCGGGCTCGAAGCCACACAGTATGACATGCGGGGAACACA 3327
Db 3463 CCCGTGTTGGCGGGTGTATCGGGCTCGCAAGCCTCAGTACGACATCTGGGGCAATAG 3522
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Db 3523 GTGAATGTGGCAGCCGATGAGCAGCAGCGGCTGCGGACCGCATCCAGTCCACCAG 3582
Qy 3388 GACCTGTACCAAGTCTTAGCTGCCAAGGCTACCAGCTGGAGTGTGCGAGGGTGTCTCAAG 3447
Db 3583 GACATGTACCAAGTGTGGCTGCGCAACACAGTACCAGCTGGAGTGCAGGGGTGTGTCAAG 3642
Qy 3448 GTGAAGGCAAGGGGAGATGACCACTTCTTCTCAATGGGGCCCC 3495
Db 3643 GTCAAGGCAAGGGAGATGATGACCTTCTTCTCAACGGTGGGCC 3690
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## RESULT 13

AAA53922

ID AAA53922 standard; cDNA; 3924 BP.

XX AAA53922;

AC AAA53922;

XX 03-JAN-2001 (first entry)

XX Type V adenylyl cyclase coding sequence.

XX Adenylyl cyclase; type I; type II; recombinant; enzyme; CAMP;  
XX cyclic AMP; adenosine monophosphate; screening; stimulation;  
XX inhibition; treatment; cholera; pituitary tumour; heart failure;  
XX ischaemia; endocrine disorder; cell necrosis;  
XX pseudohypoparathyroidism; endocrine deficiency; human; ss.

XX Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 3..3329

FT FT /\*tag= a

FT FT /product= Type V adenylyl cyclase

XX US6107076-A.

XX

XX 22-AUG-2000.

XX

XX 04-OCT-1996; 96US-0726214.

XX

XX 04-OCT-1995; 95US-0005498.

XX





xx Novel human adenylyl and guanylyl cyclases and polynucleotides encoding  
pt the cyclases, useful for treating, diagnosing or preventing  
pt cardiovascular, neurological, vision, reproduction and smooth muscle  
pt disorders -  
pt

PS Claim 5; Page 112-113; 116pp; English.

The invention relates to human adenylyl and guanylyl cyclases (ADGUC) preferably ADGUC1-ADGUC5 and nucleic acid molecules encoding such polypeptides. ADGUC sequences are useful in the diagnosis, prevention and treatment of cardiovascular disorders (e.g. angina pectoris, myocardial infarction, ischaemic heart disease, hypertension and atherosclerosis), vision disorders (e.g. keratoconjunctivitis sicca, keratitis, iritis, cataract), neurological disorders (e.g. epilepsy, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease, Creutzfeldt-Jakob disease, stroke, schizophrenia, mental disorders including mood and anxiety and prion diseases including kuru), reproductive disorders (e.g. infertility, endometriosis, impotence, uterine fibroid and gynaecomastia), smooth muscle disorders (e.g. arrhythmias, asthma and migraine) and bacterial infections. ADGUC polynucleotides are useful for creating knock-in humanised animals or transgenic animals to model human diseases. They are useful in somatic or germline gene therapy. ADGUC polynucleotides are also useful for detecting differences in the chromosomal location due to translocation, inversion, etc. among normal, carrier or affected individuals. ADGUC polypeptides are useful in a number of drug screening techniques and in vaccines. The present sequence is human ADGUC-2 cDNA.

Sequence 3137 BP; 553 A; 973 C; 1044 G; 567 T; 0 other;

Query Match 23.8%; Score 843; DB 24; Length 3137;  
Best Local Similarity 68.4%; Pred. NO. 7.6e-195;  
Matches 1286; Conservative 0; Mismatches 500; Indels 93; Gaps 5;

QY	214	CGGAGGGCGGCCCAAGGC	AGGCAAGGCAAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTC	273
Db	712	CGCGGGGCAAGGGCGCGCCG	CCGACAGCTGGAGCGCGCCGCTCGAGGGCGGAG	771
QY	274	GAGATACCGAGGTGACAAC	AGACACGCGGGCGGGAGCGGTGAGGTGGCGCCGACGCGGGT	333
Db	772	GGGTCCGGGATGGCGGAG	CTCGCGGACCTGGGCTCGGCGCGGGCCCGCGCGGTG	831
QY	334	CCGAGAGTGGCGGATCTCTG	TGGGCGCCGTTTGTGTGACAGTGTTCAGTCCGAAGCAGTTC	393
Db	832	C---TGTCCTCGGGGCCCTG	CTGCTCGCGGTTGCTGCAGATATTCGCTCCAAAGTTC	888
QY	394	CGTTGGCCAAAGCTGGAGCG	CTGTACCAGCGGTACTTTTCCAGATGAACACAGACGAC	453
Db	889	CGCTCGGACAACTGGAGCG	CGCTGTACCAGCGCTACTTCTTCGCCCTGAACACAGAGACGC	948
QY	454	CTGACGCTGCTGGTGGCGST	GTGTGTCTCACAGCGGTGCTGTGCTGGCTTCCCAAGCC	513
Db	949	CTCACCATGCTCATGGCTGTG	TGTGTGTCTGTGCTGTGCTGTGCTGTGGCTTCCACGCG	1008
QY	514	GCACCGCGCCGCTCAGCCTG	CCCTATGTGCGACTGTGGGCTGTGCGCGGCCCTGTTTC	573
Db	1009	GGCGGCCCGCCGCTCCAGT	GCCTTACCTGCG-----	1040
QY	574	GTGGGGCTCATGGTGGTGTG	TAAACGGCATAGCTCCGCCACGACTCCATGTGGGTGGTG	633
Db	1041	-----	-----CGACCACATGGGCCCTGGCC	1059
QY	634	AGTACGTGGTCTGGGCA	TCCCTGGCGGCATGTGAGTTCGGGGGCGCTTTCGACGACAGC	693
Db	1060	TGCTATGCGCTCATGCGGCT	GTGTGTGCGCGCTCCAGGTGTGGGCCCTGCTGCTGCCCGAG	1119
QY	694	CGCGCAGCCCTCTGCGGGC	CTGTGTGCGCCCTGTGTCTTTGTATACATCGCATACACG	753
Db	1120	CCACGAGGCCCTCTGAGGG	GCATCTGTGTGACCGGTGTTCTTCATCTACACCATCTACACG	1179
QY	754	CTCTCCCATCCGCATCGG	CGCTGCCCTCTCAGCGGCCCTGGGCCCTCTCCACCTTGCAT	813

Db	1180	CTGCTGCCGTGCGCATGCGGGCCGAGTGCCTCAGCGGGGTGCTCTCTGTCGCCCTCCAC	1233
Qy	814	TTGATCTTGGCCTGGCAACTTAACCGTGTGATGCTTCCCTCTCGAAGCAGCTCGGTGCC	873
Db	1240	CTGGCCATCGCCTTGGCACCAACGCCCAGGACCAGTTTCTGCTGAAGCAGCTTGTCTCC	1299
Qy	874	AATGTGCTGCTGTTCTCTTGCAACCAAGCTCATTCAGCTATTCGACACACATATCCAGCAGAG	933
Db	1300	AATGTCTCTATTTTCTTCCCTGCAACCAACATCGTGGGTGCTCGACCCACTATCCGGCTGAG	1359
Qy	934	GTGTCACGCGCCAGSCCTTTTCAGGAGACCCGCACTATCATCCAGGCCCGGCTCCACCTG	993
Db	1360	GTCTCCAGAGACAGGCTTTTCCAGGAGACCCGAGAGTGCATTCAGGCGGGCTCCACTCG	1419
Qy	994	CAGCATGAAGTAACCGCAGCAGGAGGGGTGCTGCTGTCGGTATTGCCCCAGCAGCTTGCC	1053
Db	1420	CAGCGGAGAACCAAGCAGCAGACGGCTCTGCTGTCTGTCTTCCCGTCACTGTTGCC	1479
Qy	1054	ATGGAGATGAAGAAGACATCAACACAAAAAAGAAGAA--CATGTTCACAAGATCTAC	1110
Db	1480	ATGGAGATGAAGACAGACATCAACGCCAAGCAGGAGGATATGATGTTCATAAAGATTAC	1539
Qy	1111	ATACAGAACATGACAAATGTCAGCATCTCTGTTTGACAGACATTTAGGGCTTCACAGCGTG	1170
Db	1540	ATCCAGAAACATGACAACTGAGCATCTGTTTGTCTGACATCGAGGGCTTCACACAGCTG	1599
Qy	1171	GCATCCAGTGCACCTCGCAGGAGTGGTCACTAGCCCTGAATGAGCTCTTTGCCCGGTTT	1230
Db	1600	CGCTCCAGTGCACCTGCCACAGACATGTCATGACCCCTCAAGAGCTCTTCGCCCGCTT	1659
Qy	1231	GACAAGCTGGCTGCGGGAATCACTGCTTGAGGATCAAGATCTTTGGGGACTGTTACTAC	1290
Db	1660	GACAAGCTGGCCGACAGAAATCACTGTTTACGTATTAAAGATCTTTGGGGAATGTTATTAC	1719
Qy	1291	TGTGTGTACAGGGCTGCCGAGGGCCGGCCGACATGCCCCACTGCTGTGTGGAATGGGG	1350
Db	1720	TGGCTCTCGGGGTGCTCTGAAGCAAGGGCTGACCAAGCCCTACTGCTGTGTGGAGATGGC	1779
Qy	1351	GTAGACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGTCAACATG	1410
Db	1780	ATGGACATGATCAGGCGCATCTGTTGTTGCCGGAGGTGACAGGGGTGAACGTGAACATG	1839
Qy	1411	CGGCTGGGATCCACAGCGGGCCGTGCACTCGCGCGCTCTTGGCTTCGGAAATGGCAG	1470
Db	1840	CGTGTGGAAATTCACAGCGGCGAGTACACTCGCGTGTCTTGGTCTCAGGAAGTGGCAG	1899
Qy	1471	TTCGATGTGTGTTCCAAATGATGTACCTTGGCCACACACATGGAAGCAGGAAGCGGGCT	1530
Db	1900	TTCCAGCTGTGGTCTTAACGATGTCACTGTAGCCATAGCAACCACTAGGAGCTTGGCGCAAGCA	1959
Qy	1531	GGCCGATCCACATCACTCGGCCACACTGCACTAGTACTCTGAACGGGACTACGAAGTGGAG	1590
Db	1960	GGACGATCCACATCAACAAAGGCTACACTCAACTACCTTGAATGGGACTACGAGGTGGAG	2019
Qy	1591	CCAGCGCGTGTGGCAAGCGCACACCGTACCTCAAGGAGCAGCACATTTGACATTTCCCTC	1650
Db	2020	CCAGGCTGTGGGGCGAGCGCAAGCCCTACCTCAAGGAGCAGATATCGAGACCTTCCCTC	2079
Qy	1651	ATCCTGGGGCCACAGCAGAAACGGAAGAGGAGAAGGCATGCTGGGCCAAGCTCGACGGG	1710
Db	2080	ATCCTTCGGTGTGACCAGAAGGGGGAAGAAGAGAGAGGCCATGATCGCCCAAGATGAACCGC	2139
Qy	1711	ACTCGGGCCAACTCCATGAAAGGCTGATGCCCGCATGGGTTCCTGTATCTGCTCTCTCC	1770
Db	2140	CAGAGAAACCACTTCCATCGGGGCACAAACCCACCACTGGGGGGCTTGAGCGCCCTTCTAC	2199
Qy	1771	-----CGGACCAAGCACTTCCAAAGGCTTTCGCCAGATGGGCATTTGATGATTC	1818
Db	2200	AACCACCTGGGTGCAACCAAGTGTCCAGAGAGATGAAGCGGATGGGCTTTGAAGACCC	2259
Qy	1819	AGCAAGACAAACCGGGGCACCCCAAGATGCCCTGAACTCTGAGGATGAGGTGGATGATTC	1878
Db	2260	A-----AGCAGAAAGAACCGCCAGGAGAGTGGCAACCTCGAGGATGAAGTGGATGATTT	2313







QY	2176	GCCCTGCAACGTCTGTCTCCCGCAGCATTTGGTCCGCTCACGGGCACATAGCACCGCAGTTGGC	2239
Db	2008	AGTGTGGCTGCCCTTGTCCTCTGCTGGTGTCTTGCATCTGCTTCTCCTGGTGGCCCTGTGTCTCG	2067
QY	2236	ATCTTTTTCCGTCCTGCTGTGTGTTTACTTCTGCACATTGCCAACATGTCACCTGTAAACAC	2295
Db	2068	TACCTACACATCACCCGGGT-----CCAGTGTTTTCCAGGGTGCCTGACCATTCC	2116
QY	2296	ACCCCATATAGGAGCTCTGACGCCCGGATGCTGAATTTAACAACCTCTGCTGACATCACTGCC	2355
Db	2117	AGATCCGCACCGCTTTGTGTCATCTTATCGTGGTCTTAATCTACTCTGTGGGCCCAAGGC-	2175
QY	2356	TGCCACCTGCAGCAGCTCAATTAATCTCTGGGCTGGATGCTCCCCCTGTGTGAGGGCACC	2415
Db	2176	-----TGTGTGGTGGGTGCCTGCCCTTGTGCTGGAGCTCCAAGTCCCAACGGGTCCC	2227
QY	2416	ATGCCCACTGCAGCTTTTCTGAGGTGCCATCGGGAACATGCTGCTGAGTCTCTTTGGCC	2475
Db	2228	TGGTGGTCCCTGTCTTCTGGGGCCGGAGCCAGTGTGCTG-TCOCGCCCTTGGCAGTCT	2286
QY	2476	AGCTCTGCTCTTCCCTGCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGTCTTGGGG	2535
Db	2287	CGGCCCATCGCCCTGTGTCGGCCCTCGTGGGCACCTCCCGCTGGCCATATCTCTCGGG	2346
QY	2536	CTCATCTAATTTGGTGTCTCTCTGCTGGGTGCCCAACGCCCATCTTTTGACAACCTATGAC	2595
Db	2347	GTCTCCCTCCITGCCAAAAATGATCCTGCTGCGCGTGCACCAACCTCTACATCTCTGTC	2406
QY	2596	CTACTGCTTGGGCTCCATGCGCTTGGCTTCTTCCAAATGAGACCTTTTGATGGGCTGGACGT	2655
Db	2407	CTGGAGTCTACGC-----GGTACACGAAGGCCATG	2436
QY	2656	CCAGCTCAGGGGGTGGCCCTCAAATATATGACCCCTGTGATCTGCTGTGTCTTGGC	2715
Db	2437	GGGCGCGTGCATCTCAGGGCCGCACTTCGAGCCGATCATGGCCATCTCTGCTATCTCG	2496
QY	2716	GTGCGGTGTATCTGCATGCTCAGCAGGTGGAATCGACTGCCCGCTAAACTTCCTCTGG	2775
Db	2497	TGCACGTGGCCCTTGACGCCCGCAGGTGGATGTCAAGCTCGCGCTGSACTACCTCTCG	2556
QY	2776	AAACTACAGCCACAGGGGAAAAGAGGAGATGGAGGACTACAGCATACAAACGGAG	2835
Db	2557	CGGCCACAGGCAGGAGGAGCGGATGACATGGAGAAAGTGAAGCTGGACAACAAGAG	2616
QY	2836	CTGTGTCATAACATTTCTGCCCAAGGACGTGGGGCCCACTTCTGCCCGGGAGCGCCGC	2895
Db	2617	ATTCTCTCAACCTCCTGCCAGCCACGTTGCCAGCACTTCTTAATGCCAACCTCGC	2676
QY	2896	AATGATGAATCTACTATCATGCTGTGTAGTGTGGGTGTATGTTGTGCCTTCCATPGCC	2955
Db	2677	AACATGGACCTGTATTACCAAGTCATCTCGCAGTGGGGGTGATGTTTGATCCATCCCC	2736
QY	2956	AACTTCTGTGAGTTCTATGTGAGCTGGAGGCAAAAGTAGGGTGCAGTGCCTCGGG	3015
Db	2737	AACCTCAATGACTCTACATCGAGCTGGATGGCAACAACATGGGGTGAATGCTACGC	2796
QY	3016	CTGCTCAACGAGATCFGCTGACTTTGATGAGATTATCAGCGAGGAGCGGTTCGGGAG	3075
Db	2797	CTTCTGAATGAGATCATCGCTGACTTTGATGAGCTCATGGACAAGAAGACTTTTTACAAGGAC	2856
QY	3076	CTGAAAAGATCAAGAGATTGTGTAGCACTCATATGGCTGCCTCAGGGCTGAAGCC---	3132
Db	2857	CTAGAGAAGATCAAGACCATTTGGAGCACTACATGGCTGTGTGGGCTGGCGCCACT	2916
QY	3133	-----AGCACTACGATCAGSTGGGCCCTGCCCATCACTGCCCTGGCTGACTACGCC	3186
Db	2917	GCTGGGACCAAGGCTAAGAAGTGCATCTCTCCCACTCAGCACGTTTGGCAGATTTTGGC	2976
QY	3187	ATGGCGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCTCTCAACAATTTCCAGATG	3246
Db	2977	ATCAGAGATTGTATGCTCTGGATGAGTCACTACCAAGCTCTTATPAAGCACTTTGTGCT	3036



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2003, 22:03:11 : Search time 86,927 Seconds  
(without alignments)  
12520.796 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3549	100.0	3549	US-09-008-097-5	Sequence 5, Appli
2	3478.4	98.0	4942	US-09-474-076-1	Sequence 1, Appli
3	2990.4	84.3	4046	US-07-793-961A-1	Sequence 1, Appli
4	2990.4	84.3	4046	US-08-240-357-1	Sequence 1, Appli
5	2751.2	77.5	4131	US-08-726-214-11	Sequence 11, Appli
6	1808.4	51.0	1812	US-09-008-097-3	Sequence 3, Appli
7	1703.4	48.0	4523	US-09-473-716-1	Sequence 1, Appli
8	1648.2	46.4	3924	US-08-726-214-9	Sequence 9, Appli
9	595	16.8	3978	US-08-726-214-1	Sequence 1, Appli
10	505.2	14.2	3518	US-09-412-210-2	Sequence 2, Appli
11	463.6	13.1	4601	US-08-726-214-15	Sequence 15, Appli
12	459	12.9	4008	US-08-307-896-5	Sequence 5, Appli
13	459	12.9	4008	US-08-726-214-3	Sequence 3, Appli
14	459	12.9	4008	PCT-US95-11808-5	Sequence 5, Appli
15	441.6	12.4	4533	US-08-726-214-5	Sequence 5, Appli
16	433	12.2	5199	US-08-726-214-13	Sequence 13, Appli
17	428	12.1	3357	US-08-726-214-7	Sequence 7, Appli
18	393.2	11.1	1652	US-08-726-214-17	Sequence 17, Appli
19	295.2	8.3	314	US-09-008-097-1	Sequence 1, Appli
20	288.2	8.1	2092	US-08-307-896-6	Sequence 6, Appli
21	288.2	8.1	2092	PCT-US95-11808-6	Sequence 6, Appli
22	216.8	6.1	4473	US-08-894-173-1	Sequence 1, Appli
23	216.8	6.1	4473	US-09-398-193-1	Sequence 1, Appli
24	209.4	5.9	4985	US-09-473-717-1	Sequence 1, Appli
25	207.8	5.9	5515	US-09-398-193-98	Sequence 98, Appli
26	73	2.1	7218	US-08-232-463-14	Sequence 14, Appli
27	64.4	1.8	1259	US-08-997-080-123	Sequence 123, App

ALIGNMENTS

RESULT 1  
US-09-008-097-5  
; Sequence 5, Application US/09008097  
; Patent No. 6306830  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, H. Kirk  
; APPLICANT: Insel, Paul A.  
; APPLICANT: Ping, Peipei  
; APPLICANT: Post, Steven R.  
; APPLICANT: Gao, Weihua  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE  
; TITLE OF INVENTION: HEART FAILURE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/008,097  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dylan, Tyler M  
; REGISTRATION NUMBER: 37,612  
; REFERENCE/DOCKET NUMBER: 22000-20567.21  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3549 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 1...3501  
; OTHER INFORMATION:

Sequence 123, App  
Sequence 123, App  
Sequence 123, App  
Sequence 123, App  
Sequence 176, App  
Sequence 176, App  
Sequence 176, App  
Sequence 176, App  
Sequence 173, App  
Sequence 173, App  
Sequence 173, App  
Sequence 173, App  
Sequence 44, Appl  
Sequence 44, Appl  
Sequence 44, Appl

US-09-008-097-5

Query Match 100.0%; Score 3549; DB 4; Length 3549;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGTCATGGTTAGTGGGCTCTGTGCTCCCTAAAGTGGATGAACGGAACACGCTGGGGT	60
Db	1	ATGTCATGGTTAGTGGGCTCTGTGCTCCCTAAAGTGGATGAACGGAACACGCTGGGGT	60
Qy	61	GAACCAATGGCAGAAAGCTTCGGCGCGCTGCGCATCCGGCAGGTGGCTTCCTGCAGG	120
Db	61	GAACCAATGGCAGAAAGCTTCGGCGCGCTGCGCATCCGGCAGGTGGCTTCCTGCAGG	120
Qy	121	CCCCCTATATAGCTGCTCCGGGATGACAGCCACCCAGCCCTCGCGGCCCC	180
Db	121	CCCCCTATATAGCTGCTCCGGGATGACAGCCACCCAGCCCTCGCGGCCCC	180
Qy	181	CTTCGGTGCCTCGCAGATGACGCCCTTCATCCGGAGGGGGCCAGGCAAGGCAAG	240
Db	181	CTTCGGTGCCTCGCAGATGACGCCCTTCATCCGGAGGGGGCCAGGCAAGGCAAG	240
Qy	241	GAGCTGGGGCTCGGGCAGTGGCTTGGCTTCGAGGATACGGAGGTGACACACGAGG	300
Db	241	GAGCTGGGGCTCGGGCAGTGGCTTGGCTTCGAGGATACGGAGGTGACACACGAGG	300
Qy	301	GCGGGAGGGCTGAGGTGGCGCCCGACGCGGTGCCAGAGTGGCGATCCTGCTGGCGC	360
Db	301	GCGGGAGGGCTGAGGTGGCGCCCGACGCGGTGCCAGAGTGGCGATCCTGCTGGCGC	360
Qy	361	CGTTGGTGCAGGTGTTCCAGTGAAGCAGTTCCTTCGGCCAAAGCTGAGCGCCTGTAC	420
Db	361	CGTTGGTGCAGGTGTTCCAGTGAAGCAGTTCCTTCGGCCAAAGCTGAGCGCCTGTAC	420
Qy	421	CAGCGGTACTTTTCCAGATGAACAGACAGCCTGAGCTGCTGGTGGCGGTGCTGCTG	480
Db	421	CAGCGGTACTTTTCCAGATGAACAGACAGCCTGAGCTGCTGGTGGCGGTGCTGCTG	480
Qy	481	CTGCTCACAGGGTCTGCTGGCTTTTCCAAAGCGCGACCGCGCCCTCAGCCTGCCTAT	540
Db	481	CTGCTCACAGGGTCTGCTGGCTTTTCCAAAGCGCGACCGCGCCCTCAGCCTGCCTAT	540
Qy	541	GTGGCAGCTGTTGGCTGTGGCGCCCTGTTCGTGGGGCTCATGGTGGTGTAAACGG	600
Db	541	GTGGCAGCTGTTGGCTGTGGCGCCCTGTTCGTGGGGCTCATGGTGGTGTAAACGG	600
Qy	601	CATAGCTTCGCGCAGGACTCATATGTGGTGTAGTAAAGTGTGCTGGGCATCCTGGG	660
Db	601	CATAGCTTCGCGCAGGACTCATATGTGGTGTAGTAAAGTGTGCTGGGCATCCTGGG	660
Qy	661	GCAGTGCAGGTGGGGGCTTTCGACAGACCGCGAGCCCTCTCGGGGCTCTGG	720
Db	661	GCAGTGCAGGTGGGGGCTTTCGACAGACCGCGAGCCCTCTCGGGGCTCTGG	720
Qy	721	TGCCCTGTGTTTGTATATACATACAGCTTCTCCGATCCGATCCGATGGGGCTGCC	780
Db	721	TGCCCTGTGTTTGTATATACATACAGCTTCTCCGATCCGATCCGATGGGGCTGCC	780
Qy	781	GTCTTCAGCGGCTTCCACCTTGCATTTGATTTGGCTTGGCTTGAACCTTAAACGT	840
Db	781	GTCTTCAGCGGCTTCCACCTTGCATTTGATTTGGCTTGAACCTTAAACGT	840
Qy	841	GGTATGCTTCTCCTGGAAGAGCTCGGTGCCAATGTGCTGCTCCTCTGCACCAAC	900
Db	841	GGTATGCTTCTCCTGGAAGAGCTCGGTGCCAATGTGCTGCTCCTCTGCACCAAC	900
Qy	901	GTCATTAGCATGTGACACACTATCCAGCAGAGGTGTCTCAGCGCCAGCCCTTTCAGAG	960
Db	901	GTCATTAGCATGTGACACACTATCCAGCAGAGGTGTCTCAGCGCCAGCCCTTTCAGAG	960
Qy	961	ACCCGAGTTACATCCAGGCCCGGCTCCACCTGACAGTGAATCGGCAGCAGGAGCGG	1020
Db	961	ACCCGAGTTACATCCAGGCCCGGCTCCACCTGACAGTGAATCGGCAGCAGGAGCGG	1020

Qy	1021	CTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCATGGAGATGAAAGACATCAACACA	1080
Db	1021	CTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCATGGAGATGAAAGACATCAACACA	1080
Qy	1081	AAAAAAGAACATGTTCCACAAGATCTACATACAGAGCATGACAATGTACAGATCCTG	1140
Db	1081	AAAAAAGAACATGTTCCACAAGATCTACATACAGAGCATGACAATGTACAGATCCTG	1140
Qy	1141	TTTGACAGCATTTGAGGGCTTCCACAGCTTCCAGCTGCGCAGGAGCTGGTC	1200
Db	1141	TTTGACAGCATTTGAGGGCTTCCACAGCTTCCAGCTGCGCAGGAGCTGGTC	1200
Qy	1201	ATGACCTGAATGAGCTCTTTGCCCGGTTTGACAAAGCTGGCTGCGGAGAAATCACTGCC	1260
Db	1201	ATGACCTGAATGAGCTCTTTGCCCGGTTTGACAAAGCTGGCTGCGGAGAAATCACTGCC	1260
Qy	1261	AGGATCAAGATTTTGGGGACTTGTACTGTGTGTCAGGGCTGCCGAGGCCCGGGCC	1320
Db	1261	AGGATCAAGATTTTGGGGACTTGTACTGTGTGTCAGGGCTGCCGAGGCCCGGGCC	1320
Qy	1321	GACCATGCCACTGCTGTGGAGATGGGGTAGACATGATTGAGGCCATCTCGCTGGTA	1380
Db	1321	GACCATGCCACTGCTGTGGAGATGGGGTAGACATGATTGAGGCCATCTCGCTGGTA	1380
Qy	1381	CCTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCTGCAC	1440
Db	1381	CCTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCTGCAC	1440
Qy	1441	TGCGCGCTCCTTGGGTTGCGGAAATGGCAGTTTCGATGTGTGTTGTTCAATGATGTAC	1500
Db	1441	TGCGCGCTCCTTGGGTTGCGGAAATGGCAGTTTCGATGTGTGTTGTTCAATGATGTAC	1500
Qy	1501	GCCACCACTGGAAGAGGAGCGGGCTGCCCATCCACATCCTCGGCAACACTG	1560
Db	1501	GCCACCACTGGAAGAGGAGCGGGCTGCCCATCCACATCCTCGGCAACACTG	1560
Qy	1561	CAGTACCTGAACGGGGACTACGAAGTGGAGCGAGCGCGTGGTGGCAACGCGTAC	1620
Db	1561	CAGTACCTGAACGGGGACTACGAAGTGGAGCGAGCGCGTGGTGGCAACGCGTAC	1620
Qy	1621	CTCAAGGAGCAGCATTTGAGACTTTCTCATCTCTGGGGCCAGCAGCAACGGAAG	1680
Db	1621	CTCAAGGAGCAGCATTTGAGACTTTCTCATCTCTGGGGCCAGCAGCAACGGAAG	1680
Qy	1681	GAGAAAGCATGCTGGCCAAAGCTGCGGAGCTCGGGCAACTCCATGGAAGGGCTGATG	1740
Db	1681	GAGAAAGCATGCTGGCCAAAGCTGCGGAGCTCGGGCAACTCCATGGAAGGGCTGATG	1740
Qy	1741	CGCGATGGTTCCTGATGCTGCTCTCCGAGCAACAGGACTCCAAGGCTTCCGCCAG	1800
Db	1741	CGCGATGGTTCCTGATGCTGCTCTCCGAGCAACAGGACTCCAAGGCTTCCGCCAG	1800
Qy	1801	ATGGCATTGATGATTCAGCAAAAGAACACCGGGGCAACCAAGATGCCCTGAACCTGAG	1860
Db	1801	ATGGCATTGATGATTCAGCAAAAGAACACCGGGGCAACCAAGATGCCCTGAACCTGAG	1860
Qy	1861	GATGAGTGGATGAGTCTCTGAGCGCTGCATGATGCCGAGCATTTGATCAGCTGCGG	1920
Db	1861	GATGAGTGGATGAGTCTCTGAGCGCTGCATGATGCCGAGCATTTGATCAGCTGCGG	1920
Qy	1921	AAGGACCATGTGCGCGGTTTTTGTCTCACTTCCAGAGAGAGATTTTGAAGAAGTAC	1980
Db	1921	AAGGACCATGTGCGCGGTTTTTGTCTCACTTCCAGAGAGAGATTTTGAAGAAGTAC	1980
Qy	1981	TCCCGGAGGTGGATCCCGCTTCCGAGCCTACGTTGCTGCTGCTGCTGCTGCTGCTG	2040
Db	1981	TCCCGGAGGTGGATCCCGCTTCCGAGCCTACGTTGCTGCTGCTGCTGCTGCTGCTG	2040
Qy	2041	TTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCTGATGCTGGGATTTAT	2100
Db	2041	TTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCTGATGCTGGGATTTAT	2100

Db	3181	TACGCCATGCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCCTTCAACAATTC	32400
Qy	3241	CAGATGAAGATTGGCTGAAATATGGCCAGATCGTGGCAGGTGTCTATCGGGCTCGGAAG	33000
Db	3241	CAGATGAAGATTGGCTGAAATATGGCCAGATCGTGGCAGGTGTCTATCGGGCTCGGAAG	33000
Qy	3301	CCACAGTATGACATCTGCGGGGAACACAGATGAATGTCTTAGTCTGATGACAGCACGGGG	33600
Db	3301	CCACAGTATGACATCTGCGGGGAACACAGATGAATGTCTTAGTCTGATGACAGCACGGGG	33600
Qy	3361	GTCCCCGACCAATCCAGGTGACCCAGGACCTGTACCAAGGTTCTAGCTGCCAAGGGCTAC	34200
Db	3361	GTCCCCGACCAATCCAGGTGACCCAGGACCTGTACCAAGGTTCTAGCTGCCAAGGGCTAC	34200
Qy	3421	CAGTGGAGTGTCCAGGGGTGGTCAAGGTGAAGGCGAAGGGGAGATGACCACTACTTC	34800
Db	3421	CAGTGGAGTGTCCAGGGGTGGTCAAGGTGAAGGCGAAGGGGAGATGACCACTACTTC	34800
Qy	3481	CTCAATGGGGCCCCAGCAGTTAAACAGSGCCCGACCCACAATACTAGCTGAAGGGACCAAG	35400
Db	3481	CTCAATGGGGCCCCAGCAGTTAAACAGSGCCCGACCCACAATACTAGCTGAAGGGACCAAG	35400
Qy	3541	GTGGGCACCT 3549	
Db	3541	GTGGGCACCT 3549	

RESULT 2

US-09-474-076-1

; Sequence 1, Application US/09474076

; Patent No. 6465237

; GENERAL INFORMATION:

; APPLICANT: Tomlinson, James E.

; APPLICANT: COR Therapeutics, Inc.

; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL

; TITLE OF INVENTION: CYCLASE

; FILE REFERENCE: 44481-5028-01-US

; CURRENT APPLICATION NUMBER: US/09/474, 076

; CURRENT FILING DATE: 1999-12-12

; PRIOR APPLICATION NUMBER: PCT/US98/13694

; PRIOR FILING DATE: 1998-07-01

; PRIOR APPLICATION NUMBER: 60/070, 904

; PRIOR FILING DATE: 1997-07-01

; PRIOR APPLICATION NUMBER: 08/886, 550

; PRIOR FILING DATE: 1997-07-01

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 4942

; TYPE: DNA

; ORGANISM: human type VI adenylyl cyclase

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (145)..(3648)

US-09-474-076-1

Query Match 98.0%; Score 3478.4; DB 4; Length 4942;

Best Local Similarity 98.9%; Pred. No. 0;

Matches 3513; Conservative 0; Mismatches 36; Indels 3; Gaps

Qy	1	ATGTCATGGTTTATGTGGCTTCCTGGTCCCTAAAGTGGATGAACGGAACACAGCTGGGGT 60
Db	145	ATGTCATGGTTTATGTGGCTTCCTGGTCCCTAAAGTGGATGAACGGAACACAGCTGGGGT 204
Qy	61	GAACGCAATGGCAGAAGCGTTCCGCGGCCCGCTGGCACTCGGGCAGGTGGCTTCTGTCACG 120
Db	205	GAACGCAATGGCAGAAGCGTTCCGCGGCCCGCTGGCACTCGGGCAGGTGGCTTCTGTCACG 264
Qy	121	CCCGCTATATGAGTGCCTCCGGGATGAGAGCCACCAGCCGCCCTTCGCGGGCCCC 180
Db	265	CCCGCTATATGAGTGCCTTCGGGATGAGAGCCACCAGCCGCCCTTCGCGGGCCCC 324



Db 2485 CCTGCTGACATCACTGCTGCCACCTGCAGAGCTCAATTAATCTCTGGGCGCTGGATGCT 2544  
QY 2398 CCCCCTGTGTGAGGCGACCACTGCCACCTGCAGCTTTCTCTGAGGTGTCCATCGGGAACATG 2457  
Db 2545 CCCCCTGTGTGAGGCGACCACTGCCACCTGCAGCTTTCTCTGAGTACTTTCATCGGGAACATG 2604  
QY 2458 CTGCTGAGTCTCTTGGGCGACTCTGTCTTCTGACATCAGCAGCATCGGGAAGTTGGCC 2517  
Db 2605 CTGCTGAGTCTCTTGGGCGACTCTGTCTTCTGACATCAGCAGCATCGGGAAGTTGGCC 2664  
QY 2518 ATGATCTTTCTTGGGCGCTCACTATTGTTGCTGCTTCTGCTGGTCCGCCAGCCGCC 2577  
Db 2665 ATGATCTTTCTTGGGCGCTCACTATTGTTGCTGCTTCTGCTGGTCCGCCAGCCGCC 2724  
QY 2578 ATCTTTGACAACTATGACCTACTGCTTGGCGCTCATGGCTTGGCTTCTTCAATGAGACC 2637  
Db 2725 ATCTTTGACAACTATGACCTACTGCTTGGCGCTCATGGCTTGGCTTCTTCAATGAGACC 2784  
QY 2538 TTTGATGGGCTGAGCTTCCAGCTGCGAGGAGGTGGCCCTCAAAATATATGACCCCTGTG 2697  
Db 2785 TTTGATGGGCTGAGCTTCCAGCTGCGAGGAGGTGGCCCTCAAAATATATGACCCCTGTG 2844  
QY 2698 ATTCTGCTGCTGTTGGGCTGGCGCTGATCTGATGCTCAGCAGGTGGAATGACTGCC 2757  
Db 2845 ATTCTGCTGCTGTTGGGCTGGCGCTGATCTGATGCTCAGCAGGTGGAATGACTGCC 2804  
QY 2758 CGCTTAACTTCTCTGGAACCTACAGGCAACAGGGGAAAGAGGAGATGGAGGAGCTA 2817  
Db 2905 CGCTAGACTTCTCTGGAACCTACAGGCAACAGGGGAGGAGGAGATGGAGGAGCTA 2964  
QY 2818 CAGGATACAAACCGGAGGCTGCTGCATAAATTTGCCCCAAGGACGTTGGCGGCCCACTTC 2877  
Db 2965 CAGGATACAAACCGGAGGCTGCTGCATAAATTTGCCCCAAGGACGTTGGCGGCCCACTTC 3024  
QY 2878 CTGGCCCGGAGCGCCCAATGATGAACTCTACTATCAGTCGTTGAGTGTGGCTGTT 2937  
Db 3025 CTGGCCCGGAGCGCCCAATGATGAACTCTACTATCAGTCGTTGAGTGTGGCTGTT 3084  
QY 2938 ATGTTTGCCTCCATTGCAACTTCTCTGAGTCTCTATGAGCTGGAGGAGCAACAATGAG 2997  
Db 3085 ATGTTTGCCTCCATTGCAACTTCTCTGAGTCTCTATGAGCTGGAGGAGCAACAATGAG 3144  
QY 2998 GGTGCGGAGTGCCTGGGCTGCTCAAGGAGATCATGCTGACTTTGATGAGATTATCAGC 3057  
Db 3145 GGTGTCGAGTGCCTGGGCTGCTCAAGGAGATCATGCTGACTTTGATGAGATTATCAGC 3204  
QY 3058 GAGGAGGGTTCCGGCAGCTGGAAAGATCAAGACGATTGGTAGCACCCTACATGGCTGCC 3117  
Db 3205 GAGGAGGGTTCCGGCAGCTGGAAAGATCAAGACGATTGGTAGCACCCTACATGGCTGCC 3264  
QY 3118 TCAGGGCTGAACGCCAGCAGCTACGATCAGTGGCGGCTCCACATCACTGCGCTGGCT 3177  
Db 3265 TCAGGGCTGAACGCCAGCAGCTACGATCAGTGGCGGCTCCACATCACTGCGCTGGCT 3324  
QY 3178 GACTACGCCATGGGCTCATGAGCAGATGAAGCAGATCAATGAGCAGCTCTTCAACAAT 3237  
Db 3325 GACTACGCCATGGGCTCATGAGCAGATGAAGCAGATCAATGAGCAGCTCTTCAACAAT 3384  
QY 3238 TTCAGATGAAGATTGGGCTGAACATGAGGCGGCTCCACATCACTGCGGCTCGG 3297  
Db 3385 TTCAGATGAAGATTGGGCTGAACATGAGGCGGCTCCACATCACTGCGGCTCGG 3444  
QY 3298 AAGCCAGTATGACATCTCGGGGAACACAGTGAATCTCTAGTCTGATGATGAGCAGCAG 3357  
Db 3445 AAGCCAGTATGACATCTCGGGGAACACAGTGAATCTCTAGTCTGATGAGCAGCAG 3504  
QY 3358 GGGGTCCCGACCGAATCCAGGTGACCCAGGCTGTACAGGTTCTAGTGTCCCAAGGCG 3417  
Db 3505 GGGGTCCCGACCGAATCCAGGTGACCCAGGCTGTACAGGTTCTAGTGTCCCAAGGCG 3564  
QY 3418 TACCAGTGGAGTGTGAGGGGTGTTCAAGGTGAAGGGCAAGGGGAGATGACCACTAC 3477  
Db 3565 TACCAGTGGAGTGTGAGGGGTGTTCAAGGTGAAGGGCAAGGGGAGATGACCACTAC 3624

QY 3478 TTCTCTCAATGGGGCCCCAGCAGTTAAACAGGGCCCCAGCCCAAAATTCAGCTGAAGGACC 3537  
Db 3625 TTCTCTCAATGGGGCCCCAGCAGTTAAACAGGGCCCCAGCCCAAAATTCAGCTGAAGGACC 3684  
QY 3538 AAGTGGGCACT 3549  
Db 3685 AAGTGGGCACT 3696

RESULT 3  
US-07-793-961A-1  
; Sequence 1, Application US/07793961A  
; Patent No. 5334521  
; GENERAL INFORMATION:  
; APPLICANT: Yoshihiro Ishikawa  
; TITLE OF INVENTION: Cloning and Character-  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Alan M. Gordon  
; STREET: 1937 West Main Street,  
; STREET: P.O. Box 60  
; CITY: Stamford  
; STATE: Connecticut  
; COUNTRY: USA  
; ZIP: 06904  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC AT  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: ASCII from DM4  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07793,961A  
; FILING DATE: 19911118  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gordon, Alan M.  
; REGISTRATION NUMBER: 30,637  
; REFERENCE/DOCKET NUMBER: 31,705  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 203 321 2719  
; TELEFAX: 203 321 2971  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4046 base pairs listed  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-07-793-961A-1

Query Match 84.3%; Score 2990.4; DB 1; Length 4046;  
Best Local Similarity 90.9%; Pred. No. 0;  
Matches 3229; Conservative 0; Mismatches 311; Indels 12; Gaps 4;  
QY 1 ATGTCATGTTTGTAGTGGCTTCTGCTCCCTAAAGTGATGAACGGAACAGAGCTGGGT 60  
Db 131 ATGTCGTGTTTGTAGTGGCTTCTGCTCCCAAGAGTGATGAACGGAACAGAGCTGGGT 190  
QY 61 GAACGCAATGGCAGAGCGTTCCGCGCGCTGGGACTCGGGCAGGTGGCTTCTGCACG 120  
Db 191 GAACGCAATGGCAGAGCGT---CCACGCGCGGGGACTCGGACCACTGGCTTCTGCACG 247  
QY 121 CCCCCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCCCCTTGGGGGCCCC 180  
Db 248 CCCCCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGTCCACCCCTGGCGCTCC 307

QY 181 CTTGGTGGCCCTGGCAGGATGACGCTTTCATCCCGAGGGCGGCCAAGGCAAG 240  
Db CCTGGTGGCCCTGGCAGGATGAGGCTTTCATCCCGAGAGGGCGGCCAAGGCAAG 367  
QY 241 GAGCTGGGGCTGGGGCAGCTGGCCCTGGGCTTCGAGGATACCGAGGTGACACGACAGCG 300  
Db GAGCTGGGGCTGGGGCAGCTGGCCCTGGGCTTCGAGGATACCGAGGTGACAGG - --CCATGTCAGGG 424  
QY 301 GCGGGGAGGCTGAGGTGGCGGCGGACGCGGTGCCAGGAGTGGGCGATCCTGCTGGCGC 360  
Db GTTGGGAGCTGAGGTGGCGGCGGACGCGGTGCCAGGAGTGGGCGATCCTGCTGGCGC 484  
QY 361 CGTTTGGTCCAGGTGTTCCAGTGAAGCAGTTCGCTGGGCGGCGGAGGCGGCTGTAC 420  
Db CTTTGGGCGGAGGTGTTCCAGTGAAGCAGTTCGCTGGGCGGCGGAGGCGGCTGTAC 544  
QY 421 CAGCGGTACTTTTCCAGATGAACAGAGCAGCCTGACGCTGCTGGTGGCGGTGCTGGTG 480  
Db CAGCGGTACTTTTCCAGATGAACAGAGCAGCCTGACGCTGCTGGTGGCGGTGCTGGTG 604  
QY 481 CTGCTCACAGCGTGTGCTGGCTTTCCAGCGCGCACCGCGCCCTCAGCGCTGCTAT 540  
Db CTGCTCACAGCGTGTGCTGGCTTTCCAGCGCGCACCGCGCCCTCAGCGCTGCTAT 664  
QY 541 GTGGCACTGTGGCTGTGCGCGCGGCTGTGCTGGGGGCTCATGGTGTGTGAACCGG 600  
Db GTGGCGCTGTGGCTGTGCGCGCGGCTGTGCTGGGGGCTCATGGTGTGTGAACCGG 724  
QY 601 CATAGCTTCGGCAGGACATTCATGTGGTGGTGAAGTGGTGGCGATCCTGGCG 660  
Db CACAGCTTCGGCAGGACATTCATGTGGTGGTGAAGTGGTGGCGATCCTGGCG 784  
QY 661 GCAGTGCAGGTGCGGGGCGCTTCGCGAGCAGCCGCGAGCCCTCTCGCGGCGCTCGG 720  
Db GCGGTTGAGGTTGGGGTGGCGGCGGCGAGCAGCCGCGAGCCCTCTCGCGGCGCTCGG 844  
QY 721 TGGCTGTGCTTTTGTATACATCGATACAGCTGCTCCCTCCATCGCGATGGGGTGGC 780  
Db TGGCTGTGCTTTTGTATACATCGATACAGCTGCTCCCTCCATCGCGATGGGGTGGC 904  
QY 781 GTCTTCAGCGGCTGGGCGCTCCACCTTGCATTTGATCTGGCGTGGCAACTTAACCT 840  
Db GTCTTCAGTGGCGCTGGGCGCTCCACCTTGCATTTGATCTGGCGTGGCAACTTAACCG 964  
QY 841 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTGCTCTGCAACCAAC 900  
Db GGTGAGCGCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTGCTGCAACCAAC 1024  
QY 901 GTCATTTAGCATCTGCACACACTATCCAGCAGAGGTGCTCAGCGCGGCGGCTTCAGGAG 960  
Db GTCATTTAGCATCTGCACACACTATCCAGCAGAGGTGCTCAGCGCGGCGGCTTCAGGAG 1084  
QY 961 ACCCGAGTTATCATCCAGCGCGGCTCCACCTGACAGATGAGATCGGCGAGGAGCGG 1020  
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Db CTGCTGCTCGGATTTGCCCGCAGCAGTGGCATGGAGATGAAGAGATCAACACA 1204  
QY 1081 AAAAAGAAGAC - --ATGTTCCACAGATCTACATACAGAAGCATGACAAATGTACGATC 1137  
Db AAGAAGAAGACATGATGTTCCACAGATCTACATCCAGAAGCATGACAAATGTACGATC 1264  
QY 1138 CTGTTTGCAGACATGAGGCGTTACCGCTGGCATCCAGTGCAGTGCAGGAGCTG 1197  
Db CTGTTTGCAGACATGAGGCGTTACCGCTGGCATCCAGTGCAGTGCAGGAGCTG 1324  
QY 1198 GTCATGACCTGAATGAGCTCTTTGCCCGGTTGACAAGCTGGCTGCGGAGAACTCACTGC 1257  
Db GTCATGACCTGAACGAGCTCTTCGCCCGGTTGACAAGCTGGCTGCGGAGAACTCACTGC 1384  
QY 1258 CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGAGGCCGG 1317

Db 1385 CTGAGGATCAAGATCTTAGGGGACTTACTACTGTGTCGGGGTCCGAGGCGCCG 1444  
QY 1318 GCCGACCATGCCCACTGCTGTGTGGAGATGGGGTAGACATGATTGAGGCCATCTCGCTG 1377  
Db GCAGACCATGCCCACTGCTGTGTGGAGATGGGGTAGACATGATCGAGGCCATCTCGCTG 1504  
QY 1378 GTACGTGAGTGCACAGGTGTGAATGTGAATCGCGTGGGATCCACAGCGGCGCGTG 1437  
Db GTGCGTGAAGTGCACAGGTGTGAACGTGAACATCCCGTGGCATCCACAGCGGCGTG 1564  
QY 1438 CACTCGGCGCTCCTTGGCTTGGGAAATGGCAGTTTCGATGTGTGTGTCATGATGTGACC 1497  
Db CACTGTGTGTCTTGGCTTGGGAAATGGCAGTTTCGATGTGTGTGTCATGATGTGACC 1624  
QY 1498 CTGGCCAAACACATGGAAGCAGGAGCGGCTGGCGCATCCACATCACTCGGGCAACA 1557  
Db CTGGCCAAACATGATGAGCGG - --CCCGGGCGCGCGCATCCACATCACTCGGGCGCAG 1681  
QY 1558 CTGCACTACTGAAAGGGGACTACGAAGTGGAGCCAGCGCGTGGTGGCAAGCGCAACGCG 1617  
Db CTGCACTACTGAAAGGGGACTACGAAGTGGAGCGGCGCGTGGTGGCAAGCGCG 1741  
QY 1618 TACCTCAAGGAGCAGCAGATGAGACTTTCCTCATCTCTGGGCGCCAGCCAGAAACGGA 1677  
Db TACCTCAAGGAGCAGCAGATGAGACTTTCCTCATCTCTGGGAGCCAGCCAGAAACGGA 1801  
QY 1678 GAGGAGAAAGGATGCTGCGCAAGCTGACGCGACTCGGCGCAACTTCCATGGAAGGCGT 1737  
Db GAGGAGAAAGGATGCTGCGCAAGCTGACGCGACTCGGCGCAACTTCCATGGAAGGCGT 1861  
QY 1738 ATGCGCGCATGCGTCTGATCGTCTCTCCCGACCAAGGACTTCAAGGCTTCCG 1797  
Db ATGCGCGCATGCGTCTGATCGTCTCTCCCGACCAAGGACTTCAAGGCTTCCG 1921  
QY 1798 CAGATGGGATTTGATGATTCAGAGAAAGACAAACCGGGGCGCCAGATGCCCTGAACCT 1857  
Db CAGATGGGATTTGATGATTCAGAGAAAGACAAACCGGGGCGCCAGATGCCCTGAACCT 1981  
QY 1858 GAGGATGAGTGGATGAGTTCCTGAGCGCTGCATCGATCGCGCAGCATGATGATGAGCTG 1917  
Db GAGGATGAGTGGATGAGTTCCTGAGCGCTGCATCGATCGCGCAGCATGATGATGAGCTG 2041  
QY 1918 CGGAAGGACCATGTGCGCGGTTTGTCTACCTTCCAGAGAGAGATTTGAGAAAGAG 1977  
Db CGGAAGGACCATGTGCGCGGTTTGTCTACCTTCCAGAGAGAGATTTGAGAAAGAG 2101  
QY 1978 TACTCCGGAAGTGGATCCCGCTTCGAGCGCTAGTTGCGCTGTCCTGTGGTCTTC 2037  
Db TACTCCGGAAGTGGATCCCGCTTCGAGCGCTAGTTGCGCTGTCCTGTGGTCTTC 2161  
QY 2038 TGTCTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCTGATGCTTGGGAT 2097  
Db TGTCTCATCTGCTTCATCCAGCTTCTAATTTTCCACACTCCACCTGATGCTTGGGAT 2221  
QY 2098 TATGCGAGCATCTTCTGCTGTCTTAATCACCCTGCTGATCTGTGCTGTGTACTCTGT 2157  
Db TATGCGAGTATCTTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2281  
QY 2158 GGTCTCTGTTCCCTAAGGCGCTTGAACGTCTGTCCCGCAGCATGCTCGCTCAGCGGCA 2217  
Db GGTCTCTGTTCCCTAAGGCGCTTGAACGTCTGTCCCGCAGCATGCTCGCTCAGCGGCA 2341  
QY 2218 CATAGCAGCGAGTGGGATCTTTTCCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2277  
Db CATAGCAGCGAGTGGGATCTTTTCCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2401  
QY 2278 ATGTTTCACTGTAACACACACCCCATACGAGCTGTGACGCGGATGCTGAATTTAACA 2337  
Db ATGTTTCACTGTAACACACACCCCATACGAGCTGTGACGCGGATGCTGAATTTAACA 2461  
QY 2338 CTTGTGTACATCACTGCTGCGCATCTGACAGCTCAATTTACTCTCTGGGCTGGATGCT 2397  
Db CTTGTGTACATCACTGCTGCGCATCTGACAGCTCAATTTACTCTCTGGGCTGGATGCT



Db	2462	CCGCCTGACATCACTCGCTGGCCACCTGCGACGAGCTCAATTA	CTCTCTGGGCGCTGGAGTGC	2529
Qy	2398	CCCTGTGTGAGGGCCACCATTGCCACCTGCAGCTTTCCTGAGGTG	TCCATCGGGAACATG	2457
Db	2522	CCGCTGTGTGAGGGCACCGCACCTTGCAGCTTCCCTGAGTACT	TCGTTGGGAAACATG	2581
Qy	2458	CTGCTGAGTCTCTTTGGCCAGCTCTGTCTTCCTGACATCAGCAG	AGCATCGGGAAGTTGGCC	2517
Db	2582	CTGCTGAGTCTCTTTGGCCAGCTCTGTTTTCCTGACATCAGT	TAGCATCGGGAAGTTGGCC	2641
Qy	2518	ATGATCTTTTCTCTTGGGCGTCATCTATTTTGGTGCTCTCTCT	GTGGGTGCCCGACCGCC	2577
Db	2642	ATGATCTTTTCTCTTGGGCGTCATTTATTTTGGTGCTCTCTCT	GTGGCGCCCGCCAGCACC	2701
Qy	2578	ATCTTTGACAACTATGACCTACTGCTTGGCTGCCATGCTTGG	CTTGTCCCAATGAGACC	2637
Db	2702	ATCTTTGACAACTATGACCTGCTGTTGGTGTCATGAGCTTGG	CTTCTCCCAATGACACC	2761
Qy	2638	TTTGATGGGTGGACTGTCCAGCTCGAGGGAGGGTGGCCCTCA	ATAATATGACCCTGTG	2697
Db	2762	TTTGATGGGTGGACTGCCAGCTGGGGAGGGTGGCAC	TGAATACATGACCCCTGTG	2821
Qy	2698	ATTCTGCTGTGTGTTTGGCTGGCGGTGTATCTGCA	TGCTCAGCAGGTGGAATCAGACTGCC	2757
Db	2822	ATTCTGCTGTGTGTTTGGCTGGCGGTGTATCTGCA	CGCCAGCAGGTGGAATCAACATGCA	2881
Qy	2758	CGCTAAACTTCTCTGTGAAACTACAGGCCAACAGGGGAAAG	AGGAGATGSGAGAGCTA	2817
Db	2882	CGTCTGGACTTCTCTGTGAAACTGCAAGGCACGGGGAGA	AGGAGAGATGGAGGAGCTC	2941
Qy	2818	CAGGCATACAAACCGGAGGCTGCTGCATAACATTC	TGCCCAAGGACGTGGCGCCCACTTC	2877
Db	2942	CAGSCCTACAAACGAAGGCTGCTGCATAACATTC	TGCTGCCTAAGGACGTGCGCTGCCACTTC	3001
Qy	2878	CTGGCCCGGAGGCGCGCAATGATGACTCTACTATCAGT	CGTGTGAGTGTGTGGCTGTT	2937
Db	3002	CTGGCCCGGAGGCGCGCAACATGAGCTCTACTAC	CAGTCTGTGAGTGTGTGGCGGCTC	3061
Qy	2938	ATGTTTGGCTTCCATTCGCCAACCTTCTCTGAGTTCTAT	TGTGGAGCTGGAGGCAACAATGAG	2997
Db	3062	ATGTTTGGCTTCCATTCGCCAACCTTCTCTGAGTTCT	ATGTGTGGAGCTGGAGGCAACAATGAG	3121
Qy	2998	GGTGCCGAGTGCTGCGGCTGCTCAACGAGATCATCG	TGACTTGTGATGAGATTAATCAGC	3057
Db	3122	GGTGCGAGTGCTGCGGCTGCTCAACGAAATCATCG	CCGACTTTGATGAGATCATCAGC	3181
Qy	3058	GAGGAGGGTTTCGGCAGCTGGAAGAAGATCAAGAC	GATTTGTTAGCAGCTACATGGCTGCC	3117
Db	3182	GAGGAGGGTTTCGGCAGCTGGAGAAAATCAAGAC	GATTCGGTAGCAGTACATGGCTGCG	3241
Qy	3118	TCAGGGCTGAAGCCAGCACCTACGATCAGGTGGCGCG	CTCCACATCAGTCCCTGGCT	3177
Db	3242	TCGGGGCTGNAAGCCAGCACCTACGATCAGGCCG	CGCGCTCCACATCAGTGGCCCTGGCC	3301
Qy	3178	GACTACGCCATCGCGCTCATGAGCAGAGATGAAG	CACATCAATGAGCACTCCCTTCAACAAT	3237
Db	3302	GACTATGCCATCGCGCTCATGAGCAGATGAAG	CACATCAAGCAGCACTCCCTTCAACAAC	3361
Qy	3238	TTCCAGATGAAGATTGGGCTGAACATGGGCCCG	AGTCTGGCAGGTGTATCGGGGCTCGG	3297
Db	3362	TTCCAGATGAAGATTGGGCTGAACATGGGCCCG	AGTCTGGCAGGCGTCA	3421
Qy	3298	AAGCCACAGTATGACATCTGGGGGAACACAGTGA	ATGTCTAGTCTGATGAGCAGCAGC	3357
Db	3422	AAGCCACAGTATGACATCTGGGGGAACACAGTGA	ATGTCTAGTCTGATGAGCAGCAGC	3481
Qy	3358	GGGGTCCCGACCGAATCCAGGTGACCAAGGAC	CTGTACCAGGTTCTAGCTGCCAAGGGC	3417
Db	3482	GGGGTCCCTGACCGGAATCCAGGTGACCAAGG	ACTTGTACCAGGTTCTAGCTGCCAAGGGC	3541
Qy	3418	TACACGTGGAGTGTGAGGGTGGTCAAGTGAAG	GCGCAAGGGGAGATGACCACTTAC	3477
Db	3542	TACACGTGGAGTGTGAGGGTGGTCAAGTGAAG	GCGCAAGGGGAGATGACCACTTAC	3601

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QY 3478 TTCTCTCAATGGGGCCCCCAGCAGTTCACAGGGGCCCCAGCAGCACAATTCAGCTGAAGGGACC 3537
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Db 3602 TTCTCTCAATGGGGCCCCCCCCCAGTTCAGCAGAGCCAGCTACAAGTTTCAGCTGTCAGGACC 3661
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QY 3538 AAGTGGGCACCT 3549
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Db 3662 AAGTGGGCATT 3673
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RESULT 4
US-08-240-357-1
; Sequence 1, Application US/08240357
; Patent No. 5578481
; GENERAL INFORMATION:
; APPLICANT: Ishikawa, Yoshihiro
; TITLE OF INVENTION: Cloning and Characterization of a
; TITLE OF INVENTION: Cardiac Adenylyl Cyclase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Americap Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,357
; FILING DATE: 10-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,705-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4046 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 131..3625
; US-08-240-357-1

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	Query Match	84.3%	Score 2990.4	DB 1	Length 4046
	Best Local Similarity	90.9%	Pred. No. 0		
	Matches 3229	Conservative 0	Mismatches 311	Indels 12	Gaps
Qy	1	ATGTCATGGTTT	TAGTGGCTCTCCTGGTCCCTAACTGATGAACGAAACAGCCTGGGT	60	
Db	131	ATGTCGTGGTTT	TAGTGGCTCTCTGTCCTCCCAAAATGATGAACGAGACACAGCCTGGGT	190	
Qy	61	GAACGCAATGGC	AGAGCGTTTCGGCGGCGCGTGGCACTCGGGCAGGTGGCTTCTGCACG	120	
Db	191	GAACGCAATGGC	AGAGCGT---CCACGCGCGGGGACTCGGACAGTGGCTTCTGCACG	240	
Qy	121	CCCGCTATATAG	CTGCTCTCCGGGATGTCAGAGCCACCCAGCCCCACCTCGCGGGCCCC	180	
Db	248	CCCGCTATATAG	CTGCTCTCGGGATGCGCAGCCCCCCAGTCCACCCCTCGCGGCTCCC	300	
Qy	181	CCTCGGTGCCCT	TGGCAGGATGACGCCCTTCATCCGAGGGCGGCCCGCAGGGCAAG	240	
Db	308	CCTCGTCCCTCT	TGGCAGGATGAGCCCTTCATCCGAGAGGCGGCCCGCGCAGGGCAGC	360	

[illegible]

Qy	1318	CCCAGCACCATGCCACACTGCTGTGTGGAGATGTGGGGGTAGACATGATGATTGAGGCCATCTCGCTG	1317
Db	1445	GCAGACCATGCCACACTGGTGTGTGGAGATGTGGGGGTGGACATGATGCAGAGGCCATCTCGCTG	1504
Qy	1378	GTACGTGAGGTGACAGGTTGGAATGTGAACATGCGCGTGGGGCATCCACAGCGGGCGGCTG	1437
Db	1505	GTGCGTGAAGTGAACAGGTTGAACGTGAACATCCGGGTGGGCATCCACAGCGGGGTGTG	1564
Qy	1438	CACCTGCGCGCTTCCTTTGGCTTTGCCGAATGGCAGTTTCGATGTGTGTGTCCAAATGATGTGACC	1497
Db	1565	CACGTGTGTCTTGCCCTGCGGAAATGGCAGTTTCGAGCTGTGTGTTCCAATGACGTGACT	1624
Qy	1498	CTGGCCCAACACATGGAAGACAGAACGCCGGGCTGGCGGATCCACATCACTCTGGGCAACA	1557
Db	1625	CTGGCCCAACCATATTTGAGGCGG---CCCGGGCGCGGCATCCATCACCCTGGGGCCACG	1681
Qy	1558	CTGCAGTACCTGAAGCGGGACTACGAAGTGGAGCGACAGGCGCGTGTGTGGCAAGCGAAGCGG	1617
Db	1692	CTGCAGTACCTGAACCGGGGACTACGAAGTGGAGCGCGGGCGCGGTGTGGCGAGCAACGCG	1741
Qy	1618	TACCTCAAGGAGCAGCACATTGAGACTTTTCCTCATCTTGGGCGCCAGCGCAGAAACGGAAA	1677
Db	1742	TACCTCAAGGAGCAGCACATCGAGACCTTCTCCTCATCTTGGGAGCCAGCAGAAACGGAAA	1801
Qy	1678	GAGGAGAAAGCATGTGTGGCCAAAGCTGCAGCGGACTCTGGGCGCACTCCATGGAAGGGCTG	1737
Db	1802	GAGGAGAAAGCCATGCTGGCCAAAGCTGCAGCGGAGCGCGGGCCCACTCCATGGAAGGGCTG	1861
Qy	1738	ATGCCGCGATGGGTTCTTGATCGTGCCTTCTCCCGGACCAAGGACTCCAAAGGCTTCGCG	1797
Db	1862	ATGCCAGCGTGGGTGGCGGACGCGGCTTCTTCCGGACCAAGGACTCCAAAGGCTTCGCG	1921
Qy	1798	CAGATGGGCATTGATGATCCAGCAAGACAAACCGGGGCAACCAAGATGCCCTGAACCCCT	1857
Db	1922	CAGATGGGCATTGATGATCCAGCAAGACAAACCGGGGTGCCAAGATGCCCTGAACCCCT	1981
Qy	1858	GAGGATGAGTGGATGAGTTCTTGAGCCGTGCCATCGATGCCCGCAGCATTTGATCAGGTG	1917
Db	1982	GAGGATGAGTTCGATGATGTTCTTGGCCGTGGCATCGATGCCCGCAGCATCGATCAGTA	2041
Qy	1918	CGGAAGACCATGTGCGCCGGTTTTTGCTACCTTCCAGAGAGAGGATTTTGAAGAAG	1977
Db	2042	CGGAAGACCATGTGCGCCGCTTCTTGCCTCACCTTCCAGAGAGAGGATTTTGAAGAAG	2101
Qy	1978	TACTTCCGGAAGTGGATCCCGCTTCGGAGCTACGTTTGCCTGTGCCCTGTGGCTTTC	2037
Db	2102	TACTCAAGGAAGTGGACCCCGCTTCGGAGCCTACGTTGGCCTGTGGCTGTGGCTTTC	2161
Qy	2038	TGCTTACTCTGCTTCATCCAGCTTCTAATTTTCCCACTCCACCTCATGCTTGGGAT	2097
Db	2162	TGCTTACTCTGCTTTATCCAGCTCTCTGCTTCCCACTCAACCGTCTGCTTGGGATC	2221
Qy	2098	TATGCCAGCATCTTCTGCTGCTGCTTAATCAGCTGTGATCTGTGCTGTGCTACTCTGT	2157
Db	2222	TACGCCAGTATCTTTGTGTGTGTGCTGATCACCGTCTGACCTGTGCGCTGTACTCTGT	2281
Qy	2158	GGTTCCTGTTCCTTAAGGCCCTGCAACGCTGTCCCGCAGCATTCGCTCAGCGGCA	2217
Db	2282	GGCTCTCTTCTTCCCAAGGCCCTGCGACGCTTCTCCCGCAGCATCGTCCGCTCTCGGGCA	2341
Qy	2218	CATAGCACCCAGTTGGCATCTTTTCCGCTCCTGTGTGTGTACTTCTGCCATTTGCCAAC	2277
Db	2342	CACAGCACTGTGGTTGGCATTTTTTTCAGTCTTGTAGTGTTCACCTCTGCCATCGCCAAC	2401
Qy	2278	ATGTTTACCTGTGAACACACCCCCCATPACGGAGCTGTGCAGCCCGGATGCTGAATTTAACA	2337
Db	2402	ATGTTTACCTGTGAACACACCCCCCATCCCGGAGCTGTGCAGCCCGGATGCTGAATTTAACA	2461
Qy	2338	CCTGCTCACATCACTGCCTGCCACCTGCAGAGCTCAATTACTCTCTGSGGCTCGATGCT	2397
Db	2462	CCGCTGACATCACTGCCTGCCACCTGCAGAGCTCAATTACTCTCTGSGGCTCGATGCT	2521
Qy	2398	CCCTGTGTGAGGGGCACCATGCGCCACCTTCGAGGCTTCTCTGAGGTGTCCATCGGGAACATG	2457

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Db 3602 TTCTCTCAATGGGGGCCCCCCCCAGTTTAGCAGAGCCCGAGCTACAAGTTTCAGCTGTGTCAGGACC 3661
Qy 3538 AAGTGGGCAC 3549
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Db 3662 AAGTGGGCATT 3673

RESULT 5
US-08-726-214-11
: Sequence 11, Application US/08726214
: Patent No. 610706
: GENERAL INFORMATION:
: APPLICANT: Tang, Wei-Jen
: APPLICANT: Gilman, Alfred G.
: TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
: TITLE OF INVENTION: AND USES THEREOF
: NUMBER OF SEQUENCES: 31
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: Texas
: COUNTRY: United States of America
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/726,214
: FILING DATE: Concurrently Herewith
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/005,498
: FILING DATE: 04-OCT-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Highlander, Steven L.
: REGISTRATION NUMBER: 37,642
: REFERENCE/DOCKET NUMBER: UTSD:450
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (512) 418-3000
: TELEFAX: (512) 474-7577
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4131 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
us-08-726-214-11

Query Match 77.5%; Score 2751.2; DB 3; Length 4131;
Best Local Similarity 86.7%; Pred. No. 0;
Matches 3080; Conservative 0; Mismatches 463; Indels 11; Gaps

Qy 1 ATGTCATGGTTTAGTGGCCCTCTCGTCCCTAAAGTGGATGAACGGAAACACGCTGGGGT 60
Db 56 ATGTCATGGTTTAGCGCCCTCTCGTTCCAAAGTGGATGAACGGAAACACGCTGGGGC 115
Qy 61 GAACGCAATGGGCAGAACGGTTCCGGCCCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACG 120
Db 116 GAACGCAATGGACAGAAGCG--CCACGCGCAGGGGACCCGAGCCCGTGGCTTCTGCAGC 172
Qy 121 CCGCGCTATATGAGTCGCTCCGGGATGCAGAGCCACACAGCCACCCCTGCGGGCCCC 180
Db 173 CCGCGCTACATGAGTCGCTTCAAGAATGTGGAGCACCCAGCCCCCTTCTGCACTGCG 232
Qy 181 CCTCGGTGCCCTTGGCAGGATGACGCTTCATCCGAGGGGGCGCCCGCAAGGCGCAAG 240
Db 233 ACTCGGTGCCCTTGGCAGGATGAGGCTTCATCAGGAGGGCTGGCCCGGGAAGGGGTGTG 292
Qy 241 GAGCTGGGGCTGCGGGCAGTGGCCCTTGGCTTCGAGGATACCGAGGTGACCAACGACGC 300
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Db 293 GAGCTGGGCTCGGCTGAGTGGCTTTGGTTTGAATGACACTGAGGTG---ACCACCG 349  
QY 301 GCGGAGCGCTGAGGTGGCGCCGACGCGGTGCCAGGAGTGGCGATCCTGCTGGCG 360  
Db 350 ATGGGACAGCTGAAGTGGCACCCACACATCGCTCGAAGCGTCCGCTGCTGGCAC 409  
QY 361 CTTTTGGTGAAGTGTTCAGTGAAGCAGTTCCTTGGGCCAAGCTGAGCGCTGTAC 420  
Db 410 CGGCTAGCGAGCTGTTCAGTCTAAGCAGTTCCTCGTCCGCAAGCTGAGCGTCTGTAC 469  
QY 421 CAGCGGTACTTTTCCAGATGAACAGAGCAGCCTGACGCTGCTGGTGGCGTGTGGTG 480  
Db 470 CAGCGGTACTTCTCCAGATGAACAGAGCAGCCTGACGCTGCTATGCGGTGCTGTG 529  
QY 481 CTGCTCACAGCGGTGCTGCTGGCTTTCCAAGCGCACCGCGCCCTCAGCGCTGCCAT 540  
Db 530 CTCCTCATGGCTGTACTGTGTACCTTCCAGCGCGCTGCGCTGCCCTGAGCCTGCTAT 589  
QY 541 GTGGCACTGTTGGCTGTGCCCGCCCTGTTTCGTGGGCTCATGGTGTGTAAACGG 600  
Db 590 GTGGCCCTGCTGACCTGTGCTCCGCTCTTTTGTGGTACTCATGTGTGTAAACGA 649  
QY 601 CATAGCTTCGCCAGGACTCCATGTGGGTGTGAGTAAAGTGTGCTGGCATCTGGG 660  
Db 650 CATAGCTTCGCCAGGACTCCATGTGGGTGTGAGTATGTGTTCTGGGCATCTAGCA 709  
QY 661 GCAGTGAAGTGGGGGCTTTTCGACGACAGCCGCGAGCCCTCTCGGGGCTCTGG 720  
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QY 841 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCCATGTGCTGCTCTCTGTCACCAAC 900  
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QY 1081 AAAAAAAGAC---ATGTTCCAAAGATCTATACATACAGCATGACAATGTACGATC 1137  
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QY 1198 GTCATGACCTGAATGAGCTTTTCCCGGTTTGACAAGCTGGCTGGGAGAAATCACTGC 1257  
Db 1250 GTCATGACCTGAATGAGCTTTTCCCGGTTTCGACAAAGCTGGCTGGCAGAACTCATGT 1309  
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QY 1378 GTACGTGAGTGCACAGGTGTAATGTGAACATGCGCTGGGCATCCACAGCGGGCGCTG 1437  
Db 1430 GTGCGTGAAGTAAACGGGTGTAATGTGAACATGCGCTGGGCATCCACAGCGGGCTGTA 1489  
QY 1438 CACTCGGCGTCTTGGCTTGGGAAATGGCAGTTTCGATGTGTGTGTCCTCAATGATGTACC 1497  
Db 1490 CACTCGGCTGCTTGGTCTGGGAAATGGCAGTTTGTGTGTGTCCTCAACATGTGACC 1549  
QY 1498 CTGGCCAAACCATGAAGCAGGAGCGGCTGCGCCATCCACATCACTCTCGGCCACA 1557  
Db 1550 CTGGCCAAACCATGAAGCGGGGGCGGGCCGCGCATCCACATCACTCTCGGCCACA 1609  
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Db 1670 TACCTCAAGGAGCAGCTTGGTCAAGCTGAGAGCTTCTCTATAGGAGCCAGCGAAGCGAAA 1729  
QY 1678 GAGGAGAAAGCATGCTGGCCAAAGCTGAGCGGACTCGGGCCAACTCCATGCGAAGGGCTG 1737  
Db 1730 GAGGAGAAAGCATGCTGGTCAAGCTGAGCGGAGCGCGGCCAACTCCATGCGAAGGGACTG 1789  
QY 1738 ATGCCCGCATGCTGCTGCTTCTCCCGGACCAAGGACTTCCAAAGCGCTTCCGC 1797  
Db 1790 ATGCCCGCTGGTCTGAGCGCTCTCTCCCGGACCAAGGACTTCCAAAGCGCTTCCGC 1849  
QY 1798 CAGATGGGCTATGATTTCCAGAAAGCAACCGGGGACCCAAAGATGCCCTGAACCGT 1857  
Db 1850 CAGATGGGCTATGATTTCCAGAAAGCAACCGGGGTCGCCAAGATGCTCTGAACCGT 1909  
QY 1858 GAGGATGAGTGGATGCTGAGCGCTGCGATGCGCCGAGCATCGATGCGCGAAGCATCAGAGCTG 1917  
Db 1910 GAGGATGAGTGGAGAGTTCCTGGCGGAGCATCGATGCGCGAAGCATCAGAGCTG 1969  
QY 1918 CGGAAGGACCATGTGCGCGGTTTGTCTCACTTCCAGAGAGAGGATTTTTCAGAGAGAG 1977  
Db 1970 CGTAAGGACCATGTGCGCGGTTTGTCTCACTTCCAGAGAGAGGATCTCAGAGAGAG 2029  
QY 1978 TACTCCGGAAGTGGATCCCGCTTCGAGAGCTACGTTGCTGTGCGCTGTGTCCTTC 2037  
Db 2030 TATTACGAGAAATAGACCTGTTTCGAGAGCTACGTCGCTGTGCGCTTCTGTTTC 2089  
QY 2038 TGCTTCATCTGCTTATCCAGCTTCTAATTTCCACACTCCACCTGATGCTTGGGAT 2097  
Db 2090 TGCTTCATCTGTTTATCCAGTTCCTGATTTCCACACTCCCGCTGATCTCGGAT 2149  
QY 2098 TATGCCAGCATCTTCTGCTGCTAATCACTGCTGATCTGCTGTGTGCTGCTGCT 2157  
Db 2150 TATGCCGGAATCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2209  
QY 2158 GGTTCCTGTTCCCTAAGCCCTGCAAGCTGTGTCGCGAGCATTTGCTGCTCAGGGCA 2217  
Db 2210 GGGTCTTTTCCCAACGCGCTGCGAGCGCTGTGCGCGAGTATGCTGCTGCTGCTGCT 2269  
QY 2218 CATAGCAGCGAGTGGCATCTTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2277  
Db 2270 CACACAGCGCTGTTGGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2329  
QY 2278 ATGTTTCACTGTAACACACACCCCATACGAGCTGTGCGAGCCGATGCTGAATTAACA 2337  
Db 2330 ATGTTTCACTGTAACACACACCCCATGAGGACTGTGCGCGCGGATGCTGAATTAACA 2389  
QY 2338 CCGTGTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2397  
Db 2390 CCGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2449  
QY 2398 CCGCTGTGTGAGGCGACCATGCGCCACTGCGAGCTTTCTGAGGTGTCCATCGGGAACATG 2457  
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QY 2458 CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCTGCACATCAGCAGCATCGGGAAGTTGGCC 2517  
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; Sequence 3, Application US/09008097  
; Patent No. 6306830  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, H. Kirk  
; APPLICANT: Insel, Paul A.  
; APPLICANT: Ping, Peipei  
; APPLICANT: Post, Steven R.  
; APPLICANT: Gao, Meihua  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE  
; TITLE OF INVENTION: HEART FAILURE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/008,097  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dylan, Tyler M  
; REGISTRATION NUMBER: 37,612  
; REFERENCE/DOCKET NUMBER: 22000-20567.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1812 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 1...1812  
; OTHER INFORMATION:  
; US-09-008-097-3

Query Match 51.0%; Score 1808.4; DB 4; Length 1812;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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QY 696 GCACAGCCCTCTCTCGGGGCTCTGGTCCCTGTGTCTTTGTATACATCGCATACAGCT 755  
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Db 123 CCTCCCATCCGATCGGGGCTGCCGTCTCAGGGGCTGGGCTCTCCACCTTGCATTT 182  
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QY 3373 ATCTGGGGAACACAGTGAATCTCTATGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 3432  
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QY 3433 CGAGGGGTGCTCAAGGTGAAGGGAAGGGGAGATGAGACACCTACTTCTCAATGGGGC 3492  
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QY 3493 CCC 3495  
Db 3910 CCC 3912  
RESULT 8  
US-08-726-214-9  
; Sequence 9, Application US/08726214  
; Patent No. 6107076  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Wei-Jen  
; APPLICANT: Gilman, Alfred G.  
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE  
; TITLE OF INVENTION: AND USES THEREFOR  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/726,214  
; FILING DATE: Concurrently herewith  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/005,498  
; FILING DATE: 04-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L.  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: UTSD:450  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3924 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-726-214-9

Query Match 46.4%; Score 1648.2; DB 3; Length 3924;  
Best Local Similarity 71.4%; Pred. No. 0;  
Matches 2365; Conservative 0; Mismatches 873; Indels 33; Gaps 6;

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QY 405 GCTGGAGCGCTGTACACGCGTACTTTTCCAGATGAACACAGCAGCAGCTGCTGCT 464  
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QY 465 GGTGGCGGTGCTGGTGTCTCAGCAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 524  
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US-08-726-214-1
; Sequence 1, Application US/08726214
; Patent No. 6107076
; GENERAL INFORMATION:
; APPLICANT: Tang, Wei-Jen
; APPLICANT: Gilman, Alfred G.
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,214
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435

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QY 916 ACACATATCCAGCAGAGGTGCTCTCAGCGCCAGGCTTTTCAGGAGACCCGAGTTACATC 975  
Db 799 GTGAGGATCTGGCTGAGCGCCGACGAGGAGGCCCTTCCTGCGAGCCCGGAACTGATTT 858  
QY 976 CAGCGCCGGCTCCACCTGACGATGAGAATCGGAGGAGCGGCTGCTGCTCGGTA 1035  
Db 859 GAGCACCCTGAGGCTGGAGGATGAGAAATGAGAAGCAGGAGCGGCTGCTCATGAGCTC 918  
QY 1036 TTGCCCCAGCAGCTTGCCATGAGAGATGAAGAAGACACATCAACAAAAAAGAAGACATG 1095  
Db 919 CTGCTCCGGAATGTTGCCATGAGATGAAGGAGACTTCCTGAAGCCGCCCTGAGAGGAT 978  
QY 1096 TTCCACAAGATCTACATACAGAAGCATGACAATGTCAGCATCCCTGTTGACAGACATTGAG 1155  
Db 979 TTCCACAAGATTTACATCCAGCGCATGACAACTGAGCATCTCTTTGACAGACATGCTG 1038  
QY 1156 GGCTTCCACCGCTGGCATCCCACTGCACTGCGCAGGAGCTGGTTCATGACCCCTGAATGAG 1215  
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QY 1216 CTCTTTGCCGGTTTGACAAGCTGGCTGGGAGAAATCACTGCCCTGAGGATCAAGATCTTG 1275  
Db 1099 CTCTTTGGGAAGTTTGACGAGCTGGCCACAGAGAACCACTGCCCGCCGATCAAGATCCTG 1158  
QY 1276 GGGGACTGTTACTACTGTGTGTCAGGGCTGCCGAGGCGCGGCGGACCATGCCCCTGTC 1335  
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QY 1396 GTGAATGTGAACATGCGGTGGGCATCCACAGCGGCGCGTGCACTGCGGCGTCTTGGC 1455  
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QY 1516 GCAGAAAGCGGGCTGCGCGCATCCACATCTCGGGCAACACTGCACTGAAAGCGG 1575  
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QY 1816 TCCAGCAAGAACACCGGGGACCCAAAGATGCCCTGAACCCCTGAGGATGAGGTGGATGAG 1875  
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QY 1876 TTCCTGAGCGCTGCCATCGATGCGCGCAGCATTTGATCAGGTGCGGAAGGACCATGTGCGC 1935  
Db 1743 ACTCAGAAACCGCTCGCTTCTCTACA----- 1770  
QY 1936 CGGTTTTTGTCTACCTTCCAGAGAGAGGATTTTTCAGAAAGTACTCCCGGAGGCTGGAT 1995  
Db 1771 AACGTTGTCCAAACCCCGGCACACAGTGTCAACAGGTACATCGCGCCGCTCCTCGAA 1830

QY 1996 CCCGCTTCGGAGCCTAGCTTGCCTGTGSCCCTGTGTGGTCTTCTGCTTCATCTGCTTATC 2055  
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QY 2056 CAGCTTCTTAATTTTCCACACTCCACCCCTGATGCTTGGGATTTATGCGCAGCATCTTCTG 2115  
Db 1888 CAAGCTGAGCAGAGCGAAAGTACCACAGCTTCAGGACGAGTATTTTACCAGCGCCGCTG 1947  
QY 2116 CTGCTGTCTAATCAGCGTGTGATCTGTGCTGTACTCTCTGCTGTGTTCTCTGTTCCCTAAG 2175  
Db 1948 GTTCTGCTCTCATCTTCTGGCGCCTTATTCGGCCTTGTCTACCTTCTTAATAATCCACAG 2007  
QY 2176 GCCGTGAACCTGTCTCCCGCAGCATGTCTCGCTCACGGGCACATAGCACCGCAGTTGGC 2235  
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Db 2117 AGATCCGACCGCTGTGTGCACTTTCATCTGCTGCTTAACTACTCTGTGCGCCCAAGGC- 2175  
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Db 2617 ATTCTTCTCAACCTCTGCGCAGCCACGTTGCCAGCACTTCTTAATGTTCAACCCCTGCG 2676  
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QY 2956 AACTTCTCTGAGTCTATGTGGAGCTGGAGCAACAATGAGGTTGCCGAGTGCCTTGGCG 3015  
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QY 3016 CTGCTCAACGAGATCATGCTGACTTTGATCAGATTATCAGGAGGCGGTTCCGGCAG 3075  
Db 2797 CTTCTGAATGAGATCATCGCTGACTTTGATGAGCTTGGGACAAGAGACTTTTACAAGAC 2856  
QY 3076 CTGGAAGAAGATCAAGAGGATTGGTAGCACCTTACATGGCTGGCTGCTCAGGGCTGAAGGCC--- 3132

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Db	2917	GCTGGGACCAAGGCTAAGAAAGTCATCTCTCTCCACCTCAGCAGCTTGGCAGATTTTGC	2976
Qy	3187	ATGGCGGCTCATGGAGCAGATGAAGACACATCAATAGCAGCTCTTCAACAATTTCCAGATG	3246
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Qy	3247	AAGATTGGGCTGAACATGGCCCCAGTCGTGGCAGGTCTATCGGGGCTCGGAAGCCACAG	3306
Db	3037	CGTGTGTGGCATCAATGTTGGCCCGGTGGTGGCTGGAGTGATCGGGGCTCGCAGGCCGAC	3096
Qy	3307	TATGACATCTGCGGGGAACACAGATGAATGCTCTAGTCTGATGGACAGCAGCGGGGTCCCC	3366
Db	3097	TATGACATTTGGGGGAACACAGGTCAATGTGGCCATCGGATGGACATGACCGGGCTCCAG	3156
Qy	3367	GACCGAATCCAGGTGACCCACGACCTGTACCAAGTTCCTAGTGTGCCAAGGGCTACCACTG	3426
Db	3157	GGCAGGATCCAGGTCAACAGAGGAAGTTCACCGGTGCTGCGCGGGGTTCCTACCGCTTC	3216
Qy	3427	GAGTGTGCGAGGGTGTCTAAGTGAAGGCAAGGGGAGATGACCACTTACTTCTCAAT	3486
Db	3217	GTGTGCGGAGGCAAAATCAGTGTCAAGGCAAGGGTGAGATGCTGACATACTTCTCGAA	3276
Qy	3487	GGGGGCCCC 3495	
Db	3277	GGCAGGACC 3285	
RESULT 10			
US-09-412-210-2			
; Sequence 2, Application US/09412210			
; Patent No. 6403358			
; GENERAL INFORMATION:			
; APPLICANT: Kapeller-Libermann, Rosana			
; TITLE OF INVENTION: 21529, A NOVEL ADENYLATE CYCLASE			
; FILE REFERENCE: 5800-47			
; CURRENT APPLICATION NUMBER: US/09/412,210			
; CURRENT FILING DATE: 1999-10-05			
; NUMBER OF SEQ ID NOS: 2			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 2			
; LENGTH: 3518			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: (0)...(0)			
; OTHER INFORMATION: 21529 adenylate cyclase			
; NAME/KEY: CDS			
; LOCATION: (247)...(3480)			
US-09-412-210-2			

Query Match	14.23;	Score 505.2;	DB 4;	Length 3518;
Best Local Similarity	50.0%;	Pred. No. 1.6e-115;		
Matches 1560;	Conservative	0;	Mismatches 1488;	Indels 72; Gaps 9;
QY	435	CCAGATGAACAGACAGACGCTGCTGCTGTCGGTGTGCTGCTACACAGCGT	494	
Db	318	CCAGCAGTACCCGCTGCTGCTGCTGCTGCGGATCGTCTCTGTGCGCTCGCGGCGCT	377	
QY	495	GCT----GCTGGCTTTCAAAGCCGACCCGCCGCCCTCAG--CCTGCCTATGTGGCCT	548	
Db	378	GCTGCGAGTGGCTGGGCCAGCGGACGAGGAGCTGACCTCAGACCCGAGCTCTCTGACCAC	437	
QY	549	GTTGGCTGTGCCGCCGCCCTTCTCGTGGGCTCATGTGGTGTATACCGGCATAGCTT	608	
Db	438	TGCTGTGTCGGCGTGGCGGGCTTCTCGCTGCTGCTGGGCTCGCTTCCCGGGAGACAGG	497	
QY	609	CCGCCAGACTCCATGTGGGCGTGAAGCTGCTGGGCGATCCTGGGGCAGTGCA	668	

Db	498	ACTGCAGCGCTGGACCGCTCCCTGTC	CGGCTGGTATG	GGTGGCGCTGCGCTGCTAGCGCTAGG	557
Qy	669	GGTCGGGGCGGCTTTCCGACAGACACCGCGGACGCCCTCTGCGGGGCTCTGGTGCCCTGT	728		
Db	558	CCACGCTTCCGTTCACCGGGGCGGTGAGCGCTGGACAGGTGCTATT	617		
Qy	729	GTTCCTTTGTATACATACGCAATACAGCTCTCTCCCATCCGCATCGGGCTCCGCTCTCAG	788		
Db	618	CTTCGTCTATTTACCGGCGTATGCCATGTGCTTGGGCAATCGGACACCGCGCTGCG	677		
Qy	789	CGGCTGGGCTCTCCACCTTGATTTGATCTTTGGCTGGCAA	838		
Db	678	GGGCTCGGCTCTCTACTCTCGCATCTGCTGGTCTCTGGGCTGTATCTTGGGCCACAGCC	737		
Qy	839	GTGTGATGCCCTTCCCTTG	--GAAGCAGCTCGGTGGCAATGTGCTGCTGTCTCTGTCAC	896	
Db	738	GGACTCACGGCTGCACTGCTGCCGAGTTGGCAGCAACGCAGTGTCTTCTGTGCGG	797		
Qy	897	CAACGTCATTAGCATCTGCACACACTATCCAGCAGAGGTGTC	956		
Db	798	GAACGTGGCAGGAGTGTACCAAGCGCTGATGGAGCGCGCTCGCGGCCACGTTCCG	857		
Qy	957	GGAGACCCGAGTTACATCCAGCGCGGCTCCACCTG	CAGCATGAGAAATCGGACGAGGA	1016	
Db	858	GGAGGCACTCAGCTCCTGCATCAGCGCGGCTGGACACCGAGAAGACCAAGA	917		
Qy	1017	GGGGCTGCTGCTCGGTATTTGCCCAGCAGCTTTGCCATGGAGATGAAGAAGACATCA	1076		
Db	918	ACACCTTCTCTTGTCTCATCTCTCTGCCACTTGGCCGAGAGATGAAGCAGAGATCAT	977		
Qy	1077	CACAA	-----AAAAGAAGACATGTTCCACAAAT	1106	
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Qy	1107	CTACATPACAGAAGCATGACAATGTCAGCATCTCTGTTTGACAGACATTCAGGGCTCAC	1166		
Db	1038	CTATGTCAAGAGAGCACCAGGAGTCAGCGTCTGTATGCTGACATCGTGGGCTTCAC	1097		
Qy	1167	CTGGCATCCCAGTGCACCTGGCAGAGCTGTCATGACCCCTGAATGAGCTCTTGCCCG	1226		
Db	1098	GCTGGCCAGGAGTGTCCCTTAGGAGCTGGTGCTCATGCTCAATGAGCTCTTTGGCAA	1157		
Qy	1227	GTTTGACAAAGCTGGCTGGGAGAATCACTGCCTGAGGATCAAGATCTTGGGGACTGT	1286		
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Qy	1287	CTACTGTGTGTCAGGCTCGCGGAGCGCGGGCCGACCATGCCACTGCTGTGTGGAGAT	1346		
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Qy	1347	GGGGTGTAGACATGATTGAGGCCATCTCGTGGTGTACGTGAGGTGACAGGTGTGAATGT	1406		
Db	1278	GGGCTTGGACATGTGCGGGCCATCAGGAACTCGCGGACGCCACTGGGTGGACATCA	1337		
Qy	1407	CATGGCGTGGGATCCACAGGGGCGGTGCACTCGCGGCTCTTGGCTTGGGAAATG	1466		
Db	1338	CATGGTGTGGCGTGCATCAGGACGCTACTGTGTGGAGTCA	1397		
Qy	1467	GCAGTTCGATGTGTGTCAAATGATGTGACCTCGGCCAACCATGAAGCAGGAAGCCG	1526		
Db	1398	GCAGTACGAGTTTGTGTACATGATCTACACTGGCTTACCATATGGACGCGGTGT	1457		
Qy	1527	GGTGGCGCATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGACTACGAAGT	1586		
Db	1458	ACGAGCGGAGTGCAATCACAGGGCTTACCTTGGCCCTGCTGGCAGGGGCTTATGCTGT	1517		
Qy	1587	GGAGCCAGGCGTGTGGCAAGCGCAACGTAACCTCAAGGAGCAGCACATTCAGACTTT	1646		
Db	1518	GGAGGACGACGATGGAGCATTCGGACCCCTACCTTCGGAGCT	1577		
Qy	1647	CCTCATCTCTGGCGCAGCCAGAAACGGAAAGAGGAGAAAGGATGCTGCCCAAGTGCA	1706		

Db 1578 TCTGGTCATCGATCCACGGGACAGGAGGAGGATGAGAGGGCACTGACAGAGGCTTGCT 1637  
QY 1707 GCGGACTCGGGCCAACTCCATGGAAGGCTGATGCGCGGATGGTCCCTGATCGTGCCTT 1766  
Db 1638 GTCTCTGCTTGAGGGCTCAAGATGGGTCCATCAGTCTGCTGATGACCGGTACCTGGAGTC 1697  
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QY 1827 CAACCGGGGACCCAGATGCCCTG--AACCCTGAGATGAGTGGA-TGAGTTCCTGAG 1883  
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QY 1944 GCTACCTTCCAGAGAGAGATTTTGAAGAAGTACTCCCGGAAGGTGGATCCCGCTT 2003  
Db 1878 CATTGACAGCTCAACTCGCAGAAACAGTGAAGCAGTGAAGGACTTCAACCCACTGAC 1937  
QY 2004 CGGAGCCTAGTTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2063  
Db 1938 ACTGTACTTCAGAGAGAAGGAGATGGAGAAGAGTACCGACTCTCTGCAATCCCGCCCT 1997  
QY 2064 AATTTTCCCACTCCACCTGATGCTTGGGATTTATGCGAGCATCTTCTGCTGCTGCT 2123  
Db 1998 CAATACTATGAGCCTGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2057  
QY 2124 AATCAGGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2183  
Db 2058 AGTGACAAACAGGCCCCAGCTGCGCCATCAG--TATAGCATCACTTTCTGCTGCT 2114  
QY 2184 AGTCTGCTCCGACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2243  
Db 2115 CTTCTCATCTTTTGTGCTTCTCAGAGACCTGATGAGTGTGCTGCTGAAAGGCC 2174  
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Db 2235 AATAGCCTTGGGACCGCCAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2294  
QY 2364 GCAGCAGCTCAATTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2423  
Db 2295 CTTCTTCCCAACATCATCAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2354  
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QY 2724 GTATCTGATGCTCAGCAGGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2783  
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QY 2784 GGCAACAGGGGAAAAAGGAGATGGAGGAGCTACAGGCATACAAACCGGAGGCTGCTGCA 2843  
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QY 2844 TAAATTTCTGCCAAGACGTTGGGCGCCACTTCTTGCGCGGAGCGCGCAATGATGA 2903  
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Db 2835 TCTCTACCAACGACTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2894  
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Db 2895 GGAGTTCTACTCTGATGATCCAAATCATGAGGGCTGAGAGTGTCTGAGGCTGCTGCTGCT 2954  
QY 3024 CGAGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3083  
Db 2955 TGAGATAAATGCTGATTTTATGAGGCTCTCCAAAGCCCAAGTTCAAGTGGGTGGAGAA 3014  
QY 3084 GATCAGACGATTTGGTAGCACCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3137  
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QY 3138 -----CTAGGATCAGGTGGGCGCTCCACATCACTGCTGCTGCTGCTGCTGCTGCT 3185  
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QY 3426 GGAGTCTCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3485  
Db 3375 CTACAGCCGGGTTGCTCATCAAGGTGAAGGCAAGGCGAGCTCTGCTGCTGCTGCTGCTGCT 3434

## RESULT 11

US-08-726-214-15  
; Sequence 15, Application US/08726214  
; Patent No. 6107076

## GENERAL INFORMATION:

; APPLICANT: Tang, Wei-Jen  
; APPLICANT: Gilman, Alfred G.  
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYL CYCLASE  
; TITLE OF INVENTION: AND USES THEREFOR  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/726,214  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/005,498  
FILING DATE: 04-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: US/D:450  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4601 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-726-214-15

Query Match 13.1%; Score 463.6; DB 3; Length 4601;  
Best Local Similarity 51.5%; Pred. No. 3.8e-105;  
Matches 1439; Conservative 0; Mismatches 1194; Indels 159; Gaps 10;

QY 712 GGCCTCTGGTCCCTGTGTTCTTTGTATACATCGCATACACGCTCCTCCCATCGGCATG 771  
DB 1575 GGCATAGGCTAGTCTTTTACACTCTCGCCACCTACAGCATGCTTCGGCTGCTCTC 1634

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DB 1635 ACCTGGGCCATTTGGCGGCTGGGCACATCTTGTCTGCAAGTCACACATTCAGGTGCTC 1694

QY 832 CTTAACCGTGGTGATGCTCTCTCTGGAAGCAGCTCGGTGCCAATGCTGCTGTTCCCTC 891  
DB 1695 ATACCCAGCTAGCGGTCTTTTCCATACACAGGTCTTGGCCCGAGGTGGTCTCTCATG 1754

QY 892 TGCACCAACGTCATTTAGCATCTGCACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCC 951  
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QY 952 TTTTCAGGACCGCCAGTTACATCCAGGCGCGGCTCCAGCTGCAGCATGAGAAATCGGAC 1011  
DB 1815 TTCTTGAGACCCCGAGGTGTGTGGAGCCAGGCTCCGCTGGAGACAGAAACCAAGA 1874

QY 1012 CAGGACCGGCTGCTGCTGCTGCTATGCCCCAGACAGCTTGCCATGGAGATGAAGAAGAC 1071  
DB 1875 CAGGACGGCTGTGCTCTGCTGCTCCCGAGGTTTGGCTCTAGAAATGATCAATGAC 1934

QY 1072 ATCAACACAAAAGAGAG-----ACATGTTTCCACAAGATCTACATACAGAG 1119  
DB 1935 ATGACCAATGTGGAGGAGGAGCACCCTGCAGCATCAGTTTCCACCGCATCTACATCCATCGC 1994

QY 1120 CATGCAATGTACAGATCCTGTTTGCAGACATTTAGGCGCTTCCAGCGCTGCATCCGAC 1179  
DB 1995 TACGAGACGTGAGTATTTCTTTTTCAGATGTCAAAGATTTACCAACCTCTCTACGACC 2054

QY 1180 TGCACGTGGCAGGAGCTGTGCTATGACCTGTAATGAGCTTTTGCCCGGTTTGCACAAGCTG 1239  
DB 2055 TTGCTGCTCAGGACCTGTGAGGATGCTCAGAGCTCTTTGCCAGATTTGATCGGCTG 2114

QY 1240 GCTGGGAGATCATGCTGAGGATCAAGATCTTTGGGGGACTGTTTACTGCTGTGTCA 1299  
DB 2115 GCGCATGAGCATCACTGTCTTGCATTAATAATCTTAAATCTTGGGGGACTGCTACTGTGTGTC 2174

QY 1300 GGGCTGCGGAGGCGCGGCGGCGGACCATGCCACTGCTGTGTGGAGATGGGGGTAGACATG 1359  
DB 2175 GGACTGCTGAGCGCGCGGCGGAGGACATGCTCATTTGCTGTGTGAAATGGGCTCAGCATG 2234

QY 1360 ATTGAGGCGCATCTCCCTGCTAGCTGAGGTGACAGGTGTGAATGTGAACATGCGCGCTGGGC 1419  
DB 2235 ATCAAACTATCAGGTTTGTGAGGTCCAGAGCAGCATGATGTTGACATGCGGAATTTGA 2294

QY 1420 ATCCACAGCGGGCGGTGCACCTGCGCGCTCTTGGCTTCGGAATGGCAGTTCCGATG 1479  
DB 2295 ATCCATTGAGGCTCTGTGCTGTGTGGCTGTGGCTGAGAAATGGCAGTTTATGATGTC 2354

QY 1480 TGGTCCAATGATGTGACCTTGCCCAACCACTGGAAGCAGGAGCGGGCTGCGCGCATC 1539  
DB 2355 TGGTCTTGGGATGTGACATCGCAAACTTGAATCTGGAGGAATCCTCGGAGAAAT 2414

QY 1540 CACATCACTCGGGCAACACTGCAGTACCTGACGGGGACTACGAAGTGGAGCCAGCCGT 1599  
DB 2415 CACATTTCCAAAGCCACACTGGATTCCTCAGTGTGACATATATGTAAGAGAGGCCAC 2474

QY 1600 GGTGCAAGCGCAACGCTACCTCAAGGAGCAGACATGAGACTTTCCTCATCTCGGCG 1659  
DB 2475 GGTAGGAGGAATGAATCTTTGAGGAAGCATATATAGACACCTATTTGATTAGCAG 2534

QY 1660 GCCAGCCAG-----AAACGGAAAGAGGAGAAAGCATGCTTGGGCA 1699  
DB 2535 CCCGAGAGAGTTTGTCTATCTTGCCTGAAGATATAGTTAAGGAGTCGGTGAGCTGCTCG 2594

QY 1700 AGCTCAGCGGACTCGGGCCCACTCCATGGAAGGCTGATCCCGGATGGGTTCTCTGATC 1759  
DB 2595 GACAGGAAACAGTGGGGCAACGTTACAGAAGGATCTCGAGCCCAAGCATGCCATTC 2654

QY 1760 GTGCTTCTCCCGACCAAGGACTCCAAGGCTTCGCGCAGATGGGCATTTGATGATTC-- 1817  
DB 2655 GACAACATCGTGGGCAACAGATACTCTGGCTGCCCTAACAAAGAAATTCATAAATCTG 2714

QY 1818 --CAGCAAAAGACAACCGGGGCAACCAAGATGCCCTGAAACCTTGAGGATGAGTGGATG 1875  
DB 2715 CTTCCAAACCATCTCGCAACAGCTTTTGCATGTCCAGTCTGGCCCTGAGGAAATTAACA 2774

QY 1876 TTCTGAGCGGTGCGATCGATCCGCGCAGCATGATCAGTCGGAAGGACCATGTCGCGC 1935  
DB 2775 AGAATAGACATACCATCGACTTGGGAGTGGCGATAGTTGAGAAGAGAGCATATCAAG 2834

QY 1936 CGGTTTTTGTCTACCTTCCAGAGAGAGGATTTTGAAGAAGTACTCCCGGAAGTGGAT 1995  
DB 2835 CCATTTCTCAGTGTGTTAAAGACTCCAGCTTGGAGCACAAGTATTTCTCAAAATCGGGAT 2894

QY 1996 CCCCGCTTGGAGCCTACGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2055  
DB 2895 GAAGTATTCAAGTCAAACTTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2954

QY 2056 CAGCTTCTAAATTTTCCACACTCCACCTGATGCTTGGGATTTATGCCAGCATCTTCCTG 2115  
DB 2955 CAAAGTTTGTCTT---CCTTCTCGAGGCTGATGCTATGACCATCCAGTCTTCCATCTG 3011

QY 2116 CTGCTGCTAAATACCGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2175  
DB 3012 ATCATGCTGCACTCGCGCTGGT-----CCTCA 3039

QY 2176 GCCCTGCAACGCTGTCTCCGCGAGCAATGTCGCTCAGGGGACATAGCACCCAGCTTGGC 2235  
DB 3040 TCACACCGGCAAGACATATAAGTGTCTGCTCTCTCATTTCTCGCAAAACCTGTTGTTG-- 3097

QY 2236 ATCTTTTCCGCTCTGCTGCTGCTTACTTCTGCAATGTCGAACATGTTCACTGTAAACAC 2295  
DB 3098 -----GATTAAACGAGACCTATTTGGCCCGCAAGTCATCATCTTGTGCTCC 3143

QY 2296 ACCCCCATACGAGGCTGTGACGCCGCGGATGCTGAATTAACACCTGCTGACATCACTGCT 2355  
DB 3144 ATCTTGAATTAATTTCTGGGAGCGCTCATATAATATCTGTGTGTGATTTTGCACAGTCG 3203

QY 2356 TGCCACCTTGCAGCAGCTCAATTTACTTCTGCGGCTTGGATGCTCCCTGCTGTGTGAGGGCACC 2415  
DB 3204 ATACCTTTGAAGAACCTGACTTTCAAT-----TCCTCAGCTGTGT-----TT 3245

QY 2416 ATGCCCACTGAGCTTCTTCTGAGGTGTCATCGGGAACATGCTGCTGCTGCTGCTGCTGCTG 2475  
DB 3246 ACAGATATCTGCTCTACCCAGAGTACTTTGCTTCACTGGGCTGTTGCCCATGCTGAGC 3305

QY 2476 AGCTCTGCTTCTTCTGCATCATCAGCAGCATCGGGAAAGTTGGCCATGATCTTTGCTTGGGG 2535





QY 1662 CAGCCAGAAACGGAAGAGGAGAAAGGATGCTGGCCCAAGCTGCAGCGGACTTCGGGCCAA 1721  
Db 1458 -----CAATCCCAAGGAGAGCGAGGAGTCTCTCAGCATCTCTTCAGACCTCGACACAC 1511  
QY 1722 CTCCTAGGAGGCTGATGTCGCCGATGAGGTTCTCTGATCGTGGCTTCCTCCGACCAAGGA 1781  
Db 1512 TCTGACGAGGACCAAGATGAGAGCATCTGTCCG-----CATGACCGGTACTTGA 1562  
QY 1782 CTCCTAAGGCTTCGCCAGATGGGATGATGATTCAGCAAGAACAAACCGGGGACCCA 1841  
Db 1563 GTCCTGGGAGCAGCCAGCCATTCCGACATCTGCACACAGATAGATGACACACAGA 1622  
QY 1842 AGATGCCCTGAACCTGAGGATGAGGTGATGAGTTCCTGAGCCGTCGCATCGATCCCG 1901  
Db 1623 GAATGGGAAGATTAGTACCACGGATGTCGAATGGTCAACATAATTTTCAAAATCGCAC 1682  
QY 1902 CAGCATGATGACCTGCGGAAGGACCATGTGCGCCGGTTTGTGTCACCTTCCAGAGAGA 1961  
Db 1683 CTTAAGAACTAAGTCACAGAAGAAGAGATTTGAAGAAGAACTGAATGAAGGATGATCCA 1742  
QY 1962 GGATTTTGAAGAAGTACTCCCGAAGGTGGATCCCGCTTCGGAGCTACGTTGCCGTG 2021  
Db 1743 AGCAATTGATGGATCAATGCACAGAGCAATGGCTCAAGTCAGAGACATTCAAAGAT 1802  
QY 2022 TCCCTGTGTGCTTCTGCTTCATCTGCTTCATCCAGCTTCTTAATTTTCCACACTCCAC 2081  
Db 1803 CTCCTGTCTTTCTATAACAAGAAATATAGAGAAAGAAATACCGAGCTACTGCACTGCCAGC 1862  
QY 2082 CCTGATG---CTTGGGATTTATGCCAGCATCTTCCTGCTGCTGCTTAATCACCGTCTGAT 2138  
Db 1863 ATTCAAGTACTACGTGACCTGTGCGTGCCTCATCTTCTGTCATCTTCAATGTTACAGAT 1922  
QY 2139 CTGTGCTGTG-----TACTCCTGTGTGTTCTCTGTGTC--CTAAGGCCCTGCAAGC 2186  
Db 1923 ACTTGATTTGCCAANAACGTCCATCCTTGGCTTCTCTTGGAGCTGCAATTTCTCTCCT 1982  
QY 2187 TCTGTCCCGACATTTGCTGCTCAGGGGCACATAGCACCGCAGTTGGCATCTTTTCGGT 2246  
Db 1983 CATCTTCATCTCTTGTCTGTCTGCTGGCAGACGCTTTTGAATGACGACAAAGGCGCTC 2042  
QY 2247 CCGTCTGTGTTTACTTCTGCCATTTGCCAATGTTCACTGTACCTTAACCAACACCCCATAGC 2306  
Db 2043 CACCTCTCTCATGTGGCTTTTGAATCATCAGGCATCATGCGCAACCGGCCATGGCCAG 2102  
QY 2307 GAGCTGTGAGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCTGCCACTGCA 2366  
Db 2103 GATCTCCCTCAACATCGTCACCCAGCTATCATATAACCATGGCTGTGTTCAACATGTT 2162  
QY 2367 GCAGCTCAATTAATCTCTGGGCTGGATGCTCCCTGTGTGAGGGCACCATGCCACCTG 2426  
Db 2163 TTTCTGAGCAACTCTGAGGAGACAAACCTTCCCACTGCCAATACATCAAAATGCAAGGT 2222  
QY 2427 CAGCTTTCTGAGGTGCTCATCGGAACATGCTGCTGAGTCTCTTGGCCAGCTCTGCTT 2486  
Db 2223 TTTCTGCGCGGATACACAGCGCTCATCTTCATGCTCGAAACTTGTTTTCTCCCTCCCGTA 2282  
QY 2487 CCTGCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGTCTTGGGCTCATCTATT 2546  
Db 2283 CTTCATATACACTGATUCCCTGGGTTGATCTCTGCTCCGTTTCTCTGAGGGTGAACATA 2342  
QY 2547 GGTGTGCTTCTGCTGGTTCGCCCGCCCATCTTTGACAACTATGACCTACTGCTTGG 2606  
Db 2343 TGAGTTAAAAATGTTAATCATGATGGTGGCACTCGTGGGCTACAACACATTTCTACTCCA 2402  
QY 2607 CTTCCATGGCTTGGCTTCTTCAATGAGACCTTTGATGGGCTGGAGTGTCCAGCTGACAG 2666  
Db 2403 CACCCATGCC---CATGTTCTGAGTGCCTTACAGCCAGGTCTCTTTCAGAGACCAAGCAT 2459  
QY 2667 GAGGTGGCCCTCAATATATACCCCTGTGATTTCTGCTGGTGTGCTGGCGCTGTA 2726  
Db 2460 TTGGAAGACCTGAAGACCATGGCTCCGTGTCACTCTCCCATATTCTTCATCACGCTGT 2519

QY 2727 TCTGCATGCTCAGCAGGTGGATCGACTCCCGCCTAAACTTCTCTTGGAAACTACAGGC 2786  
Db 2520 GGTTCCTGGCAGACAGAGTGAATATTACTGTAGGTTAGACTTCTTGTGGAACAAGTT 2579  
QY 2787 AACAGGGGAAAAGAGGAGATGGAGGAGCTACAGCATACAAACCGAGGCTGCTCATAA 2846  
Db 2580 CAAAAGAGGGGAGGAGATAGAAACCATGGAGAACCTAAATCGAGTGTCTGTGGAGAA 2639  
QY 2847 CATTCCTGCCAAGGAGCTGGGGGCCACTTCTGCGCCGGAGCGCCCAATGATGAAT 2906  
Db 2640 CGTGTCTCTGCACACAGTGGCTGAACACTTCTGCGCAGGAGCTGAAAATGAGGAGCT 2699  
QY 2907 CTACTATCAGTCGTGTGAGTGTGTGCTGTATGATTTGCTTCCATTTGCCAATCTCTCTGA 2966  
Db 2700 GTACCACCACTCTACGACTGTGTGTCTATGTTTGCCTCATTCGGGACTTCAAGGA 2759  
QY 2967 GTTCTATCTGGAGCTGGAGGCAACAATGAGGTGCCAGTCCCTGCGGCTGCTCAACGA 3026  
Db 2760 GTTCTACACAGATCAGATGTGAACAAGAGGCTTGAATGCTTCCGCTCCTGAATGA 2819  
QY 3027 GATCATCTGCTGACTTTGATGAGATTATCAGGAGGAGGCTTCCGCGAGCTGGAAGAT 3086  
Db 2820 GATCATCTGCTGACTTTGATGATCTGCTTTCTAAGCCAAAGTTTCAGTGTGTGAAGAT 2879  
QY 3087 CAAGCAGATTGGTAGCCTACATGCTGCTCAGGCTGAGGTGAGCCAGACACTACGATCA 3146  
Db 2880 CAAGACCATTTGGGAGCACATACATGGCAGCCACGGGACTGAGTGCATACCCAGCCAGGA 2939  
QY 3147 GGTGGGCC-----GCTCCACATCACTGCCCTGGCTGACTACGCCAT 3188  
Db 2940 GCACGCCCAGGAACCTGAGCGTCACTATGCATAGGCACATAGGCTGGAGTTGTCATA 2999  
QY 3189 GCGGCTCATGTGAGCAGATGAAGCACATCAATGAGCAGCTCTTCAACAATTTTCCAGATGAA 3248  
Db 3000 TGCCCTGTGGGAAACTGGATGCCATCAATAAGCACCTTCAACAGACTTCAAACTGCG 3059  
QY 3249 GATTTGGGTGAACATGGGCCAGCTGCTGGCAGGTCTATCGGGGCTCGGAAGCCACAGTA 3308  
Db 3060 AGTGGGTATCAACCATGGGCTGTAAATAGTGGCTCATAGGGGCTCAAAAGCCACAGTA 3119  
QY 3309 TGACATCTGGGGAACACAGTGAATGCTCTAGTCTGATGGACACAGCGGGGTCCCGGA 3368  
Db 3120 TGACATCTGGGGAACACATGTCACGTGGCCAGCAGATGAGACACACCGGGGTCTGGA 3179  
QY 3369 CGAATCCAGGTGACCGGACCTGTACCGGTTCTAGCTGCCAAGGCTACCACTCTCTCA 3485  
Db 3180 CAAAATACAGTGTGACTGAGGAGACAAGCTCATCTTGCAGACGCTTGGCTACACGTGTAC 3239  
QY 3429 GTGTCAGGGGTGTCACAGGTGAAGGGCAAGGGGAGATGACCACCTACTTCTCTCAA 3485  
Db 3240 ATGTCAGGTATCATCAATGTGAAGGGGAAAGGGGACCTGGAAGACATATTTTGTAAA 3296

## RESULT 13

US-08-726-214-3

; Sequence 3, Application US/08726214

; Patent No. 6107076

; GENERAL INFORMATION:

; APPLICANT: Tang, Wei-Jen

; APPLICANT: Gilman, Alfred G.

; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE

; TITLE OF INVENTION: AND USES THEREFOR

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White &amp; Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: United States of America

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible



OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICANT: US/08/726,214  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/005,498  
FILING DATE: 04-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: UTSD:450  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4008 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-726-214-3

Query Match 12.9%; Score 459; DB 3; Length 4008;  
Best Local Similarity 50.8%; Pred. No. 4.9e-104;  
Matches 1370; Conservative 0; Mismatches 1240; Indels 87; Gaps 8;

QY 852 CCTCTGGAACGAGCTCGGTGCCAATGTGCTGCTTCTCTGACCAACGCTATTAGCAT 911  
DB 624 CCGTCTTGGCAGATATGCGCAATGTGATCAATTTTCAATTTGGGAACCTTGGCGGAGC 683  
QY 912 CTGCACACATATCCAGCAGAGTGTCTCAGCGCCAGGCGCTTTCAGGAGACCGCGAGTTA 971  
DB 684 CTACCACAACACCTCATGAGAGTTCCTTGCAGCAACCTATCGGACACGTTGTAATG 743  
QY 972 CATCCAGGCCGGTCCACCTGCAGCATGAGAAATCGGCAGCAGGCGGTGCTGTGTC 1031  
DB 744 CATCAAGTCCCGGATCAAGTGAATTTGAAAAACGCGCAGCAGGCGGTCTGCTCTC 803  
QY 1032 GGTATTGCCCCAGCAGTTCGCCATGGAGTGAAGAAGACATCA----- 1075  
DB 804 CTGTGCTGCCAGCTCACATCGCCATGGAGATGAAGCTGAAATCATTCAGAGGCTGCAGGG 863  
QY 1076 -----ACACAAAAAAGAGACATGTTCCACAAGATCTACATACAGAAGCA 1121  
DB 864 CCCAAAGCAGGACAGATGAAACACAAACACTTCCACAATCTGTATGTCAAACGACA 923  
QY 1122 TGACATGTGAGATCCTGTTTGCAGACATGAGGGCTTCCAGCGCTGCGATCCCAAGTG 1181  
DB 924 CACCAACGTGAGCATATTATACGCTGACATTTGTTGGCTTCCACCGCGCTTGAAGCGATTG 983  
QY 1182 CACTGCGCAGAGCTGTGTATGACCTGATGAGCTCTTTGCCCGGTTTCACAAGCTGGC 1241  
DB 984 CTCCCTGGCGAACTGGTCCACATGCTGAATGAACCTTTTGGAAAGTTTGAATCAATAGC 1043  
QY 1242 TGGCGAAGATCACTGCTGAGGATCAAGATCTTTGGGGAGCTGTACTACTGTGTGTCAGG 1301  
DB 1044 AAAGGAGAAATGAATGCATGAGAATTAATAATTTAGGAGACTGTATTACTGTGTGTTCCGG 1103  
QY 1302 GCTGCGCGAGCGCGCGCCACCATGCCCACTGCTGTGTGGAGATGGGGGTAGACATGAT 1361  
DB 1104 GCTCCCTATATCACTCCCTTAACCATGCCAAGAACTGTGTGAAATGGGATTTGATATGTG 1163  
QY 1362 TGAGGCCATCTCCTGTGATGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCAT 1421  
DB 1164 CGAAGCCATAAAGAGTGAAGGATGCTACCGGAGTTGATCAACATGGCTGAGAGT 1223  
QY 1422 CCACAGCGGCGGCTGACTGCGGCGCTTGTGCTTGGCGAAATGCGAGTTTCGATGTGTG 1481  
DB 1224 GCATTCTGGGAAGCTTCTCTGTGTGTGATGCTCTCCAGAACTGGCAGTATGATGTG 1283  
QY 1482 GTCCAAATGATGTGACCTCGGCCAACCAACATGGAAGCAGGAAAGCCGGGCTGGCGCATCCA 1541

DB 1284 GTCTCATGATGTTACTCTGGCAAAACCATGGAAAGCTGGAGGAGTCCCTGGCGGTGTCA 1343  
QY 1542 CATCACTCGGCAACACTGACGTACCTGAACGGGGAGTACAAAGTGGAGCGAGCCCTGG 1601  
DB 1344 CATTTCTTCAGTCACTCTGGAGCACTTGAATGGGGCTTATAAGTGGAGGAAGAGATGG 1403  
QY 1602 TGCAAGCGCAAGCGGTACCTCAAGGAGCAGACATTTGAGACTTTCCCTCATCTCTGGGCGC 1661  
DB 1404 TGAGATAAGAGACCCATATTTAAAGCAGACACTTGGTGAACACCTACTTTGTAAT----- 1457  
QY 1662 CAGCCAGAAACGGAAAGAGGAAAGCATGCTGGGCAAGCTGCAGCGGACTTCGGGCCAA 1721  
DB 1458 -----CAATCCCAAGGAGAGCGAGTCTCTCAGCATCTCTTCAGACCTCGACACAC 1511  
QY 1722 CTCCATGGAAGGGCTGATGCCGCGATGGGTTCCTGTGATCGTCCCTCTCCCGGACCAAGGA 1781  
DB 1512 TCTGGACGGAGCCAAAGATGAGAGCATCTGTCCG-----CATGACCCGGGTACTTTGGA 1562  
QY 1782 CTCGAAGGCTTCGCCAGATGGGCATTTGATGATTCAGCAAAAGACAAACCGGGGCACCCA 1841  
DB 1563 GTCTGGGAGCAGCCAAAGCCATTCGCACATCTGCCACCACAGATAGCATGACCACAGA 1622  
QY 1842 AGATGCCCTGAACCTGAGGATGAGGTGGATGATTCCTGAGCCGTGCCATFCGATGCCCG 1901  
DB 1623 GAATGGGAAGATTAGTACACGAGTGTGCCAATGGGTCAACATAAATTTCAAAATCGCAC 1682  
QY 1902 CAGCATTTGATCAGCTCGGGAAGGACCATGTGCGCCGGTTTTTGTCTCACCITCCAGAGAGA 1961  
DB 1683 CTTAAGAACTAAGTTCACAGAAGAAGAGATTTTGAAGAAGAACTGAATGAAAGGATGATCCA 1742  
QY 1962 GGATTTTGAGAAGAAGTACTCCCGGAAGGTGGATCCCGGCTTCGGAGCCTACGTTGCGCTG 2021  
DB 1743 AGCAATTTGATGGGATCAATGCACAGAAGCAATGGCTCAAGTCAGAAGACATTTCAAGAAT 1802  
QY 2022 TGCCCTGTTGGTCTTCTGCTTTCATCTGCTTCAATCCAGCTTCTAATTTTCCCACTCCAC 2081  
DB 1803 CTCCTCTGTTTCTATTAACAAGAATATAGAGAAAGAAATACCGAGCTACTGCACTGCCAGC 1862  
QY 2082 CTTGATG- --CTTGGGATTTATGCCAGCATCTTCTCTGCTGCTGCTATATCACCGTCTGAT 2138  
DB 1863 ATTCAAGTACTAGTGACCTGTGCTGCTGCTCTCATCTTCTCTGCACTCTTCATTTGACAGAT 1922  
QY 2139 CTGTGCTGTG-----TACTCCTGTGTGTTCTCTGTGTTCC--CTAAGGCCCTGCAACG 2186  
DB 1923 ACTTGATTTGCCAAAACGCTCATCTTGGCTTCTCTCTCTTGGAGCTGCAITTTCTCTCCT 1982  
QY 2187 TCTGTCCCGCAGCATTTGTCGCTCAGGGCAGACATAGCACCGCAGTTGGCATCTTTCCGT 2246  
DB 1983 CATCTTTCATCTCTTGTCTGCTTGGCTGGACAGCTTTTGCAATGCAAGAAAAGGCTC 2042  
QY 2247 CTTGCTTGTGTTTACTTCTGCCATTGGCAACATGTTCCACCTGTAACACACACCCCATACG 2306  
DB 2043 CACCTCTCATGTGGCTTTTGAATCATCAGGCATCATCGCCAAACCGCCCATGGCCAG 2102  
QY 2307 GAGCTGTGACGCGGATGCTGAATTTAAACCTGCTGTGACATCATGCTGCCCTGCCACTGCA 2366  
DB 2103 GATCTCCCTCACAATCTGCACACGGCTATCATACTAACCATGGCTGTGTTCACATGTT 2162  
QY 2367 GCAGCTCAATTTACTCTCTGGCCCTGGATGCTCCCTGTGTGAGGGGACCATGCCACCTG 2426  
DB 2163 TTTCTGTGAGCAACTCTGAGGAGACAAACCTTCCCACCTGCCAATACATCAATGCAACG 2222  
QY 2427 CAGCTTTCTGTGAGTGTCCATCGGGAACATGCTGCTGAGTCTCTTGGCCAGCTCTGTCTT 2486  
DB 2223 TTTGTGCGCGGATTAACAGCGCTCGATTTCTCATGCTCGAAACTTTGTTTTCTCCCGTA 2282  
QY 2487 CCTGCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGTCTGTGGGGCTCATCTATTT 2546  
DB 2283 CTTTCATATACAGTGCATCTCGGCTTGTATCTCTGCTCGCTTTTCTGAGGGTGAACATA 2342  
QY 2547 GGTGCTGCTTCTGCTGGGTCCCCCAGCGCCATCTTTTGACAACTATGACCTACTGCTGG 2606

Db 2343 TGAGTTAAATGTTAATCATGATGTCGACCTCGTGGGCTACAAACACATCTTACTCCA 2402  
QY 2607 CFTCCATGGCTGGCTCTTCCAAATGAGACAGCTTTTGATGGCTGGACTGCCAGCTCAGG 2666  
Db 2403 CACCCATGCC---CATGTTCTGGATCGTACAGCAGGTCCTGTTTCAGAGACCAGCAT 2459  
QY 2667 GAGGTGGCCCTCAAAATATATGACCCTGTGATCTGCTGCTGGTGTTCGCTGGCGGTGA 2726  
Db 2460 TTGGAAGACCTGAAGACCATGGCTCCGTCGTCACCTCTCATATTTTCATCACGCTGT 2519  
QY 2727 TCTGCACTGCTCAGCAGGTGAAATCGACTGCCGSCCTAACTTCCCTGCTGAAACTACAGC 2786  
Db 2520 GGTTCGGGCACACAGAGTGAATTAATCTAGTGGTGTAGACTTCTGTGGAAGAACAGTT 2579  
QY 2787 AACAGGGGAAAAGAGAGATGAGAGCTACAGGCATACACCGGAGGCTGCTGCATAA 2846  
Db 2580 CAAAAGAGCGGGAGAGATGAACACCATGGAGACCTAATCGAGTCTGCTGGAGAA 2639  
QY 2847 CATTCGCCAAGGACGTGGCGCCACATTCCTGGCCCGGAGCGCCGCAATGATGAAT 2906  
Db 2640 CGTGTCTCTGCACACGTGGCTGAACACTTCTGCGCAGGAGCTGAAAAATGAGGAGCT 2699  
QY 2907 CTACTATCATGCTGCTGAGCTGTGGCTGTTATGTTGCTTCATTTGCCAACTTCTCTGA 2966  
Db 2700 GTACCACTGCTCTAGCACTGTCTGTGTCATGTTGCTCTCATTTCCGGACTTCAAGGA 2759  
QY 2967 GTTCTATGAGAGCTGGAGGCAACAAATGAGGCTGCCGAGTGCCTGCGGCTGCTCAAGCA 3026  
Db 2760 GTTCTACACAGATCAGATGTGNACAGGAAGCTTGGATGCTGCGGCTCTGNATGA 2819  
QY 3027 GATCATCGCTGACTTTGATGAGATTATACGAGGAGCGGTTCCGSCAGCTGGAAGAAT 3086  
Db 2820 GATCATTTGCTGACTTTGATGATCTGCTTTCTAAGCCAAAGTTCAGTGGTGTGAAAAAT 2879  
QY 3087 CAAGACGATTGTAGACCTACATGCTGCTCAGGCTGAAGCCAGCAGCAGCTACGATCA 3146  
Db 2880 CAGACCAATTGGGAGCACATACATGCGACGCCAGCGGACTGAGTGCCATACCCAGCCAGGA 2939  
QY 3147 GGTGGGCC-----GCTCCACATCACTGCGCTGGCTGACTACGCCAT 3188  
Db 2940 GCAGCGCCAGGAACCTGACCGTCAGTACATGCACATAGCAGCACCATTGGTGGAT 2999  
QY 3189 GCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCTTCAACAATTTCCAGATGAA 3248  
Db 3000 TGCCTGTGTGGGAAACTGGATGCCATCAATAAGCACTCTTCAACGACTTCAAACTGCG 3059  
QY 3249 GATTGGCTGAACATGGGCCAGTCTGTGCGAGGTGTCTATCGGGGCTCGGAAAGCCACAGTA 3308  
Db 3060 AGTGGGTATCAACCATGGGCGCTGTAAATGCTGGCGTATAGGGGCTCAAAAGCCACAGTA 3119  
QY 3309 TGACATCTGGGGAACACAGTGAATGCTCTAGTGTATGGACAGCAGCGGGGTCCCGCA 3368  
Db 3120 TGACATCTGGGCAACACTGTCAAGTGGCCAGCAGATGGACAGCAGCGGGTCTGTGA 3179  
QY 3369 CGGAATCCAGGTGACACCGGACTGTACAGGTTCTAGTGTGCAAGGGGTACAGCTGGA 3428  
Db 3180 CAAAATACAGGTGACTGAGGAGCAACAGCTCATCTTGCAGAGCTTGGCTACAGCTGTAC 3239  
QY 3429 GTGTCGAGGGTGTCAAGGTGAAGGGCAAGGGGAGGATGACCACCTACTTCTCTAA 3485  
Db 3240 ATGTCGAGGTATCATCAATGTGAAGGGGAAAGGGGACCTGAAAGACATATTTTGTAAA 3296

RESULT 14

PCT-US95-11808-5  
; Sequence 5, Application PC/TUS9511808  
; GENERAL INFORMATION:  
; APPLICANT: Iyengar, Srinivas Ravi V.  
; TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND  
; TITLE OF INVENTION: ADENYL  
; TITLE OF INVENTION: CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brumbaugh, Graves, Donohue and  
; ADDRESSEE: Raymond  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.  
; ZIP: 10112-0228  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/11808  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/307,896  
; FILING DATE: 16-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Richard S.  
; REGISTRATION NUMBER: 26,154  
; REFERENCE/DOCKET NUMBER: 29970 165/28755  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 408-2500  
; TELEFAX: (212) 765-2519  
; TELEX: 650 6111063  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4008 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
PCT-US95-11808-5

Query Match 12.9%; Score 459; DB 5; Length 4008;  
Best Local Similarity 50.8%; Pred. No. 4.9e-104;  
Matches 1370; Conservative 0; Mismatches 1240; Indels 87; Gaps 8;

QY 852 CTTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTGCTCTCTGCACCAACGTCATAGCAT 911  
Db 624 CCGTCTCTGGCAGACTGCGCAATGTGATCATTTTCATTTTGGGAACCTTGGCGGAGC 683  
QY 912 CTGCACACACTATCAGCAGAGGTGCTCAGCGCCAGGCTTTTCAGGACACCGCAGTTA 971  
Db 684 CTACACACAGCACCCTATGAGAGCTTGCCTTGAGCAGAACCTATCGGAGACAGTGTAA 743  
QY 972 CATCCAGGCGGCTCCACCTGCAGCATGAGAAATCGGCAGCAGGAGCGCTGCTGCTGC 1031  
Db 744 CATCAAGTCCCGGATCAAGCTGGAATTTGAAAAAGGCGCAGGAGGAGCTCTCTGCTCTC 803  
QY 1032 GGTATTTGCCAGCAGGTTGCCATGGAGATGAAAGAACATCA----- 1075  
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Job time : 136.927 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 921786

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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; Sequence 5, Application US/09750240  
; Patent No. US20020103147A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammon, H. K.  
; APPLICANT: Insel, P. A.  
; APPLICANT: Ping, P. A.  
; APPLICANT: Post, S. R.  
; APPLICANT: Gao, M.  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART FAILURE  
; FILE REFERENCE: 220002056723  
; CURRENT APPLICATION NUMBER: US/09/750,240  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/472,667  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: US 09/008,097  
; PRIOR FILING DATE: 1998-01-16  
; PRIOR APPLICATION NUMBER: US 08/924,757  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/048,933  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: US 08/708,661  
; PRIOR FILING DATE: 1996-09-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 3549  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-750-240-5

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; Patent No. US20020103147A1			
; GENERAL INFORMATION:			
; APPLICANT: Hammon, H. K.			
; APPLICANT: Insel, P. A.			
; APPLICANT: Ping, P.			
; APPLICANT: Post, S. R.			
; APPLICANT: Gao, M.			
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART			
; TITLE OF INVENTION: FAILURE			
; FILE REFERENCE: 220002056723			
; CURRENT APPLICATION NUMBER: US/09/750,240			
; CURRENT FILING DATE: 2001-10-12			
; PRIOR APPLICATION NUMBER: US 09/472,667			
; PRIOR FILING DATE: 1999-12-27			
; PRIOR APPLICATION NUMBER: US 09/008,097			
; PRIOR FILING DATE: 1998-01-16			
; PRIOR APPLICATION NUMBER: US 08/924,757			
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; ORGANISM: Homo sapiens			
US-09-750-240-10			
Query Match 98.2%; Score 3484.8; DB 10; Length 3552;			
Best Local Similarity 99.0%; Pred. No. 0;			
Matches 3517; Conservative 0; Mismatches 32; Indels 3; Gaps			
Qy	1	ATGTCATGTTTACTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAACACCTGGGGT 60	
Db	1	ATGTCATGTTTACTGGCTCTCTGGTCCCTAAAGTGGATGAACGGAACACCTGGGGT 60	
Qy	61	GAACGCAATGGGCAAGGCTTCGGGGCCCTGGCACTCGGGCAGGTGGCTTCTGCACG 120	
Db	61	GAACGCAATGGGCAAGGCTTCGGGGCCCTGGCACTCGGGCAGGTGGCTTCTGCACG 120	
Qy	121	CCCGCGTATATAGCTGCCTCCGGGATGCAGAGCCACCCAGCCGCCCTTCGGGGCCCC 180	
Db	121	CCCGCGTATATAGCTGCCTCCGGGATGCAGAGCCACCCAGCCGCCCTTCGGGGCCCC 180	
Qy	181	CTCTGGTGCCCTTGCAGAGTGAACCCCTTCATCCGAGGGGGCCGCCAGGCAAGGCAAG 240	
Db	181	CTCTGGTGCCCTTGCAGAGTGAACCCCTTCATCCGAGGGGGCCGCCAGGCAAGGCAAG 240	
Qy	241	GAGCTGGGGTTCGGGCACGTGGCCCTTGGGCTTCGAGGATACCGAGGTGACAACACACGCG 300	
Db	241	GAGCTGGGGTTCGGGCACGTGGCCCTTGGGCTTCGAGGATACCGAGGTGACAACACACGCG 300	



Db 2461 CTGCTGAGTCTCTGGCCAGCTCTGCTTCCCTGCACATCAGCAGCATCGGAAATTGGCC 2520  
QY 2518 ATGATCTTTGCTTTGGGGCTCATCTATTTGGTGTCTGCTGTGGTGTCCCGCAGCGCC 2577  
Db 2521 ATGATCTTTGCTTTGGGGCTCATCTATTTGGTGTCTGCTGTGGTGTCCCGCAGCGCC 2580  
QY 2578 ATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACC 2637  
Db 2581 ATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACC 2640  
QY 2638 TTTGATGGGTGAGCTTCCAGCTGACGGAGGGTGGCCCTCAAAATATATGACCCCTGTG 2697  
Db 2641 TTTGATGGGTGAGCTTCCAGCTGACGGAGGGTGGCCCTCAAAATATATGACCCCTGTG 2700  
QY 2698 ATTCTGCTGGTGTGTTGGCTGGCGCTGTATCTGCATGCTCAGCAGTGGAAATGAGTGC 2757  
Db 2701 ATTCTGCTGGTGTGTTGGCTGGCGCTGTATCTGCATGCTCAGCAGTGGAGTGCAGTGC 2760  
QY 2758 CGCTTAACTTCTCTGGAACCTACAGGCAACAGGGGAAAGAGGAGATGGAGGAGCTA 2817  
Db 2761 CGCTAGACTTCTCTGGAACCTACAGGCAACAGGGGAGAGAGATGGAGGAGCTA 2820  
QY 2818 CAGGCATACAAACCGGAGGTGCTGCATAAATCTGCCAAAGACGTGGCGCCCACTTC 2877  
Db 2821 CAGGCATACAAACCGGAGGTGCTGCATAAATCTGCCAAAGACGTGGCGCCCACTTC 2880  
QY 2878 CTGGCCGGGAGGCGCGCAATGATGAACCTACTATCAGTCGTGAGTGTGGTGTGTT 2937  
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Db 3001 GGTGTCGAGTGCCTGCGGTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC 3060  
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QY 3418 TACCAGTGGAGTGTGAGGGTGGTCAAGGTGAAGGGCAAGGGGAGATGACCACTAC 3477  
Db 3421 TACCAGTGGAGTGTGAGGGTGGTCAAGGTGAAGGGCAAGGGGAGATGACCACTAC 3480  
QY 3478 TTCTCAATGGGGGCCCCAGCAGTTTAAAGGGGCCAGGCCACAAATTCAGTGAAGGAGCC 3537  
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QY 3538 AAGGTGGGCACT 3549  
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Db 3541 AAGGTGGGCACT 3552  
RESULT 3  
US-10-201-000-1  
; Sequence 1, Application US/10201000  
; Publication No. US20020187540A1  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, James E.  
; APPLICANT: COR Therapeutics, Inc.  
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYL  
; FILE REFERENCE: 44481-5028-01-US  
; CURRENT APPLICATION NUMBER: US/10/201,000  
; CURRENT FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: US/09/474,076  
; PRIOR FILING DATE: 1999-12-12  
; PRIOR APPLICATION NUMBER: PCT/US98/13694  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/070,904  
; PRIOR FILING DATE: 1997-07-01  
; PRIOR APPLICATION NUMBER: 08/886,550  
; PRIOR FILING DATE: 1997-07-01  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4942  
; TYPE: DNA  
; ORGANISM: human type VI adenylyl cyclase  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (145)..(3648)  
US-10-201-000-1  
Query Match 98.0%; Score 3478.4; DB 9; Length 4942;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 3513; Conservative 0; Mismatches 36; Indels 3; Gaps 1;  
QY 1 ATGTCATGTTTGTAGTGGCTTCTGCTTAAAGTGGATGAACGGAAACAGCTGGGT 60  
Db 145 ATGTCATGTTTGTAGTGGCTTCTGCTTAAAGTGGATGAACGGAAACAGCTGGGT 204  
QY 61 GAACCAATGGGCAGAAAGCTTCCGGCGCGCTGGGACTCGGCAGGTGCTTCTGCACG 120  
Db 205 GAACCAATGGGCAGAAAGCTTCCGGCGCGCTGGGACTCGGCAGGTGCTTCTGCACG 264  
QY 121 CCCCCTATATGAGTGCCTCCGGGATGACAGCCAGCCAGCCAGCCAGCCAGCCAGCC 180  
Db 265 CCCCCTATATGAGTGCCTCCGGGATGACAGCCAGCCAGCCAGCCAGCCAGCCAGCC 324  
QY 181 CCTCGTGGCCCTGGCAGGATGACGCTTCCATCCGGAGGGCGGCGCCAGGAGGCAAG 240  
Db 325 CCTCGTGGCCCTGGCAGGATGACGCTTCCATCCGGAGGGCGGCGCCAGGAGGCAAG 384  
QY 241 GAGCTGGGCTGCGGCGAGTGGCCCTTGGGCTTCGAGGATACCGAGGTGACACGACAGCG 300  
Db 385 GAGCTGGGCTGCGGCGAGTGGCCCTTGGGCTTCGAGGATACCGAGGTGACACGACAGCG 444  
QY 301 GCGGAGCAGGCTGAGGTGGCGCCGAGCGGTCGCCAGGAGTGGCGATCCTGCTGGCGC 360  
Db 445 GCGGAGCAGGCTGAGGTGGCGCCGAGCGGTCGCCAGGAGTGGCGATCCTGCTGGCGC 504  
QY 361 CGTTTGTGTCAGTGTTCAGTGAAGCAGTTCGTTCCGCCAAGCTGGAGCGCTGTAC 420  
Db 505 CGTCTGGTGCAGGTGTTCAGTGAAGCAGTTCGTTCCGCCAAGCTGGAGCGCTGTAC 564  
QY 421 CAGCGTACTTTTCCAGATGAACAGAGCAGCTGACGCTGCTGTTGGTGGTGGTGGT 480  
Db 565 CAGCGTACTTTTCCAGATGAACAGAGCAGCTGACGCTGCTGATGGCGGTGCTGGT 624  
QY 481 CTGCTCACAGCGGTGCTGCTGGCTTTCCAAAGCCGACCCCGCCCTCAGCTGCCTAT 540  
Db 625 CTGCTCACAGCGGTGCTGCTGGCTTTCCAGCGCCCGCCCTCAGCTGCCTAT 684



[illegible]

## RESULT 4

RESOLUTION 4  
US-09-750-240-12  
; Sequence 12, Application US/09750240  
; Patent No. US20020103147A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammon, H. K.  
; APPLICANT: Insel, P. A.  
; APPLICANT: Ping, P. A.  
; APPLICANT: Post, S. R.  
; APPLICANT: Gao, M.  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART  
; TITLE OF INVENTION: FAILURE  
; FILE REFERENCE: 220002056723

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; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 3582
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified AC-VI
US-09-750-240-12

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Query Match 95.2% Score 3379.2 DB 10: Length 3582:

Best Local Similarity 97.4%; Pred. No. 0;  
Matches 3458; Conservative 88; Indels 6; Gaps 2;

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Qy	61	GAAGCAATGG	CAGAGCCGTCGCGCGCCGTGGCACATCGGCGACGTGCTTCTGCACG	120
Db	82	GAAGCAATGG	CAGAGCCGTCGCGCGCCGTGGCACATCGGCGACGTGCTTCTGCACG	141
Qy	121	CCCGCTATAT	GAGCTGCCCTCCGGGATCAGAGCCACCCAGCCCCACCCCTCGCGGCCCC	180
Db	142	CCCGCTATAT	GAGCTGCCCTCCGGGATCAGAGCCACCCAGCCCCACCCCTCGCGGCCCC	201
Qy	181	CTCTGGTGCC	CCCTGGCAGGATGACGCCCTTCATCCGAGGGCGGCCAGAGGCAAG	240
Db	202	CTCTGGTGCC	CCCTGGCAGGATGACGCCCTTCATCCGAGGGCGGCCAGAGGCAAG	261
Qy	241	GAGCTGGGGT	CGGGCAGTGGCCCTTGGAGTATCCAGGATACCGAGTGCACACGACAGCG	300
Db	262	GAGCTGGGGT	CGGGCAGTGGCCCTTGGAGTATCCAGGATACCGAGTGCACACGACAGCG	321
Qy	301	GGCGGACGCT	GAGGTGGCGCCGACGCGGTGCCAGGAGTGGCGCATCTCTGCTGGCG	360
Db	322	GGCGGACGCT	GAGGTGGCGCCGACGCGGTGCCAGGAGTGGCGCATCTCTGCTGGCG	381
Qy	361	CGTTTGGTGC	AGGTGTTCCTCAGTCCGAAGCAGTTCCTGTCGSCCAAGCTGGAGCGCCTGTAC	420
Db	382	CGTCTGCTGC	AGGTGTTCCTCAGTCCGAAGCAGTTCCTGTCGSCCAAGCTGGAGCGCCTGTAC	441
Qy	421	CAGCGGTAC	TTTTCAGATGAACAGAGCAGCGCTGACGCTGCTGTGTGGCGGTGCTGGTG	480
Db	442	CAGCGGTACT	TTTTCAGATGAACAGAGCAGCGCTGACGCTGCTGTGTGGCGGTGCTGGTG	501
Qy	481	CTGCTCACAG	GGGTGCTGCTGCTTTCCAGACCGCGCACCCCGCCGCTCAGCCTGCCTAT	540
Db	502	CTGCTCACAG	GGGTGCTGCTGCTTTCCAGCGCGCACCCCGCCGCTCAGCCTGCCTAT	561
Qy	541	GTGCACTGTT	GTGCGTGGCGCCGCTCTGTCGTTGGGGCTCATGTGTGTGTGTAACCGG	600
Db	562	GTGCACTGTT	GTGCGTGGCGCCGCTCTGTCGTTGGGGCTCATGTGTGTGTGTAACCGG	621
Qy	601	CATAGCTTCC	CGCAGGACTCCATGTGGGTGGTGAAGCTGGTGTGGGCATCTCTGGCG	660
Db	622	CATAGCTTCC	CGCAGGACTCCATGTGGGTGGTGAAGCTGGTGTGGGCATCTCTGGCG	681
Qy	661	GCAGTGCAG	TCTCGGGGCGCTTTCGACAGACACCCGACGCCCTCTCTCGGGCCCTTGG	720
Db	682	GCAGTGCAG	TCTCGGGGCGCTCTCGACAGACCCGCGCAGCCCCCTCTCTCGGGCCCTTGG	741

Qy	721	TGCCCTGTGTTCTTTGTATACATCGCATACAGCTCTCCCCATCCCGCATCGGGCTGCC	780
Db	742		
Qy	781	GTCTCTACGGCGCTGGCGCTCTCCACCTTGCATTGTATGCTTGGCTGGCACTTAAACCGT	840
Db	802	GTCTCTACGGCGCTGGCGCTCTCCACCTTGCATTGTATGCTTGGCTTGGCACTTAAACCGT	861
Qy	841	GGTGATGCCTTCTCTGGAAGCAGCTCGGTGCCAATGCTGCTGTTCCTCTGCACCAAC	900
Db	862	GGTGATGCCTTCTCTGGAAGCAGCTCGGTGCCAATGCTGCTGTTCCTCTGCACCAAC	921
Qy	901	GTCAATTAGCATCTGCACACACTATCCAGCAGAGTGTCTCAGCGCCAGGCGCTTTCAGGAG	960
Db	922	GTCAATTGGCATCTGCACACACTATCCAGCAGAGTGTCTCAGCGCCAGGCGCTTTCAGGAG	981
Qy	961	ACCCGAGATTACATCCAGGCGCGGCTCCACCTGCAGCATGAGAAATCGCGCAGCAGAGCGG	1020
Db	982	ACCCGCGTTTACATCCAGGCGCGGCTCCACCTGCAGCATGAGAAATCGCGCAGCAGAGCGG	1041
Qy	1021	CTGCTGCTGTGCGTATGTCCTGGAAGCAGCTCGGTGCCATGGAATGAAAGAGACATCAACACA	1080
Db	1042	CTGCTGCTGTGCGTATGTCCTGGAAGCAGCTCGGTGCCATGGAATGAAAGAGACATCAACACA	1101
Qy	1081	AAAAAGAAAGAC---ATGTTCCACAAGACTCTACATACAGAAAGCATGACAATGTCAAGATC	1137
Db	1102	AAAAAGAAAGACATGATGTTCCACAAGATCTACATACAGAAAGCATGACAATGTCAAGATC	1161
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Db	1162	CTGTTTGCAGACATTTGAGGCTTTCACGAGCTTGGCATCCCATGTCGACTGGCAGGAGCTG	1221
Qy	1198	GTATGACCCCTGAATCAGCTCTTTGCCGGTTTGACAAGCTGGCTGGGAGAAATCACTGC	1257
Db	1222	GTATGACCTTGAATCAGCTCTTTGCCCGTTTGACAAGCTGGCTGGGAGAAATCACTGT	1281
Qy	1258	CTGAGGATCAAGATCTTGGGGACTTTACTACTGTGTGTCAGGGCTGCCGAGGCCCGG	1317
Db	1282	CTGAGGATCAAGATCTTAGGAGACTTTACTACTCGTGTGTCAGGGCTGCCGAGGCCCGG	1341
Qy	1318	GCGACCATGCCACATCGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG	1377
Db	1342	GCAGATCACGCCACATCGTGTGGAGATGGGGGTAGACATGATCGAAGCCATCTCGCTG	1401
Qy	1378	GTACGTGAGTGCAGGTGTAATGTGAACATGCGCGTGGCATCCACAGCGGCGCGTG	1437
Db	1402	GTGCGTAGGTAAACAGGTGTAACGTGAACATGCGTGTGGCATCCACAGCGGAGCTGTG	1461
Qy	1438	CACGTGGCGCTCCTTGGCTTGGGAAATGGCAGTTCGATGTGTGGTCCATGATGTGACC	1497
Db	1462	CATTGGGCGCTCCTTGGCTTACGAAATGGCAATTTGATGTCTGGTCAAAAGATGTGACC	1521
Qy	1498	CTGGCCAAACCACATGGAAGCAGGAAGCGGGCTGGCCCATCCACATCACTCGGGCAACA	1557
Db	1522	CTGCTAAACCACATGAGGCGCGGGGC--GGCCGGCGCATCCACATCACTCGGGCTACA	1578
Qy	1558	CTGCAGTACTGAAACGGGACTACGAATGGCAGCAGCGCCGTGTGGCAGCGCAACGCG	1617
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Db	1639	TACCTCAAGGAGCATGTGACCTTTCTCATCTTGGCGCCAGCCAAAACGGAAA	1698
Qy	1678	GAGGAAAGGCATGCTGGCCAAAGCTGCAGCGACTCGGGCCAACTCCATGGAGGGCTG	1737
Db	1699	GAGGAAAGGCCATGCTGGCCAAAGCTTCAGCGGACACGGGCCAACTCCATGTAAGGACTG	1758
Qy	1738	ATGCCCGGATGGTTCCTGATCGTGCCTTCTCCGGACCAAGGACTCCAAGGCGCTCCCG	1797
Db	1759	ATGCCCGGCTGGGTTCCTGAACCGTCCCTTCTCCCGGACCAAGGACTCTAAGGCATTCGCG	1818

QY	1798	CAGATGGCATTTGATGATTCACCAAGAACAACCGGGGACCCCAAGATGCCCTGAACCCCT	1857
DB	1819	CAGATGGGCATTTGATGATTTACCAAGAACAACCGGGGTGCCCAAGATGCTCTGAACCCCT	1878
QY	1858	GAGATGAGGTGGATGAGTTCTGTACCGCTGCATCGATGCCCGCAGCATTTGATCAGCTG	1917
DB	1879	GAAGATGAGGTGGATGAGTTCTTGGCCGAGCGCATCGATGCCCGCAGCATTTGATCAGCTG	1938
QY	1918	CGGAAGGACCATGTGGCCGGTTTTTGTCTCACTTCCAGAGAGAGGATTTTTGAGAAGAAG	1977
DB	1939	CGGAAGGACCATGTGGCCGGTTTTTGTCTCACTTCCAGAGAGAGGATCTTTGAGAAGAAG	1998
QY	1978	TACTTCCGGGAAGTGGATCCCCGCTTCGAGCGCTACGTTGGCTGTGCCCTGTGGTCTTC	2037
DB	1999	TACTTCCGGGAAGTGGATCCCCGCTTCGAGCGCTACGTTGGCTGTGGCCCTGTGGTCTTC	2058
QY	2038	TGCTTCATCTGCTCATCCAGCTTCTAAATTTTCCACACATCCACCGCTGATCGTTGGGANTT	2097
DB	2059	TGCTTCATCTGCTCATCCAGCTTCTCATCTTCCACACACTCCACCGCTGATCGTTGGGATC	2118
QY	2098	TATGCCAGCATCTTCTGCTGCTGCTTAATCAACCGCTGCTGATCTGTGCTGTGCTACTCCTGT	2157
DB	2119	TATGCCAGCATCTTCTGCTGCTGCTTAATCAACCGCTGCTGATCTGTGCTGTGCTACTCCTGT	2178
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DB	2179	GGTTCTCTGTTCCTTAAGGCGCTGCAACGCTCTGTCCCGCAGCATTTGCCGCTCACGGGCA	2238
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DB	2359	CCTGCTGACATCACTGCTGCGCACCTGTGCAGCAGCTCAATTTACTCTCTGGGCGCTGGATGCT	2418
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DB	2659	TTTGATGGGTGGACTGTCCAGCTCGAGGGAGGGTGGCCCTCAATATATGACCCCTGTGTG	2718
QY	2698	ATTCTGCTGTGTTTGGCTGGCGCTGATCTGCATGCTCAGCAGGTGGAATCGACTGCC	2757
DB	2719	ATTCTGCTGTGTTTGGCTGGCGCTGATCTGCATGCTCAGCAGGTGGAATCGACTGCC	2778
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DB	2779	CGCTTAGACTTCTCTGGAACTTACAGGCAACAGGGGAAAAAGAGGAGATGGAGAGCTA	2838
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DB	2839	CAGCATACAAACCGGAGGCTGTGCATACATTTCTGCCCAAGGAGCTGGCGGCCACTTC	2898
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Db 2899 CTGGCCGGAGGCGCCCAATGATGAATCTACTATCAGTCGCTGAGTGTGGCTGTT 2958  
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QY 2998 GGTGCCGAGTGCCTGCGGCTGCCTCAACGAGATCATCGCTGACTTTTGATGAGATTATCAGC 3057  
Db 3019 GGTGTCGAGTGCCTGCGGCTGCTCAAGGAGATCATCGCTGACTTTTGATGAGATTATCAGC 3078  
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Db 3559 AAGTGGGCCT 3570

RESULT 5  
US-09-750-240-3  
; Sequence 3, Application US/09750240  
; Patent No. US20020103147A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammon, H. K.  
; APPLICANT: Insel, P. A.  
; APPLICANT: Ping, P.  
; APPLICANT: Post, S. R.  
; APPLICANT: Gao, M.  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART  
; FILE REFERENCE: FAILURE  
; CURRENT APPLICATION NUMBER: US/09/750,240  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/472,667  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: US 09/008,097  
; PRIOR FILING DATE: 1998-01-16  
; PRIOR APPLICATION NUMBER: US 08/924,757  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/048,933  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: US 08/708,661  
; PRIOR FILING DATE: 1996-09-05

; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1812  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-750-240-3  
Query Match 51.0%; Score 1808.4; DB 10; Length 1812;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1809; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 636 TAACTGTTGCTGCGGATCCTGCGGAGTCAGGTGCGGGGCGCTTTCGAGCAGACCC 695  
Db 3 TAACTGTTGCTGCGGATCCTGCGGAGTCAGGTGCGGGGCGCTTTCGAGCAGACCC 62  
QY 696 GCGAGCCCTCTGCGGGCCTCTGGTCCCTGTTTGTATATACATGACAGCT 755  
Db 63 GCGAGCCCTCTGCGGGCCTCTGGTCCCTGTTTGTATATACATGACAGCT 122  
QY 756 CTTCCCATCCGATCGGGCTGCCGTCCTCAGGGCTGGGCTCTCCACCTTGCATTT 815  
Db 123 CTTCCCATCCGATCGGGCTGCCGTCCTCAGGGCTGGGCTCTCCACCTTGCATTT 182  
QY 816 GATCTTGGCTGGCAACTTAACGTTGATGCTTCTCTGGAAGCAGCTCGGTGCCAA 875  
Db 183 GATCTTGGCTGGCAACTTAACGTTGATGCTTCTCTGGAAGCAGCTCGGTGCCAA 242  
QY 876 TGTCTGCTCTTCTCTGCAACAGTCATTAGCATCTGCACACACTATCCAGCAGGT 935  
Db 243 TGTCTGCTCTTCTCTGCAACAGTCATTAGCATCTGCACACACTATCCAGCAGGT 302  
QY 936 GTCTCAGCCGAGCCCTTTCAGAGACCCGAGTTACATCCAGGCCGCGCTCCACCTGCA 995  
Db 303 GTCTCAGCCGAGCCCTTTCAGAGACCCGAGTTACATCCAGGCCGCGCTCCACCTGCA 362  
QY 996 GCATGAAATCGGAGGAGCGGCTGCTGCTGGTATTGCCCCAGCAGCTTGCAT 1055  
Db 363 GCATGAAATCGGAGGAGCGGCTGCTGCTGGTATTGCCCCAGCAGCTTGCAT 422  
QY 1056 GGAGATGAAAGAGACATCAACACAAAAAAGAGACATGTTCCACAAGATCTACATACA 1115  
Db 423 GGAGATGAAAGAGACATCAACACAAAAAAGAGACATGTTCCACAAGATCTACATACA 482  
QY 1116 GAAGCATGAAATGTCAGCATCTGTTTGCAGACATTTAGGGCTTCACCGCTGGCATC 1175  
Db 483 GAAGCATGAAATGTCAGCATCTGTTTGCAGACATTTAGGGCTTCACCGCTGGCATC 542  
QY 1176 CCAGTGCACCTGCGAGGAGCTGGTGCATGACCTGAATGAGCTTTTCCCGGTTTGACAA 1235  
Db 543 CCAGTGCACCTGCGAGGAGCTGGTGCATGACCTGAATGAGCTTTTCCCGGTTTGACAA 602  
QY 1236 GCTGGCTGCGGAGAACATCACTGCTGAGGATCAAGATCTTGGGGACTGTTACTACTGT 1295  
Db 603 GCTGGCTGCGGAGAACATCACTGCTGAGGATCAAGATCTTGGGGACTGTTACTACTGT 662  
QY 1296 GTCAGGGCTCCCGAGGCGCGGCGGACCATGCCACTGCTGTGTGAGATGGGGTAGA 1355  
Db 663 GTCAGGGCTCCCGAGGCGCGGCGGACCATGCCACTGCTGTGTGAGATGGGGTAGA 722  
QY 1356 CATGATTGAGGCCATCTCGCTGGTGTACGTGAGGTGACAGGTGTGAATGTGAACATGCCGT 1415  
Db 723 CATGATTGAGGCCATCTCGCTGGTGTACGTGAGGTGACAGGTGTGAATGTGAACATGCCGT 782  
QY 1416 GGGCATCCACAGCGGCGCTGCACTGCGGCTCTTGGTGTGCGGAAATGGCAGTTGCA 1475  
Db 783 GGGCATCCACAGCGGCGCTGCACTGCGGCTCTTGGTGTGCGGAAATGGCAGTTGCA 842  
QY 1476 TGTGTGTTCAATGATGTACCTGTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 1535  
Db 843 TGTGTGTTCAATGATGTGACCTGTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 902  
QY 1536 CATCCACATCACTCGGCAACACTGCACTACCTGAACGGGGACTACGAAGTGGAGCCAGG 1595









Db 3490 CAGCTCGAGAAGATCAAGACATCGGCAGACCTACATGGCTCGGCTCCAGCAC 3549  
 QY 3133 AGCACTACGATCAGGTGGCGCGCTCCACATCACTTGCCCTGGCTAGCTAGCCATCGG 3192  
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 QY 3193 CTGATGGAGCAGATGAAGCAGACATCAATGAGCAGCTCTTCAACAATTTCCAGATGAAGATT 3252  
 Db 3610 CTGATGGAGCAGATGAAGTACATCAATGAGCAGCTCTTCAACAATTTCCAGATGAAGATC 3669  
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 Db 3670 GGCTCAACATCGGCCCGCTGCTGGCCGGGTGTAGGGGCACGAAAGCCCTCAGTACGAC 3729  
 QY 3313 ATCTGGGGGAACACAGTGAATGCTCTAGTGTATGGACACGGGGTCCCGGACCGA 3372  
 Db 3730 ATCTGGGGCAATACCGTGAACGTGGCCAGCCGATGGACACACCGGTGTATCCGACCGC 3789  
 QY 3373 ATCCAGGTGACCACGGAGCTGTACCAGTTCTAGCTGCCAAGGCTACCACTTCTCAATGGGGC 3432  
 Db 3790 ATCCAGGTCAACACAGACATGTACCAGTTCTAGCTGCCAAGGCTACCACTTCTCAATGGAGTC 3849  
 QY 3433 CGAGGGGTGCTCAAGTGAAGGGCAAGGGGAGATGACCACTTCTCAATGGGGC 3492  
 Db 3850 CGGGGGCTGCTCAAGGTCAAGGGCAAGGGGAGATGATGACCTTCTTCTCAATGGAGG 3909  
 QY 3493 CCC 3495  
 Db 3910 CCC 3912  
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 ; Sequence 23, Application US/09989442  
 ; Publication No. US20030013649A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; FILE REFERENCE: PJ208  
 ; CURRENT APPLICATION NUMBER: US/09/989,442  
 ; CURRENT FILING DATE: 2001-11-21  
 ; PRIOR APPLICATION NUMBER: 60/179,065  
 ; PRIOR FILING DATE: 2000-01-31  
 ; PRIOR APPLICATION NUMBER: 60/180,628  
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Query Match 16.5%; Score 586; DB 9; Length 837;  
Best Local Similarity 85.3%; Pred. No. 1.7e-135;  
Matches 652; Conservative 1; Mismatches 111; Indels 0; Gaps 0;  
  
QY 2732 ATGCTCAGCAGGTGGAATCGACTGCCGCGCTAAACTTCTCTGGAACATACAGGCAACAG 2791  
Db 1 ACGCCAGCAGGTGGAGTCCACTGCCGCGCTCGACTTCTCTTGAGAGCTGCAGGCCACAG 60  
  
QY 2792 GGGAAAAAGAGGAGATGGAGGAGCTACAGGCATACAAACCGAGGCTGCTGCATACATTC 2851  
Db 61 AGGAGATAGAGGAGATGGAGGAGCTGCAGGCTACAAACCGGCGCTGCTGCACACATCC 120  
  
QY 2852 TGCCCAAGGAGTGGCGGCCACTTCTTGCCCGGAGCGCCGAATGATGAATCTACT 2911  
Db 121 TGCCCAAGGAGTGGCGGCCACTTCTTGCCCGGAGCGCCGAATGATGAATCTACT 180  
  
QY 2912 ATCAGTCGTGTGAGTGTGCTGTTATGTTGCTCCATTGCCAATCTCTCAGTTCT 2971  
Db 181 ATCAGTCGTGTGAGTGTGCTGTTATGTTGCTCCATTGCCAATCTCTCAGTTCT 240  
  
QY 2972 ATGTGGAGCTGGAGGCAAAACAATGAGGCTGCCGAGTGCCTGCGGCTGCTCAACGAGATCA 3031  
Db 241 ACGTTGAGCTGGAGGCCAACAAACGAGGCTGTCGAGTGCCTGCGGCTACTCAATGAGATCA 300  
  
QY 3032 TCCTGACTTTGATGAGATTATCAGCGAGGAGCGGTTCCGGCAGCTGGAAGAATCAAGA 3091  
Db 301 TCCTGACTTTGATGAGATTATCAGCGAGGAGTCCGTTCCGGCAGCTGGAAGAATCAAGA 360  
  
QY 3092 CGATTGGTAGCACCCTACATGCTGCCCTCAGGCTGGAAGCCAGCACCTACGATCAGTGG 3151  
Db 361 CCATCGCAGCACCTACATGCTGCCCTCAGGCTTCAAGACTCTACCTACGCAAGTGG 420  
  
QY 3152 GCCGCTCCCATCAGTCCCTGGCTGACTACGCCCTACGCCCTCATGGAGCAGATGAAGC 3211  
Db 421 GCAAGACCCACATCAAGGCACTGSCCGACTTTGCCATGAAGCTGAGCCAGATGAAGT 480  
  
QY 3212 ACATCAATGAGCACTCCTTCAACAAATTTCCAGATGAAGATGGGCTGAACATGGGCCAG 3271  
Db 481 ACATCAATGAGCACTCCTTCAACAAATTTCCAGATGAAGATGGGCTGAACATGGGCCAG 540  
  
QY 3272 TCGTGGCAGGTGTCATCGGGCTCGGAAGCTCGAGATGATGACATCTGGGGGAACACAGTGA 3331  
Db 541 TGGTGGCGGGGTGATAGGGGCAGCAAGGCTCAGTACGACATCTGGGGCAATACCGTGA 600  
  
QY 3332 ATGTCTCTAGTTCGTATGGACAGCAGCGGGGTGCCCGACCGAATCCAGGTGACCCAGACC 3391  
Db 601 ACGTGGCCAGCCGATGGACAGCAGCCGGTGTACCCGACCGCTACAGGTCAACACAGACA 660  
  
QY 3392 TGTACCAAGTTCTAGCTGCCAAGGGCTACCAAGTGGAGTGTCCAGGGGTGGTCAAGGTGA 3451  
Db 661 TGTACCAAGTGTCTGGCTGCCAAGACAGTACCAGTGGAGTGGCGGKGGTGGTCAAGGTGA 720  
  
QY 3452 AGGCAAGGGGAGATGACCAACCTACTTCTCAATGGGGCCCC 3495  
Db 721 AGGCAAGGGGAGATGATGACCTACTTCTCAATGGGGCCCC 764



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Query Match 14.9%; Score 529.6; DB 9; Length 915;  
Best Local Similarity 85.2%; Pred. No. 1.6e-121;  
Matches 600; Conservative 2; Mismatches 101; Indels 1; Gaps 1;

QY	2792	GGGAAAAGGAGATGGAGGAGCTACAGGCATCAACCCGGAGGCGTCTGCATACAAATTC	2851
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QY	2852	TGCCCAAGGACGTGGCGGCCACTTCCTGGCCGGGAGCGCGCAATGATGAACCTTACT	2911
Db	71	TGCCCAAGGACGTGGCGGCTCACTTCCTGGCCGGGAGCGCGGCATGATGAGCTCTACT	130
QY	2912	ATCAGTCGTGTGAGTGTGGCTGTATGTTTGGCTTCCATTGCCAACTTCTCTGAGTTCT	2971
Db	131	ATCAGTCCTGTAGTGTGGCGGTCATGTTCCGCTCCCATGCCAACTTCTCCGAGTTCT	190
QY	2972	ATCTGAGCGTGGAGGCAACAATGAGGTTGCCGAGTGCGTGGGCTGCTCAACGAGATCA	3031
Db	191	ACGTTGAGCTGGAGGCCAACACGAGGGTGTGAGTGGCTCGGGCTACTCAATGAGATCA	250
QY	3032	TCGCTGACTTTGATGAGATTATCAGCGAGGAGCGGTTCCGGCAGCTGGAAAAGATCAAGA	3091
Db	251	TCGCTGACTTTGATGAGATCATCAGCGAGGATCGGTTCCGGCAGCTGGAGAAGATCAAGA	310
QY	3092	CGATTGGTAGCACCTACATGGCTGCGCTCAGGGCTGAACCGCAGCACCTACGATCAGGTGG	3151
Db	311	CCATCGGAGCACCTACATGGCTGCGCTCCGGGCTCAACGACTCTACCTACGACAAGTGG	370
QY	3152	GC CGCTCCACACATCACTGCGCTGGCTGACTACGCCATCGGCTCATGGAGCAGATGAAGC	3211
Db	371	GCAAGACCACATCAAGGCACCTGGCCGACTTTGCCATGAAGCTGATGGACCAGATGAAGT	430
QY	3212	ACATCAATGAGCACCTCTTCAACAATTTCCAGATGAAGATTGGGCTGAACATGGGCCCGAC	3271
Db	431	ACATCAATGAGCACCTCTTCAACAACATTTCCAGATGAAGATCGGCTCAACATGGGCCCGC	490
QY	3272	TCGTGCGAGGTGTCACTGGGGCTCGGAAGCCACAGATATGACATCTGGGGGAACACAGTGA	3331
Db	491	TGCTGGCCGGGTGATAGGGGCACGAAGCCCTCAGTAGCAGCATCTGGGGCAATACCTGTA	550
QY	3332	ATGTTCTTAGTCGTATGGACACACGGGGTCCCGGACCGGAATCCAGGTGACACAGGACC	3391
Db	551	ACGTGGCCAGCCGCATGGACACACCGGTGTACCCGACCGCATCCAGGTCCACACAGACA	610
QY	3392	TGTTACCAAGTTCCTAGCTGCCAAGGGCTACCAAGCTGGAGTGTCTGAGGGTGGTCAAGTGA	3451
Db	611	TGTTACCAAGTTCCTAGCTGCCAACACGTACCAAGCTGGAGTGGCGGGGCGTGGTCAAGTGA	670
QY	3452	AGGGCAAGGGGAGATGACCACCTACTTCTCTCAATGGGGGGCCCC	3495
Db	671	AGGGCAAGGGGAGATGATGACCTACTTCTCTCAATGGAGGGCCC	714

## RESULT 10

```

US-10-121-911-2
; Sequence 2, Application US/10121911
; Patent No. US20020164632A1
; GENERAL INFORMATION:
; APPLICANT: kapeller-Libermann, Rosana
; TITLE OF INVENTION: 21529, A NOVEL ADENYLATE CYCLASE
; FILE REFERENCE: 5800-47
; CURRENT APPLICATION NUMBER: US/10/121,911
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US/09/412,210
; PRIOR FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3518
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: 21529 adenylate cyclase
; NAME/KEY: CDS
; LOCATION: (247)...(3480)

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QY 1467 GCATTTTCATGTGGTCCATGATGATGACCTTGGCCCAACCATGGAAGAGGAGCGG 1526  
DB 1398 GCATACAGCTTTGGTTCACATGATGTACACTGGCTACCATCATGAGGAGCGGCTGT 1457  
QY 1527 GGTGGCGCATCCACATCACTCGGGCAACACTGCAGTACCTGAACGGGGACTACGAAGT 1586  
DB 1458 ACCAGGGCGAGTGCACATCACAGGGCTACCTTGGCCCTGTGGCAGGGGTATGCTGT 1517  
QY 1587 GGAGCCAGGCGGTGGTGGCAAGCGCAACGCGTACCTCAAGGAGCAGCAGCATTTGAGACTTT 1646  
DB 1518 GGAGCAGCAGCATGGAGCATCGGACCCCTACCTTCGGGAGCTAGGGAGCCCTACCTA 1577  
QY 1647 CTTATCTTGGGCGCCAGCCAGAAACGAAAGAGAGAGAAAGCATGCTGGCCCAAGCTGCA 1706  
DB 1578 TCTGGTCACTATCCACGGGAGAGGAGGAGATGAGAAGGCCACTGCGAGGAGGCTTGTCT 1637  
QY 1707 GCGGACTCGGCGCAACTCCATGGAAGGCTGATGCCGGATGGGTTCCTGATCTGTCGCTT 1766  
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QY 1827 CAACGGGGGACCCAAAGATGCCCTG -- AACCTGAGGATGAGGTGA -TGAGTTCCCTGAG 1883  
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QY 1884 CCGTGCCATGATGCCCGACATGATCACTGCGGAGGAGCACTGTCGCGCGTCTTTT 1943  
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QY 1944 GCTCACTTCCAGAGAGAGATTTTGAGAAGAACTACTCCCGGAAGTGGATCCCGCGTT 2003  
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QY 2004 CGGAGCTTACGTGGCTGTGCCCTGTGGTCTTCTGTCTATCTGCTTCATCCAGCTTCT 2063  
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QY 2064 AATTTTCCACACTCCACCTGATCTTGGGATTTATCCAGCACTTCTCTGCTGCTGCT 2123  
DB 1998 CAATACTATGAAGCTGCACCTTCCCTGTTTTTCTTCCAACTTTCATCCAGATGCT 2057  
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QY 2244 CTTCTGTCTGTGTTTACTTCTGCATTTGCCAATGTTCACTTCACTGTAACCCACACCCCAT 2303  
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QY 2364 GCAGAGCTCAATTTACTCTCTGGGCTGGATGCTCCCTGTGTGAGGACCACTGCCCCAC 2423  
DB 2295 CTTCTTCCAAACATCATCAGACTGCCCTTTTCCAAAGCTCCCAATGTGTCTCCATGATTC 2354  
QY 2424 CTGAGCTTTTCTGAGGTGCCATCGGGAAACATGCTGCTGAGTCTCTTTGGGCCAGCTGT 2483  
DB 2355 CAACCTCTCTCGGAGCTCCCTGGGTCTCTGCCCTCTCATAGTGTCCCATCTCCATGCA 2414

QY 2484 CTTCTGCACATACGACGATCGGGAAGTGTGGCCATGATCTTTGTCTTTGGGCTCATCTA 2543  
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QY 2784 GGCAACAGGGGAAAGAGAGAGTGGAGGAGCTACAGGCATACAAACCGGAGGCTCTGCA 2843  
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QY 3024 CGAGATCATCTGACTTTTGTAGTATGATATCAGCAGAGGCGGTTCGCGCAGCTGGAAAA 3083  
DB 2955 TGAGATAATTGCTGATTTTGTAGTGTCTCTCCAAGCCCAAGTTTCACTGGGTGAGAA 3014  
QY 3084 GATCAAGACGATTTGTAGCACCTTACATGGCTGCTCAGGGCTGAGACGCCAGCAC -- 3137  
DB 3015 GATCAAGACCATCGGCAGCACCTTACATGGCAGCCACAGGCTTAATGCGCACCTCTGAGCA 3074  
QY 3138 -----CTAGATCAGTGGGCGCTCCACATCACTGCGCTGCTGACTACGC 3185  
DB 3075 GGATGCAACACAGATGTGAACGAGTGCAGCCACCTTGGCACTATGGTGAATTTGC 3134  
QY 3186 CATCGGCTCATGGAGCAGATGAAGCAGATCAATGAGCACTCTTCAACAATTTCCAGAT 3245  
DB 3135 CGTGGCCCTGGGCTTAAGCTGGAGTTCATCAACAAGCATTCATTCAACAACACTCCGCT 3194  
QY 3246 GAAGATTGGGCTGAACATGGGCCAGTCTGGCAGGTGATCGGGGCTCGGAAGCCACA 3305  
DB 3195 GCGAGTGGGTTGAACCATGGACCCGTAGTACCTGAGTTATTGGGCGCCCAAGAACCGCA 3254  
QY 3306 GTATGACATCTGGGGAACACAGTGAATGCTCTAGTGTATGGACACACGCGGTGCC 3365  
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QY 3366 CGACGAATCCAGGTGACCGAGCTGTACAGGTTCTAGCTGCCAAGGCTACACGCT 3425  
DB 3315 TGGCAAAATCCAAGTGAAGTGAAGGAGAGGAGATGACAGTCCCTGGGCTACACCTG 3374  
QY 3426 GGAGTGTGCGGGGTGCTCAAGGTGAAGGCAAGGGGAGATGACCACTTCTCTCTCAA 3485  
DB 3375 CTACAGCGGGGTGTCTCAAGGTGAAGGCAAGGGGAGGCTCTGTGACCTACTTCTCTGAA 3434

RESULT 11

US-09-925-297-352

; Sequence 352, Application US/09925297

; Patent No. US20020081659A1





Db 1758 AAGGATTCACCCCTGGGCTCAATGGGCACTGACAGGCTGC--CCCTGGTGCCTTCCAAGTA 1815  
QY 2685 TATGACCCCTGATCTGCTGCTGTTGGCTGGGCTGTACTGCTGCTCAGCAGGT 2744  
Db 1816 CTCTATGACGGTGATGGTGCTCATGATGCTCAGCTTCTACTACTTCTCCGCCACGT 1875  
QY 2745 GGAATGAGCTGCCCGCTAAACTTCTCTGGAACACTACAGCAACAGGGGAAAAAGAGGA 2804  
Db 1876 AGAAAACTGGCAGGACACTTTCTTGTGGAAGATTGAGGTCCACGACCAAGGAACG 1935  
QY 2805 GATGGAGGAGCTACAGCATACACCGGAGGCTGCTGCATAACATCTCTGCCCAAGGACGT 2864  
Db 1936 TGTCTATGAGATCGAGCTGGAGACGAGGCTTGGTCACCAACATGTTGCTCAGCAGCT 1995  
QY 2865 GCGGGCCCACTTCTCGCCCGGAGCGCCGCAATGATGACTACTACTCAGTCTGTGA 2924  
Db 1996 GGCAGCCCAATTCCTGGGTCGAAGAGAGATGAGGAGCTGTATAGCCAGACGTATGA 2055  
QY 2925 GTGTGTGGTGTATGTTTGGCTCCCATTTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGA 2984  
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Db 2116 CATCAACAATGGTGATTGAGTGCTGCGTTTCTCCTCAATGAATCATCTCGATTTTGA 2175  
QY 3045 TGAGATTATCAGGAGAGGCGGTTCCGGCAGCTGGAAAGATCAAGACGATTTGGTAGCAC 3104  
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QY 3306 GTATGATCTGCGGGAACACAGTGAATGCTCTCTAGTCGTATGG-ACAGCAGCGGGGTCC 3364  
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QY 3365 CCAGCCGAATCCAGGTGACACCGGA 3389  
Db 2536 TGGGCAACATTCAGGTGGAGAAGGA 2560

RESULT 12  
US-09-750-240-1  
; Sequence 1, Application US/09750240  
; Patent No. US20020103147A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, H. K.  
; APPLICANT: Insel, P. A.  
; APPLICANT: Ping, P.  
; APPLICANT: Post, S. R.  
; APPLICANT: Gao, M.  
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART  
; FILE REFERENCE: 220002056723  
; CURRENT APPLICATION NUMBER: US/09/750,240  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 09/472,667  
; PRIOR FILING DATE: 1999-12-27

; PRIOR APPLICATION NUMBER: US 09/008,097  
; PRIOR FILING DATE: 1998-01-16  
; PRIOR APPLICATION NUMBER: US 08/924,757  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: US 60/048,933  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: US 08/708,661  
; PRIOR FILING DATE: 1996-09-05  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 314  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(314)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-750-240-1  
  
Query Match 8.3%; Score 295.2; DB 10; Length 314;  
Best Local Similarity 97.1%; Pred. No. 1.2e-63;  
Matches 300; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
  
QY 1 ATGTCATGTTTGTAGTGGCTCTCTGCTTAAAGTGGATGAACGGAACAGCCTGGGT 60  
Db 1 ATGTCATGTTTGTAGTGGCTCTCTGCTTAAAGTGGATGAACGGAACAGCCTGGGT 60  
  
QY 61 GAACGCAATGGGAGAGGCTTCGCGGCGCGCTGGGCACTCGGCAAGTGGCTTTCGACG 120  
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QY 121 CCCCCTATATGAGTGCCTCCGGGATGACAGCCACCCAGCCCTGCGGGCCCC 180  
Db 121 CCCCCTATATGAGTGCCTCCGGGATGACAGCCACCCAGCCCTGCGGGCCCC 180  
  
QY 181 CTTCTGGTGCCTTCGCGGATGACGCTTTCATCCGAGGGCGCGCCAGCAAGGCAAG 240  
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Db 241 GAACTGGGCTGGGGCAGTGGGCTTCGAGATACCGAGTGAACAGCAGCG 300  
  
QY 301 GCGGGGACG 309  
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RESULT 13  
US-09-915-582-11  
; Sequence 11, Application US/09915582  
; Patent No. US20020120103A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 17 Human Secreted Proteins  
; FILE REFERENCE: PS723P1  
; CURRENT APPLICATION NUMBER: US/09/915,582  
; CURRENT FILING DATE: 2001-07-27  
; PRIOR APPLICATION NUMBER: PCT/US01/01431  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/231,968  
; PRIOR FILING DATE: 2000-09-12  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 1180  
; TYPE: DNA  
; ORGANISM: Homo sapiens



QY 2969 TCATGTGGAGCTGGAGGCAACAATGAGGGTGCCCGAGTGCCCTGCGGCTGCTCAACGAGA 3028

Dbb 5895 ACTGCCAAGTTTCAGGG 5879



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model  
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Gapop 10.0 , Gapext 1.0  
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Maximum Match 100%  
Listing first 45 summaries

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- 2: em\_esthum.\*
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- 7: em\_estro.\*
- 8: em\_hic.\*
- 9: gb\_est1.\*
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- 11: gb\_hic.\*
- 12: gb\_est3.\*
- 13: gb\_est4.\*
- 14: gb\_est5.\*
- 15: em\_estfun.\*
- 16: em\_estom.\*
- 17: gb\_gss.\*
- 18: em\_gss\_hum.\*
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- 25: em\_gss\_other.\*
- 26: em\_gss\_pro.\*
- 27: em\_gss\_rod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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30	387.8	10.9	417	12	BE840138
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42	320.4	9.0	821	13	BI257644
43	320.2	9.0	2661	11	BC028085
44	311	8.8	567	13	BI739363
45	305.8	8.6	824	13	BI257519

ALIGNMENTS

RESULT 1	BM811640	1039 bp	mrna	linear	EST 05-MAR-2002
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DEFINITION	5', mRNA sequence.				
ACCESSION	BM811640				
VERSION	BM811640.1	GI:19128463			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/				
TITLE	1 (bases 1 to 1039)				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Invitrogen CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov Plate: LLM12712 row: 1 column: 10 High quality sequence stop: 644.				
FEATURES	Location/Qualifiers				
source	1. .1039				



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Qy	2366	AGCAGCTCAATTACTTCTGCGGCTTGGATGCTCCCTCTGTGTAGGGGCACCAATGCCACCT	2425
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Qy	2486	TCCTGCACATCAGCAGCATCGGGAAGTTGGCCATGATCTTTGCTTTGGGGTCACTATT	2545
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Qy	2666	GGAGGCT - GGCCCTCAAATATATGACCCCTGTGATTCCTGCTGGTGTTTGCGCTGGCCTG	2724
Db	641	GGAGGCTGGCCCTCAAATATATGACCCCTGTGATTCCTGCTGGTGTTTGCGCTGGCCTG	700
Qy	2725	TATCTGATGCTCAGCAGGTGGAACTGCACTG - CCGCCCTAAACTTCCCTCTGGAACACTACA	2783
Db	701	TATCTGATGCTCAGCAGGTGGAGTGCAGTCCCGCCCTAGACTTCCCTCTGGAACACTACA	760
Qy	2784	GGCAACAGGGGAAAAGAGAGATGG - AGGAGCTACAGGCATACACCGGAGGCTGCTGC	2842
Db	761	GGCAACAGGGGAAAAGAGAGATGGAAGAGCTACAGGCATACAAACGGAAGCTGCTGC	820
Qy	2843	ATAACATTCTGCCAAGGACGTGGCGGCCACTTCCCTGG - -CCCGGGAGCGCGCAATGA	2900
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Qy	2901	TGAACCTCTACTATCAGTC - - -GTGTGAGTGTGTGCTGTTATGTTTGCTCCATT - GCCA	2956
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Qy	2957	ACTTCTCTGAGTCTAT - GTGGAGCTGGAGGCAACAATAGGGTG	3001
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RESULT 3	
BF792125	
LOCUS	775 bp mRNA linear EST 12-JAN-2001
DEFINITION	G02252571F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4345144 5',
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ACCESSION	BF792125
VERSION	BF792125.1 GI:12097179
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 775)
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

```

Email: c9apbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9964 row: m column: 17
High quality sequence stop: 711.
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NotI; Site_2: SalI; Cloned unidirectionally; oligo-dr
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full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
184 a 199 c 239 g 153 t
BASE COUNT

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QY 2743	GTGGAATCGACTCGCCGCTAAACTTCCTCTGGAACCTACAGGCAACAGGGGAAAAAGAG	2802			
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QY 2803	GAGATGGAGGAGCTACAGGCAATACAACGGGAGGCTGTGCATACATTCTGCCCAAGGAC	2862			
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QY 2923	GAGTGTGTGGCTGTATTGTTTTCCTCCATTGCCAACTTCCTGTAGTTCTTATGTGGAGCTG	2982			
DB 191	GAGTGTGTGGCTGTATTGTTTTCCTCCATTGCCAACTTCCTGTAGTTCTTATGTGGAGCTG	250			
QY 2983	GAGGCAACAATGAGGGTGCAGTGCTCGGGCTGTCAACGAGATCATCGCTGACATTT	3042			
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QY 3103	ACCTACATGGCTGCTCAGGGCTGAACGCCAGCACCTACGATCAGTTGGGCGCTCCAC	3162			
DB 371	ACCTACATGGCTGCTCAGGGCTGAACGCCAGCACCTACGATCAGTTGGGCGCTCCAC	430			
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QY 3223	CACCTCTTCAACAATTTCCAGATGAAGATTGGGCTGAACATGGGCCACAGTCGTGGCAGGT	3282			
DB 491	CACCTCTTCAACAATTTCCAGATGAAGATTGGGCTGAACATGGGCCACAGTCGTGGCAGGT	550			
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DEFINITION BE840188
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VERSION BE840188.1 GI:10272566
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 676)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-QV0-FN0181-100
800-335-d08&t3=2000-08-10&t4=1)
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application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT 125 a 203 c 193 g 155 t
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Matches 609; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
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RESULT 5
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LOCUS BI691747
DEFINITION 603307455F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5343565 5',
mRNA sequence.
ACCESSION BI691747
VERSION BI691747.1 GI:15654376
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 1225)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11872 row: n column: 14
High quality sequence start: 2
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BG297229 1043 bp mRNA linear EST 21-FEB-2001  
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 BG297229 BG297229.1 GI:13060672  
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 house mouse.  
 Mus musculus

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
NIH-MGC <http://mgc.ncl.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.

**Tissue Procurement:** The Cepko Laboratory  
Email: [cygabus-remail@mit.edu](mailto:cygabus-remail@mit.edu)

cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be found through the TMA CF Consortium/UMI at:

http://image.llnl.gov  
plate: LLAM10382 row: 1 column: 10

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Location/Qualifiers

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Average insert size 3.3 kb. Library enriched for full-length clones and constructed by life technologies.

Note: this is a NIH\_MGC Library.

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RESULT 7
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DEFINITION mRNA sequence.
ACCESSION BI685206
VERSION BI685206.1 GI:15647834
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL 1 (bases 1 to 743)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1879 row: j column: 04
High quality sequence stop: 741.
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Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT 149 a 208 c 213 g 173 t
ORIGIN

Query Match 15.8%; Score 559.8; DB 13; Length 743;
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RESULT 8
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LOCUS 602381888F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:449589 5',
DEFINITION mRNA sequence.
ACCESSION BI687169
VERSION BI687169.1 GI:13040741
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL 1 (bases 1 to 796)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
```

Email: c9apbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Plate: LLAM10363 row: p column: 22  
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BASE COUNT 207 a 193 c 245 g 151 t  
ORIGIN  
Query Match 15.5%; Score 549.6; DB 12; Length 796;  
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Matches 613; Conservative 0; Mismatches 14; Indels 5; Gaps 5;  
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DEFINITION  
ACCESSION  
VERSION  
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Homo sapiens  
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1 (bases 1 to 581)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR3&td=MR3-HF0999-070201-003-h04&td3=2001-02-07&td4=1)  
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High quality sequence stop: 581.  
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/dev\_stage="Adult"  
/note="Organ: head\_neck; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
BASE COUNT 118 a 157 c 199 g 106 t 1 others  
ORIGIN  
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Best Local Similarity 98.2%; Pred. No. 2.6e-112;  
Matches 556; Conservative 0; Mismatches 9; Indels 1; Gaps 1;  
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QY 1316 GGCCCGACCATGCCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGCCATCTCGC 1375  
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Db 256 CCTGCGCCAAACACATGGAAGCAGGAGCCGGGCTGGCGCATCCACATCACTCTGGGCGAA 315

QY 1556 CACTGACGTACCTGAACGGGGACTACGAAGTGGAGCCAGCCGCTGTGTGCGAAGCCGAACG 1615

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LOCUS B1255147 790 bp mRNA linear EST 17-JUL-2001

DEFINITION 602977410Fl NIH\_MGC\_12 Homo sapiens cDNA clone IMAGE:5122130 5', mRNA sequence.

ACCESSION B1255147

VERSION B1255147.1 GI:14808265

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 790)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-re@mail.nih.gov](mailto:cgapbs-re@mail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Arrayed by: Life Technologies, Inc.  
cDNA Library Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLAM11298 row: d column: 03  
High quality sequence stop: 634.  
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Db 69 CTTGGCGT-C-ATGGCTTGGTCTTCCAATGAGACCTTTTGATGGGCTGACCTGTCAGCT 126

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Db 127 GCAGGAGGGTGGCCCTCAAATATATATGACCCCTGTGATTTCTGCTGGTGTGGCTGGCG 185

QY 2722 CTGTATCTCATGCTCAGCAGGTGGAATCGACTGCCCGCTAAACTTCCTCTGGAACAATA 2781

Db 186 CTGTATCTCATGCTCAGCAGGTGGAATCGACTGCCCGCTTAGACTTCCTCTGGAACAATA 245

QY 2782 CAGGCAACAGGGGAAAAGAGGAGATGGAGAGCTACAGGCATACAAACGGAGGCTGCTG 2841

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Db 306 CATAACATTCTGCCCAAGGACGTGGCGG-CCACTTCTGGCCCGGAGCGCGCAATGAT 364

QY 2902 GAACTCTACTATCATGCTGTGTGAGTGTGGCTGTATTTGCCCTCCATTGCGGTTGTC 2960

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QY 2961 CTCTGAGTTCTATGTGGAGCTGGAGCAACAATGAGGCTGCCGAGTGCCTGGCGTCT 3020

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Db 545 GAACAGATCAAGACGATTTGGTAGCCTTACATGGCTGCTCAGGCTTGAACGCCAGCA 604

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Db 785 TGACAT 790

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LOCUS BQ231940

DEFINITION BQ231940 905 bp mRNA linear EST 02-MAY-2002

5', mRNA sequence.

ACCESSION BQ231940

VERSION BQ231940.1 GI:20413340

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 905)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

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DEFINITION	UI-M-CGPp-beo-d-02-0-UI 5', mRNA sequence.				

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LOCUS
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No si sequence available.
This clone (DKFZp761N2323) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
BASE COUNT 114 a 129 c 142 g 102 t
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Db 61 GAGGTGTCGAGTGCCTGCGGTCTCAACGAGATCATCGCTGACTTTGATGAGATTATC 120
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QY 3295 CGGAAGCCACATGATGACATCTGGGGGAACACAGTGAATGCTCTAGTCTGATGACAGC 3354
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Db 361 CGGAAGCCACATGATGACATCTGGGGGAACACAGTGAATGCTCTAGTCTGATGACAGC 420
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QY 3355 ACGGGGGTCCCGACCGCAATCCAGCTGACACCGACCTGTACCGAGTTCTAGCTGCCAAG 3414
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Db 421 ACGGGGGTCCCGACCGCAATCCAGCTGACACCGACCTGTACCGAGTTCTAGCTGCCAAG 480
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QY 3415 GGCTACC 3421
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Db 481 GGCTACC 487
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RESULT 14
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VERSION
KEYWORDS
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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
WashU-HHMI Mouse EST Project
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LiNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:407635
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 417.
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/db_xref="taxon:10090"
FEATURES
source
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Db 541 GGTGAACGCAATCGGTACCTCAAGG 565

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Job time : 3447.62 secs